

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17 ; Search time 6.89987 Seconds  
(without alignments)  
368.069 Million cell updates/sec

Title: US-09-661-992B-106

Perfect score: 82  
Sequence: 1 FRWRGMTALKVSSCD 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	82	100.0	16	AA20445
2	82	100.0	23	AA279422
3	82	100.0	368	AA273020
4	82	100.0	720	AA274088
5	82	100.0	729	AA274089
6	82	100.0	740	AA276959
7	82	100.0	740	AA276961
8	82	100.0	740	AA276962
9	82	100.0	740	AA273021

10	82	100.0	740	AA274090	Factor VIII heavy
11	82	100.0	740	AA276982	Human factor VIII
12	82	100.0	1383	AA273227	Procoagulant-activ
13	82	100.0	1383	AA273228	Procoagulant-activ
14	82	100.0	1383	AA273229	Procoagulant-activ
15	82	100.0	1424	AA280268	Modified factor VI
16	82	100.0	1424	AA281169	Sequence of 740 Ar
17	82	100.0	1424	AA284842	Mutant mature huma
18	82	100.0	1424	AA284842	Human mature B-dom
19	82	100.0	1425	AA280267	Modified factor VI
20	82	100.0	1438	AA280162	B-domain deleted f
21	82	100.0	1445	AA282971	Factor VIII:SO, U
22	82	100.0	1445	AA282940	Factor VIII:SO, U
23	82	100.0	1447	AA282941	Factor VIII:SO, U
24	82	100.0	1457	AA282942	Factor VIII:SO, U
25	82	100.0	1457	AA282943	Factor VIII:SO, U
26	82	100.0	1457	AA282944	Factor VIII:SO, U
27	82	100.0	1457	AA282945	Factor VIII:SO, U
28	82	100.0	1459	AA282946	Factor VIII:SO, U
29	82	100.0	1459	AA282947	Factor VIII:SO, U
30	82	100.0	1471	AA282948	Factor VIII:SO, U
31	82	100.0	1471	AA282949	Factor VIII:SO, U
32	82	100.0	1516	AA282950	Factor VIII:SO, U
33	82	100.0	2098	AA282951	Factor VIII:SO, U
34	82	100.0	2332	AA282952	Factor VIII:SO, U
35	82	100.0	2332	AA282953	Factor VIII:SO, U
36	82	100.0	2332	AA282954	Factor VIII:SO, U
37	82	100.0	2332	AA282955	Factor VIII:SO, U
38	82	100.0	2332	AA282956	Factor VIII:SO, U
39	82	100.0	2332	AA282957	Factor VIII:SO, U
40	82	100.0	2332	AA282958	Factor VIII:SO, U
41	82	100.0	2332	AA282959	Factor VIII:SO, U
42	82	100.0	2332	AA282960	Factor VIII:SO, U
43	82	100.0	2332	AA282961	Factor VIII:SO, U
44	82	100.0	2332	AA282962	Factor VIII:SO, U
45	82	100.0	2332	AA282963	Factor VIII:SO, U

#### ALIGNMENTS

RESULT 1  
AA20445  
ID AA20445 standard; Peptide; 16 AA.  
XX  
AC AA20445;  
XX  
DT 21-JUN-2001 (first entry)  
XX  
DE Anti-FIX/FIXa antibody CDR3.  
XX  
KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;  
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;  
KW complementarity determining region; CDR.  
XX  
OS Mus musculus.  
XX  
PN WO200119992-A2.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-BP08936.  
XX  
PR 14-SEP-1999; 99AT-0001576.  
XX  
PA (BAXT) BAXTER AG.  
XX  
PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;  
XX WPI; 2001-290358/30.  
XX  
PT New factor IX/factor IXa antibodies and their derivatives useful for

PT increasing amidolytic activity of factor IXa, and for treating blood  
 XX coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 PS  
 XX Claim 7; Page 74; 138pp; English.

CC The present sequence is that of complementarity determining  
 CC region 3 (CDR3) of an antibody having anti-factor IX (FIX) or  
 CC anti-activated factor IX (FIXa) activity. Such antibodies  
 CC and their derivatives (including those that comprise the present  
 CC CDR3 peptide) have factor VIIa (FVIIa) cofactor activity or FIXa  
 CC activating activity. Administration of the antibodies or their  
 CC derivatives leads to an increase in the procoagulant activity of  
 CC FIXa, even in the presence of FVIIa inhibitors. This allows for  
 CC rapid blood coagulation even in the absence of FVIII or FVIIa, and  
 CC in the case of FVIII inhibitor patients. The antibodies or their  
 CC derivatives are used in a claimed pharmaceutical composition for  
 CC treating patients with blood coagulation disorders, especially  
 CC haemophilia A and haemorrhagic diathesis.

XX Sequence 16 AA;

Query Match 100.0%; Score 82; DB 22; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGMTALKVSSCD 16  
 |||||  
 DB 1 FRNRGMTALKVSSCD 16

#### RESULT 2

AAAG79422  
 ID AAG79422 standard; protein; 294 AA.

XX AAG79422;

XX 25-OCT-2002 (first entry)

XX Human factor VIII region 2/3.

XX Factor VIII; factor IX; coagulation; blood; cardiovascular disorder;  
 KM thrombosis; atherosclerosis; restenosis.

XX Homo sapiens.

XX WO200259268-A2.

XX 01-AUG-2002.

XX 23-JAN-2002; 2002WO-US01724.

XX 23-JAN-2001; 2001US-263431P.

XX (UTSL-) UNIV SAINT LOUIS.

XX Baja PS, Fay PJ;

XX WPI; 2002-599771/64.

PT New polypeptide inhibits interaction of blood coagulation factor VIIa  
 FT with factor IXa precluding activation of factor X, useful for  
 PT preventing or treating coagulation disorders, such as thrombosis,  
 PT atherosclerosis and restenosis -

XX Claim 2; Fig 7A; 61pp; English.

CC The sequences given in AAG79422-23 represent regions 2 and 3 of human  
 CC factors VIII and IX. Region 2 comprises the interaction between N346  
 CC of factor IXa and E455 and K570 of factor VIIa, and the interaction  
 CC between R403 of factor IXa and E633 of factor VIIa. Region 3 comprises  
 CC the interaction between K293 of factor IXa and D712 of factor VIIa, and  
 CC the interaction between E410 of factor IXa and K713 of factor VIIa.  
 CC Fragments of these polypeptides inhibit the interaction of blood

CC coagulation factor VIIa with blood coagulation factor IXa. They also  
 CC inhibit the activation of blood coagulation factor X, or inhibit blood  
 CC coagulation. These peptide fragments are useful in preventing and/or  
 CC treating coagulation disorders, in particular cardiovascular disorders  
 CC such as thrombosis, atherosclerosis and restenosis.

XX Sequence 294 AA;

Query Match 100.0%; Score 82; DB 23; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGMTALKVSSCD 16  
 |||||  
 DB 268 FRNRGMTALKVSSCD 283

#### RESULT 3

AAAR73020  
 ID AAR73020 standard; peptide; 368 AA.

XX AAR73020;

XX 25-MAR-2003 (updated)

XX 21-NOV-1995 (first entry)

XX Human Factor-VIII fragment.

XX Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.

XX Homo sapiens.

XX WO9513301-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-DK0424.

XX 12-NOV-1993; 93DK-0001281.

XX (NOVO) NOVO-NORDISK AS.

XX Persson E;

XX WPI; 1995-194038/25.

PT Crosslinked Factor VIII polypeptide which is stable - is prep'd. using  
 FT bis(sulphosuccinimidy)l suberate or disuccinimyl suberate in the  
 PT presence of polysorbate 80 to produce a coagulant with long lasting  
 PT activity

XX Disclosure; Page 19; 36pp; English.

CC This is a fragment corresponding to internal Aas 373-740 of human  
 CC Factor-VIII which may be crosslinked resulting in  
 CC increased stability and retention of high activity over extended  
 CC periods of time after activation by thrombin. The polypeptide is  
 CC used to prevent or treat diseases caused by the absence or deficiency  
 CC of Factor-VIII in a subject such as haemophilia.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 368 AA;

Query Match 100.0%; Score 82; DB 16; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGMTALKVSSCD 16  
 |||||  
 DB 325 FRNRGMTALKVSSCD 340

#### RESULT 4

AA74088  
 ID AAR74088 standard; protein; 720 AA.  
 XX  
 AC AAR74088;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 04-NOV-1995 (first entry)  
 XX  
 DE Factor-VIII heavy chain N-terminal fragment.  
 XX  
 KM human; Factor VIII; heavy chain; N-terminal fragment;  
 KM thrombin cleavage; blood-clotting.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W09513300-A1.  
 PN  
 PD 18-MAY-1995.  
 PD  
 PF 10-NOV-1994; 94WO-DK00423.  
 PF  
 PR 12-NOV-1993; 93DK-0001280.  
 PR  
 PA (NOVO ) NOVO-NORDISK AS.  
 PA  
 PI Ezban Rasmussen M, Kjalke M;  
 PI  
 DR WPI; 1995-194037/25.  
 DR  
 XX  
 PT Factor VIII polypeptide(s) comprising a heavy chain shorter than native  
 PT A1-A2 domain - are easier to produce recombinantly and retain coagulant  
 PT activity, may be used to treat patients who have developed antibodies to  
 PT C-terminal epitope(s) of Factor VIII  
 XX  
 PS Claim 3; Page 24-26; 51pp; English.  
 PS  
 CC The sequence represents N-terminal residues 1-720 of a human Factor-  
 CC VIII heavy chain. The sequence is shorter than the A1-A2 domain,  
 CC and is produced by treating a polypeptide containing the full A1-A2  
 CC domain of full-length Factor-VIII with a protease, e.g. thrombin.  
 CC The fragment has the same specific activity as full-length  
 CC Factor-VIII in a chromogenic assay, but activity is a factor of two  
 CC lower in a clotting assay, and the fragment is activated by thrombin  
 CC at a slower rate and to a lower level than fragments 1-740 (AAR74090).  
 CC 1-729 (AAR74089) and plasma Factor-VIII. The fragment may be produced  
 CC recombinantly to reduce production costs and improve safety, and  
 CC production levels and stability are higher than for the full-length  
 CC form. The fragment may be used to treat patients who have developed  
 CC antibodies against epitopes in the C-terminal part of the heavy chain.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 720 AA;  
 SQ  
 Query Match 100.0%; Score 82; DB 16; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FRNRGNTALKVSSCD 16  
 DB 697 FRNRGNTALKVSSCD 712

KM human; Factor VIII; heavy chain; N-terminal fragment;  
 KM thrombin cleavage; blood-clotting.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W09513300-A1.  
 PN  
 PD 18-MAY-1995.  
 PD  
 PF 10-NOV-1994; 94WO-DK00423.  
 PF  
 PR 12-NOV-1993; 93DK-0001280.  
 PR  
 PA (NOVO ) NOVO-NORDISK AS.  
 PA  
 PI Ezban Rasmussen M, Kjalke M;  
 PI  
 DR WPI; 1995-194037/25.  
 DR  
 XX  
 PT Factor VIII polypeptide(s) comprising a heavy chain shorter than native  
 PT A1-A2 domain - are easier to produce recombinantly and retain coagulant  
 PT activity, may be used to treat patients who have developed antibodies to  
 PT C-terminal epitope(s) of Factor VIII  
 XX  
 PS Claim 2; Page 27-29; 51pp; English.  
 PS  
 CC The sequence represents N-terminal residues 1-729 of a human Factor-  
 CC VIII heavy chain. The sequence is shorter than the A1-A2 domain,  
 CC and is produced by treating a polypeptide containing the full A1-A2  
 CC domain of full-length Factor-VIII with a protease, e.g. thrombin.  
 CC The fragment has the same coagulant specific activity as full-length  
 CC Factor-VIII in a chromogenic assay, and is activated by thrombin at  
 CC a similar rate. The fragment may be produced recombinantly to reduce  
 CC production costs and improve safety, and production levels and  
 CC stability are higher than for the full-length form. The fragment may  
 CC be used to treat patients who have developed antibodies against  
 CC epitopes in the C-terminal part of the heavy chain.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 729 AA;  
 SQ  
 Query Match 100.0%; Score 82; DB 16; Length 729;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FRNRGNTALKVSSCD 16  
 DB 697 FRNRGNTALKVSSCD 712

RESULT 6  
 ID AAR76959 standard; protein; 740 AA.  
 XX  
 AC AAR76959;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 09-MAR-1996 (first entry)  
 XX  
 DE Human Factor-VIII/Factor-VIIIa derivative.  
 XX  
 KM Factor-VIII; therapeutic; blood-clotting.  
 KM  
 OS Homo sapiens.  
 OS  
 PN Key Location/Qualifiers  
 PN  
 FT Misc-difference 403  
 FT /label= Asp absent or Asn, Ser, Thr, Ala  
 FT Misc-difference 404  
 FT /label= Asp absent or Asn, Ser, Thr, Ala  
 FT Misc-difference 433  
 FT /label= Asp absent or Asn, Ser, Thr, Ala  
 FT Misc-difference 482

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FT  /label= Asp absent or Asn, Ser, Thr, Ala
FT  Misc-difference 500
FT  /label= Asp absent or Asn, Ser, Thr, Ala
FT  Misc-difference 434
FT  /label= Glu absent or Gln, Ser, Thr, Ala
FT  Misc-difference 440
FT  /label= Glu absent or Gln, Ser, Thr, Ala
XX  W09518829-A1.
XX  13-JUL-1995.
XX  06-JAN-1995; 95WO-DK00010.
XX  07-JAN-1994; 94DK-0000030.
XX  (NOVO ) NOVO-NORDISK AS.
XX  Ezban Rasmussen M, Nicolaisen EM, Persson E;
XX  WPI; 1995-255041/33.
XX  Novel factor VIII derivative used to treat haemophilia - and
XX  comprises a functional A2 domain containing a mutation at one or
XX  more Cys residues.
XX  Disclosure; Page 11-14; 24pp; English.
XX  The new Factor-VIII/Factor-VIIa derivative comprises a functional
XX  A2 domain in which amino acid residues, as indicated in the
XX  Features, are deleted or substituted by another amino acid so as to
XX  increase the overall positive charge. Asp-403, Asp-404, Asp-433,
XX  Asp-482 and Asp-500 are preferably substituted by Asn; Glu-434 and
XX  Glu-440 are preferably substituted by Gln. The new derivative has
XX  the same activity as the wild-type Factor-VIII but with improved
XX  stability (the activity is maintained for a longer period compared
XX  to the rapid decline of the activity of wt Factor-VIII). The new
XX  derivative can be used in a composition for treating diseases caused
XX  by an absence or deficiency of Factor-VIII, especially haemophilia.
XX  (Updated on 25-MAR-2003 to correct DR field.)
XX  Sequence 740 AA;
SQ
Query Match 100.0%; Score 82; DB 16; Length 740;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRNRGWTALTKVSSCD 16
DB 697 FRNRGWTALTKVSSCD 712
RESULT 7
AAR76961
ID AAR76961 standard; protein; 740 AA.
XX
XX AAR76961;
AC
XX 09-MAR-1996 (first entry)
XX
XX Human Factor-VIII derivative.
XX
XX Factor-VIII; therapeutic; blood-clotting.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 692
XX /label= absent or Ala, Thr, Ser, Gly or Asp
XX Misc-difference 720
XX /label= absent or Gln, Ser, Thr, Val or Ala
XX Misc-difference 729
XX /label= absent or Val, Ala or Ile

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XX  W09518827-A1.
XX  13-JUL-1995.
XX  06-JAN-1995; 95WO-DK00008.
XX  07-JAN-1994; 94DK-0000032.
XX  (NOVO ) NOVO-NORDISK AS.
XX  Ezban Rasmussen M, Nicolaisen EM, Persson E;
XX  WPI; 1995-255039/33.
XX  Novel factor VIII derivative used to treat haemophilia - and
XX  comprises a functional A2 domain containing a mutation at one or
XX  more Cys residues.
XX  Disclosure; Page 14-17; 30pp; English.
XX  The new Factor-VIII derivative comprises a functional A2 domain in
XX  which Cys-692 is deleted or replaced with another amino acid
XX  residue, preferably Ser (see AAR76962). Alternatively, Glu-720 and/or
XX  Tyr-729 are deleted or substituted with various amino acids (as in
XX  the Features). The new derivative has the same activity as the wild-
XX  type Factor-VIII but with improved stability (the activity is
XX  maintained for a longer period compared to the rapid decline of the
XX  activity of wt Factor-VIII). The new derivative can be used in a
XX  composition for treating diseases caused by an absence or deficiency
XX  of Factor-VIII, especially haemophilia.
XX  Sequence 740 AA;
SQ
Query Match 100.0%; Score 82; DB 16; Length 740;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRNRGWTALTKVSSCD 16
DB 697 FRNRGWTALTKVSSCD 712
RESULT 8
AAR76962
ID AAR76962 standard; protein; 740 AA.
XX
XX AAR76962;
AC
XX 09-MAR-1996 (first entry)
XX
XX Human Factor-VIII derivative.
XX
XX Factor-VIII; therapeutic; blood-clotting.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 692
XX /label= Cys substituted by Ser
XX Misc-difference 720
XX /label= absent or Gln, Ser, Thr, Val or Ala
XX Misc-difference 729
XX /label= absent or Val, Ala or Ile
XX  W09518827-A1.
XX  13-JUL-1995.
XX  06-JAN-1995; 95WO-DK00008.
XX  07-JAN-1994; 94DK-0000032.

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PA (NOVO ) NOVO-NORDISK AS.  
XX  
XX Ezbán Rasmussen M, Nicolaisen EM, Persson E;  
XX WPI; 1995-255039/33.  
XX  
XX Novel factor VIII derivative used to treat haemophilia - and  
PT comprises a functional A2 domain containing a mutation at one or  
PT more Cys residues.  
XX  
XX Disclosure; Page 18-20; 30pp; English.  
XX  
XX The new Factor-VIII derivative comprises a functional A2 domain in  
CC which Cys-692 is replaced with Ser. For other (less preferred)  
CC substitutions at this site, see AAR76961. Alternatively, Glu-720 and/or  
CC Tyr-729 are deleted or substituted with various amino acids (as in  
CC the features). The new derivative has the same activity as the wild-  
CC type Factor-VIII but with improved stability (the activity is  
CC maintained for a longer period compared to the rapid decline of the  
CC activity of wt Factor-VIII). The new derivative can be used in a  
CC composition for treating diseases caused by an absence or deficiency  
CC of Factor-VIII, especially haemophilia.  
XX  
XX Sequence 740 AA;  
SQ  
Query Match 100.0%; Score 82; DB 16; Length 740;  
Best Local Similarity 100.0%; Pred. No. 8.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRNRGWTALLKTVSSCD 16  
DB 697 FRNRGWTALLKTVSSCD 712  
RESULT 9  
AAR73021  
ID AAR73021 standard; peptide; 740 AA.  
XX  
XX AAR73021;  
AC  
XX  
XX 25-MAR-2003 (updated)  
DT 21-NOV-1995 (first entry)  
XX  
XX Human Factor-VIII N-terminal fragment.  
DE  
XX  
XX Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9513301-A1.  
PN  
XX  
XX 18-MAY-1995.  
PD  
XX  
XX 13-NOV-1994; 94WO-DK00424.  
PF  
XX  
XX 12-NOV-1993; 93DK-0001281.  
PR  
XX  
XX (NOVO ) NOVO-NORDISK AS.  
PA  
XX  
XX Persson E;  
PI  
XX  
XX WPI; 1995-194038/25.  
DR  
XX  
XX Crosslinked Factor VIII polypeptide which is stable - is prep'd, using  
PT bis(sulphosuccinimidy1) suberate or disuccinimidy1 suberate in the  
PT presence of polysorbate 80 to produce a coagulant with long lasting  
PT activity  
XX  
XX Disclosure; Page 21; 36pp; English.  
PS  
XX  
XX This is the N-terminal fragment of human Factor-VIII which may be  
CC crosslinked resulting in increased stability and retention of high  
CC activity over extended periods of time after activation by thrombin.

CC The polypeptide is used to prevent or treat diseases caused by the  
CC absence or deficiency of Factor-VIII in a subject such as  
CC haemophilia.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 740 AA;  
SQ  
Query Match 100.0%; Score 82; DB 16; Length 740;  
Best Local Similarity 100.0%; Pred. No. 8.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRNRGWTALLKTVSSCD 16  
DB 697 FRNRGWTALLKTVSSCD 712  
RESULT 10  
AAR74090  
ID AAR74090 standard; protein; 740 AA.  
XX  
XX AAR74090;  
AC  
XX  
XX 25-MAR-2003 (updated)  
DT 04-NOV-1995 (first entry)  
XX  
XX Factor-VIII heavy chain N-terminal fragment.  
DE  
XX  
XX human; Factor VIII; heavy chain; N-terminal fragment;  
KM thrombin cleavage; blood-clotting.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9513300-A1.  
PN  
XX  
XX 18-MAY-1995.  
PD  
XX  
XX 10-NOV-1994; 94WO-DK00423.  
PF  
XX  
XX 12-NOV-1993; 93DK-0001280.  
PR  
XX  
XX (NOVO ) NOVO-NORDISK AS.  
PA  
XX  
XX Ezbán Rasmussen M, Kjalke M;  
PI  
XX  
XX WPI; 1995-194037/25.  
DR  
XX  
XX Factor VIII polypeptide(s) comprising a heavy chain shorter than native  
PT A1-A2 domain - are easier to produce recombinantly and retain coagulant  
PT activity, may be used to treat patients who have developed antibodies to  
PT C-terminal epitope(s) of Factor VIII  
XX  
XX Disclosure; Page 30-32; 51pp; English.  
PS  
XX  
XX The sequence represents N-terminal residues 1-740 of a human Factor-  
CC VIII heavy chain. The sequence contains entire A1 and A2 domains,  
CC and truncated forms (1-720 in (AAR74088) and 1-729 in (AAR74090))  
CC may be produced by treatment with a protease, e.g. thrombin. The  
CC C-terminally truncated fragments have the same coagulant specific  
CC activity as full-length Factor-VIII, and may be produced  
CC recombinantly to reduce production costs and improve safety, giving  
CC higher production levels and stability than for the full-length form.  
CC The fragments may be used to treat patients who have developed  
CC antibodies against epitopes in the C-terminal part of the heavy chain.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 740 AA;  
SQ  
Query Match 100.0%; Score 82; DB 16; Length 740;  
Best Local Similarity 100.0%; Pred. No. 8.7e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRNRGWTALLKTVSSCD 16

Db 697 FRNRGWTALKVSSCD 712

## RESULT 11

ID AAR76982 standard; protein; 740 AA.

XX AAR76982;

DT 21-FEB-1996 (first entry)

DE Human factor VIII A2-domain derivative.

KM Factor VIII; human; haemophilia; thrombin; protein C; plasmin;  
KW serine protease; recombination; therapy; deficiency.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 720 /label= Gln, Ser, Thr, Val, Ala

FT Misc-difference 729 /label= Val, Ala, Ile

PN MO9518828-A1.

PD 13-JUL-1995.

PF 06-JAN-1995; 95WO-DK00009.

PR 07-JAN-1994; 94DK-0000031.

XX (NOVO ) NOVO-NORDISK AS.

PI Ezban Rasmussen M, Nicolaissen EM, Persson E;

DR WPI; 1995-255040/33.

PT Novel factor VIII derivative with resistance to enzymatic cleavage -  
FT and comprises a functional A2 domain where Glu720 and/or Tyr729 is  
XX deleted/substituted.

PS Claim 1; Page 11-14; 26pp; English.

CC This sequence represents the A2 domain of a human factor VIII derivative.  
CC Factor VIII is a large glycoprotein which is present in plasma at low  
CC concentrations. Factor VIII is an essential part of the clotting  
CC reaction in response to a wound. Factor VIII is susceptible to cleavage  
CC by thrombin, activated protein C, plasmin, and other serine proteases.  
CC Full length factor VIII consists of three repeats of the A-domain, a  
CC B-domain and 2 repeats of the C-domain. Active factor VIII has the A1  
CC domain cleaved off. Factor VIII is too unstable for use in recombinant  
CC techniques. Factor VIII containing this sequence has improved stability  
CC and shows resistance against enzymatic activity present in mammalian  
CC cells. This means that factor VIII containing this sequence can be used  
CC in recombinant techniques. A factor VIII derivative can be used for  
CC treating diseases caused by an absence or deficiency of factor VIII (in  
CC the same way as normal factor VIII) e.g. haemophilia. The advantage with  
CC using a recombinant factor VIII also includes no need for lots of donors  
CC in order to get a sufficient amount. Also, there is no long purification  
CC process, and there is no risk of transmission of blood-borne diseases  
CC such as HIV.

SQ Sequence 740 AA;

Query Match 100.0%; Score 82; DB 16; Length 740;

Best Local Similarity 100.0%; Freq. No. 8.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALKVSSCD 16

DB 697 FRNRGWTALKVSSCD 712

## RESULT 12

ID AAM33227 standard; protein; 1383 AA.

XX AAM33227;

DT 30-APR-1998 (first entry)

DE Procoagulant-active human factor VIII:C (FVIII) mutant protein.

KM Pro-coagulant active factor VIII; FVIII; haemophilia A;  
KW recombinant secretion; pro-coagulant activity; resistance;  
KM activated protein C cleavage; APC; B domain; A2 domain; A3 domain;  
KW von Willebrand factor binding site; binding affinity;  
KM FVIII replacement therapy.

XX Synthetic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..346 /note= "factor VIIIA heavy chain"

FT Region 741..1383 /note= "factor VIIIA light chain"

FT Domain 1..329 /note= "A1 domain"

FT Domain 1..179 /note= "plastocyanin-like domain 1"

FT Domain 187..329 /note= "plastocyanin-like domain 2"

FT Domain 380..711 /note= "A2 domain"

FT Misc\_feature 711..746 /note= "a spacer of the sequence  
SFSQNRHPSTROKQENATITPEDIKTDPMF  
AARTPKIQNVSSDLML is inserted  
between domains A2 and A3"

FT Domain 380..554 /note= "plastocyanin-like domain 3"

FT Domain 564..711 /note= "plastocyanin-like domain 4"

FT Domain 746..1073 /note= "A3 domain"

FT Domain 1073..1221 /note= "C1 domain"

FT Domain 1226..1378 /note= "C2 domain"

FT Cleavage-site 372..373 /note= "by thrombin"

FT Disulfide-bond 153..179 /note= "probable"

FT Disulfide-bond 528..554 /note= "probable"

FT Misc-difference 740 /label= R740A

FT /note= "wild type Arg replaced with Ala"

PN MO9740145-A1.

PD 30-OCT-1997.

PF 24-APR-1997; 97WO-US06563.

PR 15-MAY-1996; 96US-0017785.

PR 24-APR-1996; 96US-0016117.

PA (UNMI ) UNIV MICHIGAN.

PI Amano K, Kaufman RJ, Pipe SM;

DR WPI; 1997-535830/49.

PT Modified human pro-coagulant active factor VIII - can be  
 PT administered to haemophiliacs, i.e. factor VIII replacement therapy  
 XX  
 PS Claim 20, Page -; 57pp; English.

CC The present sequence represents a novel pro-coagulant active factor  
 CC VIII (FVIII) mutant protein, comprising a deletion of the B domain and  
 CC von Willebrand factor binding site, a mutation at Arg740 and an addition  
 CC of an amino acid sequence spacer between the A2 and A3 domains. Factor  
 CC VIII, along with calcium and phospholipid, acts as a cofactor for factor  
 CC IXA, when it converts factor X to the activated form (factor XA). FVIII  
 CC is the coagulation factor deficient in the X-chromosome-linked bleeding  
 CC disorder haemophilia A. Several other mutant FVIII proteins have also  
 CC been created (see AMW33222-29). The FVIII mutant F309S (AMW33225) is  
 CC capable of recombinant secretion at higher levels than typically obtained  
 CC with wild type FVIII and retains pro-coagulant activity. The FVIII  
 CC mutant R336I (AMW33222) and R562K (AMW33223) are resistant to activated  
 CC protein C (APC) cleavage. The present FVIII mutant can form a more  
 CC stable configuration, and have an approximate 5-fold increase in  
 CC specific activity compared to purified wild type FVIII, while increasing  
 CC their binding affinity to von Willebrand factor improves their  
 CC stability. The FVIII proteins can be administered to haemophiliacs, i.e.  
 CC FVIII replacement therapy, while the nucleic acid molecule can be used  
 CC for gene therapy.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using sequences from the given references.

CC Sequence 1383 AA;

Query Match 100.0%; Score 82; DB 18; Length 1383;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FNRGWTALKVSSCD 16  
 DB 697 FNRGWTALKVSSCD 712

RESULT 13  
 ID AMW33228 standard; protein, 1383 AA.

AC AMW33228;  
 DT 30-APR-1998 (first entry)

DE Procoagulant-active human factor VIII:C (FVIII) mutant protein.

XX Pro-coagulant active factor VIII; FVIII; haemophilia A;  
 KW recombinant secretion; pro-coagulant activity; resistance;  
 KW activated protein C cleavage; APC; B domain; A2 domain; A3 domain;  
 KW von Willebrand factor binding site; binding affinity;  
 KW FVIII replacement therapy.

OS Synthetic.  
 OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..346 Region "factor VIIIA heavy chain"

FT 741..1383 Region "factor VIIIA light chain"

FT 1..329 Domain "A1 domain"

FT 1..179 Domain "plastocyanin-like domain 1"

FT 187..329 Domain "plastocyanin-like domain 2"

FT 380..711 Domain "A2 domain"

FT 711..746 Misc\_feature "a spacer of the sequence  
 FT SPQNSRHPSTRQKQFPAITPNDIEKIDPMF

FT AHRTPMKIQNVSSSLML is inserted  
 FT between domains A2 and A3"

FT Domain 380..554  
 FT /note= "plastocyanin-like domain 3"

FT Domain 564..711  
 FT /note= "plastocyanin-like domain 4"

FT Domain 746..1073  
 FT /note= "A3 domain"

FT Domain 1073..1221  
 FT /note= "C1 domain"

FT Domain 1225..1378  
 FT /note= "C2 domain"

FT Cleavage-site 372..373  
 FT /note= "by thrombin"

FT Disulfide-bond 153..179  
 FT /note= "probable"

FT Disulfide-bond 528..554  
 FT /note= "probable"

FT Misc-difference 336  
 FT /label= R336I  
 FT /note= "wild type Arg replaced with Ile"

FT Misc-difference 562  
 FT /label= R562K  
 FT /note= "wild type Arg replaced with Lys"

FT Misc-difference 740  
 FT /label= R740A  
 FT /note= "wild type Arg replaced with Ala"

FT WO9740145-A1.

FT 30-OCT-1997.

FT 24-APR-1997; 97WO-US06563.

FT 15-MAY-1996; 96US-0017785.

FT 24-APR-1996; 96US-0016117.

FT (UNMI ) UNIV MICHIGAN.

FT Amano K, Kaufman RJ, Pipe SW;

FT WPI, 1997-535830/49.

PT Modified human pro-coagulant active factor VIII - can be  
 PT administered to haemophiliacs, i.e. factor VIII replacement therapy

PS Claim 18; Page -; 57pp; English.

CC The present sequence represents a novel pro-coagulant active factor  
 CC VIII (FVIII) mutant protein, comprising a deletion of the B domain and  
 CC von Willebrand factor binding site, mutations R336I, R562K and R740A and  
 CC an addition of an amino acid sequence spacer between the A2 and A3  
 CC domains. Factor VIII, along with calcium and phospholipid, acts as a  
 CC cofactor for factor IXA, when it converts factor X to the activated form  
 CC (factor XA). FVIII is the coagulation factor deficient in the  
 CC X-chromosome-linked bleeding disorder haemophilia A. Several other  
 CC mutant FVIII proteins have also been created (see AMW33222-29). The FVIII  
 CC mutant F309S (AMW33225) is capable of recombinant secretion at higher  
 CC levels than typically obtained with wild type FVIII and retains  
 CC pro-coagulant activity. The FVIII mutant R336I (AMW33222) and R562K  
 CC (AMW33223) are resistant to activated protein C (APC) cleavage. The FVIII  
 CC mutant comprising a deletion of the B domain and von Willebrand factor  
 CC binding site, a mutation at Arg740 and an addition of an amino acid  
 CC sequence spacer between the A2 and A3 domains can form a more stable  
 CC configuration, and have an approximate 5-fold increase in specific  
 CC activity compared to purified wild type FVIII, while increasing their  
 CC binding affinity to von Willebrand factor improves their stability.  
 CC The FVIII proteins can be administered to haemophiliacs, i.e. FVIII  
 CC replacement therapy, while the nucleic acid molecule can be used for  
 CC gene therapy.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using sequences from the given references.

SQ Sequence 1383 AA;  
 Query Match 100.0%; Score 82; DB 18; Length 1383;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FNRKGTALKVSSCD 16  
 |||||  
 DB 697 FNRKGTALKVSSCD 712

RESULT 14  
 AAW33229  
 ID AAW33229 standard; protein; 1383 AA.  
 AC AAW33229;  
 XX 30-APR-1998 (first entry)  
 DT  
 XX Procoagulant-active human factor VIII:C (FVIII) mutant protein.  
 XX  
 XX Pro-coagulant active factor VIII; FVIII; haemophilia A;  
 KM recombinant secretion; pro-coagulant activity; resistance;  
 KM activated protein C cleavage; APC; B domain; A2 domain; A3 domain;  
 KM von Willebrand factor binding site; binding affinity;  
 XX FVIII replacement therapy.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX Key  
 FT location/Qualifiers  
 FT 1..346 /note= "factor VIIIA heavy chain"  
 FT 741..1363 /note= "factor VIIIA light chain"  
 FT 1..329 /note= "A1 domain"  
 FT 1..179 /note= "plastocyanin-like domain 1"  
 FT 187..329 /note= "plastocyanin-like domain 2"  
 FT 380..711 /note= "A2 domain"  
 FT 711..746 /note= "A3 domain"  
 FT /note= "a spacer of the sequence  
 SFSQNSRHSSTQKQKQWATYIPENDIEKTDPMW  
 AHRTPMKIQNVSSSDILMLL is inserted  
 between domains A2 and A3"  
 FT 380..554  
 FT /note= "plastocyanin-like domain 3"  
 FT 564..711 /note= "plastocyanin-like domain 4"  
 FT 746..1073 /note= "A3 domain"  
 FT 1073..1221 /note= "C1 domain"  
 FT 1226..1378 /note= "C2 domain"  
 FT 372..373 /note= "by thrombin"  
 FT 153..179 /note= "probable"  
 FT 528..554 /note= "probable"  
 FT 309 /label= "F309S  
 /note= "wild type Phe replaced with Ser"  
 FT 740 /label= "R740A  
 /note= "wild type Arg replaced with Ala"  
 XX Misc-difference  
 XX WO9740145-A1.

PD 30-OCT-1997.  
 XX  
 XX 24-APR-1997; 97WO-US06563.  
 PF  
 XX 15-MAY-1996; 96US-0017785.  
 PR 24-APR-1996; 96US-0016117.  
 XX  
 XX (UNMI ) UNITV MICHIGAN.  
 XX  
 PI Amano K, Kaufman RJ, Pipe SW;  
 XX WPI; 1997-535830/49.  
 DR  
 XX Modified human pro-coagulant active factor VIII - can be  
 PT administered to haemophiliacs, i.e. factor VIII replacement therapy  
 XX  
 XX Claim 13; Page -; 57pp; English.  
 XX  
 CC The present sequence represents a novel pro-coagulant active factor  
 CC VIII (FVIII) mutant protein, comprising a deletion of the B domain and  
 CC von Willebrand factor binding site, mutations F309S, R740A and addition  
 CC of an amino acid sequence spacer between the A2 and A3 domains. Factor  
 CC VIII, along with calcium and phospholipid, acts as a cofactor for factor  
 CC IXa, when it converts factor X to the activated form (factor Xa). FVIII  
 CC is the coagulation factor deficient in the X-chromosome-linked bleeding  
 CC disorder haemophilia A. Several other mutant FVIII proteins have also  
 CC been created (see AAW33222-29). The FVIII mutant F309S (AAW33225) is  
 CC capable of recombinant secretion at higher levels than typically obtained  
 CC with wild type FVIII and retains pro-coagulant activity. The FVIII  
 CC mutant R336I (AAW33222) and R562K (AAW33223) are resistant to activated  
 CC protein C (APC) cleavage. The present FVIII mutant can form a more  
 CC stable configuration, and have an approximate 5-fold increase in  
 CC specific activity compared to purified wild type FVIII, while increasing  
 CC their binding affinity to von Willebrand factor improves their  
 CC stability. The FVIII proteins can be administered to haemophiliacs, i.e.  
 CC FVIII replacement therapy, while the nucleic acid molecule can be used  
 CC for gene therapy.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using sequences from the given references.  
 CC  
 SQ Sequence 1383 AA;  
 Query Match 100.0%; Score 82; DB 18; Length 1383;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FNRKGTALKVSSCD 16  
 |||||  
 DB 697 FNRKGTALKVSSCD 712

RESULT 15  
 AAP80268  
 ID AAP80268 standard; protein; 1424 AA.  
 XX  
 XX AAP80268;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 10-OCT-1990 (first entry)  
 DT  
 XX Modified factor VIII:C sequence with the R740-D1658 deletion.  
 DE  
 XX Modified factor VIII:C; maturation polypeptide; haemophilia;  
 KM blood coagulation; RD deletion; procoagulant.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO8800831-A.  
 PN  
 XX 11-FEB-1988.  
 PD  
 XX 31-JUL-1987; 87WO-US01814.  
 PF  
 XX

```

PR 01-AUG-1986; 86US-0893375.
XX
XX (BIOJ ) BIOGEN NV.
PA (PASE/) PASEK M P.
XX
XX PASEK MP;
PI
XX
XX WPI; 1988-049866/07.
DR N-PSDB; AAN80447.
XX
PT New DNA sequences encoding modified factor VIII:C - with deletion of DNA
PT encoding maturation polypeptide, useful for high yield transformation.
XX
XX Claim 3; Page 60-61-62-63; 97pp; English.
PS
XX The RD deletion removes the DNA from Ser 741 to Ser 1657.
CC A major part of the sequence encoding the maturation polypeptide of
CC Factor VIII:C is deleted, i.e. Gln 744 - Asp 1563.
CC The full length Factor VIII:C cDNA has two changes with respect to the
CC published sequence (EPO application 160457):
CC CTG to CTA at Leu 242 and TTC to CTC change at amino acid residue 1880
CC (Phe to Leu). The product is produced in approx. 20 times higher
CC yields than previous recombinant produced factor VIII:C and are more
CC easily purified. The peptide is used for treating haemophilia A, both
CC acute and prolonged bleeding.
CC See also AAN80444 and AAN80446.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 1424 AA;

```

Query Match 100.0%; Score 82; DB 9; Length 1424;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FRNRGWTALLKVSSCD 16
   |||||
Db 697 FRNRGWTALLKVSSCD 712

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Search completed: November 7, 2003, 07:27:05  
 Job time : 7.89987 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 1.29506 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-5

Perfect score: 58  
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	72.4	626	2 B70749	probable Acyl-CoA
2	41	70.7	389	2 B90083	polyadenylate-bind
3	41	70.7	453	2 S75579	hypothetical prote
4	41	70.7	2515	2 A41519	posterior-group pr
5	39	67.2	401	2 H82175	multidrug resistanc
6	39	67.2	568	1 A55377	CPR-binding protei
7	38	65.5	402	2 D90034	hypothetical prote
8	38	65.5	488	2 AD0735	conserved hypothet
9	38	65.5	488	2 AG0621	probable bacteriop
10	38	65.5	488	2 B95521	protein F21D18.20
11	38	65.5	583	2 B87204	probable acyl-CoA
12	38	65.5	588	2 JC7206	phosphoprotein pho
13	37	63.8	205	2 T19356	hypothetical prote
14	37	63.8	223	2 B70372	polymerase
15	37	63.8	306	1 S59863	polymerase
16	37	63.8	331	2 C86413	hypothetical prote
17	37	63.8	346	2 C86413	hypothetical prote
18	37	63.8	390	2 AG6028	hypothetical prote
19	37	63.8	394	1 WHPSBA	hypothetical prote
20	37	63.8	394	1 WHPSBA	hypothetical prote
21	37	63.8	422	2 P97012	hypothetical prote
22	37	63.8	422	2 P97012	hypothetical prote
23	37	63.8	422	2 P97012	hypothetical prote
24	36	62.1	117	2 P97012	hypothetical prote
25	36	62.1	117	2 P97012	hypothetical prote
26	36	62.1	117	2 P97012	hypothetical prote
27	36	62.1	117	2 P97012	hypothetical prote
28	36	62.1	117	2 P97012	hypothetical prote
29	36	62.1	117	2 P97012	hypothetical prote

30	36	62.1	452	2 S64211	probable transcrip
31	36	62.1	611	2 S60914	lysine transport p
32	36	62.1	670	2 T02019	callus-associated
33	36	62.1	910	2 S38167	hypothetical prote
34	36	62.1	1414	1 S23809	collagen alpha 2(I
35	36	62.1	1928	2 J50610	beta-galactosidase
36	35	60.3	109	2 P30607	Ig kappa chain V-I
37	35	60.3	112	2 J00151	hypothetical prote
38	35	60.3	113	2 P84671	hypothetical prote
39	35	60.3	157	2 S76232	hypothetical prote
40	35	60.3	166	2 T39586	hypothetical prote
41	35	60.3	204	2 T39489	hypothetical prote
42	35	60.3	217	2 T50004	hypothetical prote
43	35	60.3	258	2 S25624	coat protein - cas
44	35	60.3	270	2 A81497	phosphoglycerate m
45	35	60.3	285	2 B82459	hypothetical prote

#### ALIGNMENTS

RESULT 1  
B70749  
probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C/Accession: B70749  
R/Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; G  
i Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Hol  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A/Accession: B70749  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-626 <COL>  
A/Cross-references: GB:Z74697; GB:AL123456; NID:G3261602; PIDN:CAA98985.1; PID:G  
A/Experimental source: strain H37RV  
C/Genetics:  
A:Gene: fadD26  
C/Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology  
F103-610/Domain: acetate-CoA ligase homology <ACL>  
Query Match 72.4%; Score 42; DB 2; Length 626;  
Best local similarity 77.8%; Pred. No. 8.5;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YGNSPKGFAY 9  
DB 73 YGSDPKGFA 81  
RESULT 2  
H90083  
polyadenylate-binding protein [imported] - Giardia thoma nucleomorph  
C:Species: nucleomorph Giardia thoma  
A>Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C/Accession: H90083  
R/Douglas, S.; Zauner, S.; Franholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu,  
Nature 410, 1091-1096, 2001  
A>Title: The highly reduced genome of an enslaved algal nucleus.  
A/Reference number: A99082; MUID:11323671; PMID:11323671  
A/Accession: H90083  
A>Status: preliminary  
A/Molecule type: DNA  
A:Residues: 1-389 <DOU>  
A/Cross-references: GB:AF165818; NID:G13794428; PIDN:AAK39803.1; GSPDB:GN00150  
C/Genetics:  
A:Gene: pab1  
A/Map position: 1

A:Genome: nucleomorph  
C:Keywords: nucleomorph

Query Match 70.7%; Score 41; DB 2; Length 389;  
Best Local Similarity 70.0%; Pred. No. 7.9;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
|||  
Db 222 YNSIPKGFAY 231

## RESULT 3

S75579  
hypothetical protein sl10804 - *Synechocystis* sp. (strain PCC 6803)  
C:Species: *Synechocystis* sp.  
A:Variety: PCC 6803  
C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 02-Feb-2001  
C:Accession: S75579  
R:Kaneko, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75579  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-453 <KAN>  
A:Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDD:BA18140.1; PID:g165322  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: hypothetical protein sl10804; translation elongation factor Tu homology  
C:Keywords: GTP binding; nucleotide binding; P-loop  
F:62-176/Domain: translation elongation factor Tu homology <ETU>  
F:68-75/Region: nucleotide-binding motif A (P-loop)  
F:173-176/Region: GTP-binding NKXD motif  
F:367-369/Region: GTP-binding SAK/L motif

Query Match 70.7%; Score 41; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7  
|||  
Db 224 YGNSPKG 230

## RESULT 4

A41519  
posterior-group protein tudor - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 24-Sep-1999  
C:Accession: A41519; S19019  
R:Golubetski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.  
Genes Dev. 5, 2060-2070, 1991  
A:Title: tudor, a posterior-group gene of *Drosophila melanogaster*, encodes a novel prote  
A:Reference number: A41519; MUID:92038995; PMID:1936993  
A:Accession: A41519  
A:Molecule type: mRNA  
A:Residues: 1-2515 <GOL>  
A:Cross-references: GB:X62420; NID:98753; PIDD:CAA44286.1; PID:g8754  
C:Genetics:  
A:Gene: tud  
A:Superfamily: posterior-group protein tudor

Query Match 70.7%; Score 41; DB 2; Length 2515;  
Best Local Similarity 87.5%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8  
|||  
Db 217 YGNSPKSF 2178

## RESULT 5

H82175  
multidrug resistance protein VCI634 [imported] - *Vibrio cholerae* (strain N16961  
C:Species: *Vibrio cholerae*  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: H82175  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson,  
D.; Ermolaeva, M.D.; Yamateyan, J.; Bass, S.; Qin, H.; Dreigol, I.; Se  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: H82175  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-401 <HEI>  
A:Cross-references: GB:AE004241; GB:AE003852; NID:g9656142; PIDD:AAF94785.1; GS  
A:Experimental source: serogroup O1, strain N16961, biotype El Tor  
C:Genetics:  
A:Gene: VCI634  
A:Map position: 1  
C:Superfamily: bicyclomycin resistance protein

Query Match 67.2%; Score 39; DB 2; Length 401;  
Best Local Similarity 70.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGRAY 10  
|||  
Db 251 YGNSPDGRGX 260

## RESULT 6

A55377  
CPE-binding protein - African clawed frog  
M:Alternate names: cytoplasmic polyadenylation element-binding protein  
C:Species: *Xenopus laevis* (African clawed frog)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: A55377  
R:Hake, L.B.; Richter, J.D.  
Cell 79, 617-627, 1994  
A:Title: CPEB is a specificity factor that mediates cytoplasmic polyadenylation  
A:Reference number: A55377; MUID:95042759; PMID:7954828  
A:Accession: A55377  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-568 <HAK>  
A:Cross-references: GB:U14169; NID:g987224; PIDD:AAA80483.1; PID:g624634  
C:Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat  
F:314-386/Domain: ribonucleoprotein repeat homology <RNM1>

Query Match 67.2%; Score 39; DB 1; Length 568;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
|||  
Db 357 GNSPKGYVY 365

## RESULT 7

D90034  
hypothetical protein SA2135 [imported] - *Staphylococcus aureus* (strain N315)  
C:Species: *Staphylococcus aureus*  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C:Accession: D90034  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui,  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.  
lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A/Reference number: A89758; MUID:21311952; PMID:11418146  
A/Accession: D90034  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-402 <R>  
A/Cross-references: GB:BA000018; PID:g13702296; PIDN:BA843437.1; GSPDB:GN00149  
A/Experimental source: strain N3.5  
C/Genetics:  
A/Gene: S42135  
C/Superfamily: sodium-glutamate symport carrier protein

Query Match 65.5%; Score 38; DB 2; Length 402;  
Best Local Similarity 75.0%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8  
DB 368 YGNSPKAY 375

RESULT 8  
AD0735  
Conserved hypothetical protein STY2039 [imported] - *Salmonella enterica* subsp. *enterica*  
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A/Note: this species has also been called *Salmonella typhi*  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AD0735  
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, C.; T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar AB0502; MUID:21534947; PMID:11677608  
A/Accession: AD0735  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-488 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CA05582.1; PID:g16503079; GSPDB:GN00176  
C/Genetics:  
A/Gene: STY2039  
C/Superfamily: Haemophilus influenzae hypothetical protein H11409

Query Match 65.5%; Score 38; DB 2; Length 488;  
Best Local Similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 9  
DB 323 FGSPKGF 331

RESULT 9  
AC0621  
Probable bacteriophage protein STY1048 [imported] - *Salmonella enterica* subsp. *enterica*  
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A/Note: this species has also been called *Salmonella typhi*  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AC0621  
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, C.; T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar AB0502; MUID:21534947; PMID:11677608  
A/Accession: AC0621  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-488 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CA05582.1; PID:g16502202; GSPDB:GN00176  
C/Genetics:  
A/Gene: STY1048

C/Superfamily: Haemophilus influenzae hypothetical protein H11409

Query Match 65.5%; Score 38; DB 2; Length 488;  
Best Local Similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 9  
DB 323 FGSPKGF 331

RESULT 10  
B96521  
protein P21D18.20 [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C/Accession: B96521  
R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Deansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: B96521  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-488 <STO>  
A/Cross-references: GB:AE005173; MUID:88778515; PIDN:AAF79523.1; GSPDB:GN00141  
C/Genetics:  
A/Gene: P21D18.20  
A/Map position: 1

Query Match 65.5%; Score 38; DB 2; Length 488;  
Best Local Similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGF 10  
DB 232 GNSPKGF 240

RESULT 11  
B87204  
probable acyl-CoA synthase [imported] - *Mycobacterium leprae*  
C/Species: *Mycobacterium leprae*  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 24-Aug-2001  
C/Accession: B87204  
R/Cole, S.T.; Eigmeier, K.; Parikh, J.; James, K.D.; Thomson, N.R.; Wheeler, R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares  
A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:11234002  
A/Accession: B87204  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-583 <STO>  
A/Cross-references: GB:AL450380; MUID:g13093967; PIDN:CA031874.1; GSPDB:GN00147  
C/Genetics:  
A/Gene: fadD26  
C/Superfamily: Synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase

Query Match 65.5%; Score 38; DB 2; Length 583;  
Best Local Similarity 75.0%; Pred. No. 44;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8

Db 30 YGSDPKGF 37

## RESULT 12

phosphoprotein phosphatase (EC 3.1.3.16) [validated] - shiitake mushroom  
 C/Species: Lentinula edodes (shiitake mushroom)  
 C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 20-Apr-2001  
 C/Accession: JG7206  
 R/Isizaki, T.; Yokoyama, H.; Kajiwara, S.; Shishido, K.  
 Biosci. Biotechnol. Biochem. 64, 438-442, 2000  
 A/Title: Basidiomycete fungal gene encoding a regulatory subunit A homologue of protein  
 A/Reference number: JG7206; MUID:20199469; PMID:10737208  
 A/Accession: JG7206  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-588 <ISH>  
 A/Cross-references: DDBJ:AB027711; GB:AB027711; NID:g7416049; PID:g7416050  
 C/Genetics:  
 A/Gene: paal  
 C/Superfamily: phosphoprotein phosphatase 65K regulatory chain  
 C/Keywords: phosphoric monoester hydrolase

Query Match 65.5%; Score 38; DB 2; Length 588;  
 Best Local Similarity 60.0%; Pred. No. 44;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 |||:|:|:  
 Db 544 YGNTPEGEAF 553

## RESULT 13

hypothetical protein C17E4.5 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T19356  
 R/Percy, C.  
 submitted to the EMBL Data Library, October 1996  
 A/Reference number: Z19113  
 A/Accession: T19356  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: DNA  
 A/Residues: 1-205 <WILL>  
 A/Cross-references: EMBL:Z81037; PIDN:CA802750.1; GSPDB:GN00019; CESP:C17E4.5  
 A/Experimental source: clone C17E4  
 C/Genetics:  
 A/Gene: CESP:C17E4.5  
 A/Map position: 1  
 A/Introns: 22/3; 120/2

Query Match 63.8%; Score 37; DB 2; Length 205;  
 Best Local Similarity 60.0%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 :|||:  
 Db 114 FSGHPKGFAY 123

## RESULT 14

flagellar protein FlgA - Aquifex aeolicus  
 B70372  
 C/Species: Aquifex aeolicus  
 C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
 C/Accession: B70372  
 R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
 Nature 392, 353-358, 1998  
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A/Reference number: A70500; MUID:98196666; PMID:9537320

A/Accession: B70372  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-223 <AOF>  
 A/Cross-references: GB:AE000709; NID:g2983373; PIDN:AA069662.1; PID:g2983376; GB  
 A/Experimental source: strain VFS  
 C/Genetics:  
 A/Gene: flgA

Query Match 63.8%; Score 37; DB 2; Length 223;  
 Best Local Similarity 60.0%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 |||:|:|:  
 Db 75 YGNSPKGFH 84

## RESULT 15

polyA binding protein II - bovine  
 S59863  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Nov-1999  
 C/Accession: S59863  
 R/Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jence, P.; Lustig, A.; Wahle, E.  
 Nucleic Acids Res. 23, 4034-4041, 1995  
 A/Title: Isolation of genomic and cDNA clones encoding bovine poly(A) binding protein  
 A/Reference number: S59863; MUID:96071160; PMID:7479061  
 A/Accession: S59863  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-306 <NEM>  
 A/Cross-references: EMBL:X8969; NID:g1065677; PIDN:CA62006.1; PID:g1051125  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995  
 C/Superfamily: bovine polyA binding protein II; ribonucleoprotein repeat homology  
 F,173-239/Domain: ribonucleoprotein repeat homology <RFM2>

Query Match 63.8%; Score 37; DB 1; Length 306;  
 Best Local Similarity 60.0%; Pred. No. 34;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 :|||:  
 Db 208 FSGHPKGFAY 217

Search completed: November 7, 2003, 07:36:15  
 Job time : 3.39506 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 0.720961 Seconds

(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992B-5  
Perfect score: 58  
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	72.4	583	1	FD26 MYCTU
2	41	70.7	2515	1	FD26 MYCTU
3	37	63.8	223	1	FLGA AQUAR
4	37	63.8	394	1	PHHY PSEAE
5	37	63.8	394	1	PHHY PSEAE
6	37	63.8	1180	1	RNPI DROME
7	36	62.1	452	1	HOS2 YEAST
8	36	62.1	611	1	LYPI YEAST
9	36	62.1	910	1	YK69 YEAST
10	36	62.1	1928	1	LYPI YEAST
11	35	60.3	290	1	TODE PSEPU
12	35	60.3	291	1	BHGI RHOGO
13	35	60.3	332	1	CIQ3 CAVPO
14	35	60.3	349	1	RNRP PASMU
15	35	60.3	373	1	NLPD SALTI
16	35	60.3	377	1	NLPD SALDU
17	35	60.3	377	1	NLPD SALTY
18	35	60.3	379	1	NLPD ECOLI
19	35	60.3	396	1	PRRC ECOLI
20	35	60.3	490	1	ITPI DROME
21	35	60.3	503	1	ATRI YEAST
22	35	60.3	674	1	AGUA THEMA
23	35	60.3	1230	1	UGS4 SOLTU
24	34	58.6	220	1	HB7B XENLA
25	34	58.6	246	1	Y625 MYCTU
26	34	58.6	260	1	COAT TYLCV
27	34	58.6	289	1	HXD8 MOUSE
28	34	58.6	290	1	HXD8 HUMAN
29	34	58.6	350	1	YLBS PYRAE
30	34	58.6	427	1	RUI7 ARATH
31	34	58.6	429	1	THD1 MYCTU
32	34	58.6	1058	1	YU02 ARATH
33	34	58.6	1866	1	VGNB_CPMV

34	58.6	2329	1	YLJ6 CAEEL	P34369 caenorhabdi
35	56.9	109	1	KVIG HUMAN	P04206 homo sapien
36	56.9	226	1	YB62 THEMA	O9X0P5 thermotoga
37	56.9	258	1	COAT CLIVK	P03561 caesava lac
38	56.9	258	1	COAT CLIVK	P14566 caesava lac
39	56.9	292	1	CDD HABIN	P44325 haemophilus
40	56.9	298	1	MIAA AGRTS	P38435 agrobacteri
41	56.9	317	1	TFB3 HALNI	O9Hk55 halobacteri
42	56.9	328	1	Y36X HALNI	P14321 halobacteri
43	56.9	385	1	ARGD_BACSU	P36839 bacillus su
44	56.9	403	1	MEIK_XANAC	O8PD75 xanthomonas
45	56.9	403	1	MEIK_XANCP	O8PD75 xanthomonas

## ALIGNMENTS

RESULT 1  
FD26 MYCTU STANDARD; PRT; 583 AA.  
ID FD26 MYCTU  
AC Q10976;  
DT 01-OCT-1996 (Ref. 34, Created)  
DT 16-OCT-2001 (Ref. 40, Last sequence update)  
DT 16-OCT-2001 (Ref. 40, Last annotation update)  
DE Putative fatty-acid-CoA ligase FadD26 (EC 6.2.1.-) (Acyl-CoA synthetase).  
GN FADD26 OR RV2930 OR MT2999 OR MTCY338.19.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_Taxid=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37Rv;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sutton J.E., Taylor K., Whitehead S., Barrett B.G.;  
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."  
RT Nature 393:537-544(1998).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=CDC 1551 / Oshkosh;  
RC Fleisigmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Debby R., Dodson R., Gwin M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;  
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."  
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME FAMILY.  
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CC EMBL: Z74697; CA98985.1; ALT INIT.  
CC EMBL: AE007122; AA47327.1; --  
CC TIGR: MT2999; --  
CC Tuberculist: RV2930; --  
CC InterPro: IPR000873; AMP-bind.

DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP BINDING; FALSE NEG.  
 KW Hypothetical protein; Ligase; Fatty acid metabolism;  
 KM Complete proteome.  
 SQ SEQUENCE 583 AA; 63043 MW; F97CD6E19E217435 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 583;  
 Best Local Similarity 77.8%; Pred. No. 4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGNSPKGFA 9  
 |||  
 30 YGSDPKGFA 38

## RESULT 2

TUD DROME STANDARD; PRT; 2515 AA.  
 ID TUD DROME  
 AC P25823;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Maternal tudor protein.  
 GN TUD.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9203895; Pubmed=1936993;  
 RA Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.;  
 RT "Tudor, a posterior-group gene of Drosophila melanogaster, encodes a  
 novel protein and an mRNA localized during mid-oogenesis";  
 RL Genes Dev. 5:2060-2070(1991).  
 CC -1- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF  
 CC PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.  
 CC -1- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR  
 CC REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES  
 CC OF OOGENESIS.  
 CC -1- SIMILARITY: Contains 9 Tudor domains.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 DR EMBL; X62420; CAA44286.1; -.  
 DR PIR; A41519; A41519.  
 DR HSBP; O16637; IGSV.  
 DR FLYBASE; FBgn0003891; tud.  
 DR GO; GO:0019050; P-mitochondrial rRNA, mitochondrial export; IMP.  
 DR GO; GO:0007315; P-pole plasm assembly; IMP.  
 DR InterPro; IPR001097; Maternal\_tudor.  
 DR InterPro; IPR002959; Tudor.  
 DR Pfam; PF00567; Tudor; 10.  
 DR SMART; SM00333; TUDOR; 10.  
 DR PROSITE; PS50304; TUDOR; 9.  
 KM Developmental protein; Repeat.  
 FT DOMAIN 455 513 TUDOR 1.  
 FT 641 696 TUDOR 2.  
 FT DOMAIN 1062 1122 TUDOR 3.  
 FT DOMAIN 1355 1414 TUDOR 4.  
 FT DOMAIN 1662 1718 TUDOR 5.  
 FT DOMAIN 1839 1898 TUDOR 6.  
 FT DOMAIN 2023 2082 TUDOR 7.  
 FT DOMAIN 2211 2269 TUDOR 8.  
 FT DOMAIN 2392 2451 TUDOR 9.

SQ SEQUENCE 2515 AA; 285236 MW; 683C10AD308BADA CRC64;  
 Query Match 70.7%; Score 41; DB 1; Length 2515;  
 Best Local Similarity 87.5%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGNSPKGF 8  
 |||  
 2171 YGNSPKSF 2178

## RESULT 3

FLGA AQAUE STANDARD; PRT; 223 AA.  
 ID FLGA AQAUE  
 AC O67005;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Flagella basal body P-ring formation protein flga precursor.  
 GN FLGA OR AQ.833.  
 GN Aquifex aeolicus.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VPS;  
 RX MEDLINE=9819666; Pubmed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Sneed W.A., Keller W., Aulay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus";  
 RL Nature 392:353-358(1998).  
 CC -1- FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING  
 CC FORMATION. IT MAY ASSOCIATE WITH FLGF ON THE ROD CONSTITUTING A  
 CC STRUCTURE ESSENTIAL FOR THE P-RING ASSEMBLY OR MAY ACT AS A  
 CC MODULATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE FLGA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 DR EMBL; AB000709; AAC06962.1; -.  
 DR PIR; B70372; B70372.  
 DR InterPro; IPR001924; FLGA.  
 DR Pfam; PF03240; FLGA; 1.  
 KW Flagella; Periplasmic; Signal; Complete proteome.  
 FT SIGNAL 1 POTENTIAL.  
 FT CHAIN ? 223 FLAGELLA BASAL BODY P-RING FORMATION  
 FT PROTEIN FLGA.  
 SQ SEQUENCE 223 AA; 26303 MW; 98C0A51898254CD CRC64;

Query Match 63.8%; Score 37; DB 1; Length 223;  
 Best Local Similarity 60.0%; Pred. No. 13;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGNSPKGF 10  
 |||  
 75 YGNSPKGF 84

## RESULT 4

PHHY PSBAE STANDARD; PRT; 394 AA.  
 ID PHHY PSBAE  
 AC P20586;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)  
 DE P-hydroxybenzoate hydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-  
 monooxygenase) (PHEH).  
 GN FORA OR P80247.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89138003; PubMed=2465205;  
 RA Entsch B., Nan Y., Weach K., Scott K.F.;  
 RT "Sequence and organization of poba, the gene coding for p-  
 hydroxybenzoate hydroxylase, an inducible enzyme from Pseudomonas  
 aeruginosa.";  
 RL Gene 71:279-291(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 Hickey M.J., Brinkman F.S.L., Hutnagle N.O., Kowalik D.J., Lagrou M.,  
 Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Jarbig K., Lam R.M.,  
 Smith K.A., Spencer D.H., Wong G.K.-S., Ra Z., Paulsen I.T.,  
 Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=95025875; PubMed=7939628;  
 RA Gatti D.L., Falley B.A., Lah M.S., Entsch B., Maasey V., Ballou D.P.,  
 Ludwig M.L.;  
 RT "The mobile flavin of 4-OH benzoate hydroxylase.";  
 RL Science 266:110-114(1994).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=96140232; PubMed=8555229;  
 RA Gatti D.L., Entsch B., Ballou D.P., Ludwig M.L.;  
 RT "pH-dependent structural changes in the active site of  
 p-hydroxybenzoate hydroxylase point to the importance of proton and  
 water movements during catalysis.";  
 RL Biochemistry 35:567-578(1996).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANTS.  
 RX MEDLINE=94146010; PubMed=8312276;  
 RA Lah M.S., Falley B.A., Schneider H.A., Ludwig M.L.;  
 RT "Crystal structures of mutant Pseudomonas aeruginosa  
 p-hydroxybenzoate hydroxylases: the Tyr201Phe, Tyr385Phe, and  
 Asn300Asp variants.";  
 RL Biochemistry 33:1555-1564(1994).  
 CC -1 CATALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) =  
 4-hydroxybenzoate + NADP(+) + H(2)O.  
 CC -1 COFACTOR: FAD.  
 CC -1 PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COA.  
 CC -1 SUBUNIT: Homodimer.  
 CC -1 SIMILARITY: TO P. PUTIDA SALICYLATE HYDROXYLASE.  
 CC -----  
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 CC -----  
 DR EMBL; M23173; AAA8455.1; -;  
 DR EMBL; AE004463; AAC03636.1; -;  
 DR PIR; J70384; WHSBA.  
 DR PDB; 1DOE; 30-NOV-94.  
 DR PDB; 1DOC; 30-NOV-94.  
 DR PDB; 1DOD; 30-NOV-94.

DR PDB; 1DOE; 30-NOV-94.  
 DR PDB; 1IUS; 03-APR-96.  
 DR PDB; 1IUT; 03-APR-96.  
 DR PDB; 1IUU; 03-APR-96.  
 DR PDB; 1IUV; 20-JUN-96.  
 DR PDB; 1IUW; 11-JUL-96.  
 DR PDB; 1IUX; 11-JUL-96.  
 DR PDB; 1PXA; 27-FEB-95.  
 DR PDB; 1PXB; 27-FEB-95.  
 DR PDB; 1PXC; 27-FEB-95.  
 DR PDB; 1D7L; 21-JAN-00.  
 DR PDB; 1K0J; 27-FEB-02.  
 DR PDB; 1K0L; 27-FEB-02.  
 DR InterPro; IPR007033; Flav monooxygenase.  
 DR InterPro; IPR002938; Moxv\_FAD\_binding.  
 DR InterPro; IPR003042; Rng\_mnoxygenase.  
 DR Pfam; PF01494; FAD\_binding\_3; 1.  
 DR Pfam; PF01360; Monooxygenase; 1.  
 DR PRINTS; PR00420; RINGMONOXGNASE.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;  
 KW Flavoprotein; FAD; NADP; 3D-structure; Complete proteome.  
 NP BIND 4 32 FAD (POTENTIAL).  
 FT STRAND 2 2  
 FT STRAND 5 8  
 FT HELIX 12 23  
 FT TURN 24 25  
 FT STRAND 28 31  
 FT HELIX 36 40  
 FT TURN 41 41  
 FT STRAND 47 49  
 FT HELIX 50 58  
 FT TURN 59 60  
 FT HELIX 63 68  
 FT STRAND 70 72  
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 FT TURN 80 81  
 FT STRAND 82 87  
 FT HELIX 88 91  
 FT TURN 92 93  
 FT STRAND 97 99  
 FT HELIX 102 116  
 FT TURN 117 117  
 FT STRAND 119 121  
 FT TURN 122 123  
 FT STRAND 125 130  
 FT TURN 132 133  
 FT STRAND 138 143  
 FT TURN 144 145  
 FT STRAND 146 151  
 FT STRAND 154 157  
 FT TURN 161 162  
 FT HELIX 164 167  
 FT TURN 168 168  
 FT HELIX 171 173  
 FT STRAND 175 190  
 FT TURN 200 202  
 FT STRAND 205 206  
 FT TURN 209 215  
 FT STRAND 216 217  
 FT TURN 218 225  
 FT HELIX 227 228  
 FT HELIX 231 233  
 FT HELIX 236 246  
 FT HELIX 249 252  
 FT TURN 253 254  
 FT STRAND 260 274  
 FT STRAND 277 278  
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 FT HELIX 285 287  
 FT TURN 288 288  
 FT STRAND 289 290

FT HELIX 293 295  
 FT HELIX 298 319  
 FT HELIX 322 327  
 FT HELIX 328 350  
 FT HELIX 358 373  
 FT HELIX 375 386  
 SQ SEQUENCE 394 AA; 44323 MW; 1E7232854D9EC792 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 394;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGNSPKGFA 9  
 DB 201 YANHPGRFA 209

RESURF 5  
 ID PHHY\_PSEFL STANDARD; PRT; 394 AA.  
 AC P00438;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE P-hydroxybenzoate hydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-monooxygenase).  
 GN POBA.  
 OS Pseudomonas fluorescens.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID:294;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93092974; PubMed=1459126;  
 RA van Berkel W., Westphal A., Eschrich K., Eppink M., de Kok A.;  
 RT "Substitution of Arg214 at the substrate-binding site of P-hydroxybenzoate hydroxylase from Pseudomonas fluorescens.";  
 RU Eur. J. Biochem. 210:411-419 (1992).  
 RN (2)  
 RP SEQUENCE.  
 RA MEDLINE=82257502; PubMed=6809053;  
 RA Weijer W.J., Hofsteenge J., Vereijken J.M., Jekel P.A., Beintema J.J.;  
 RT "Primary structure of p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens.";  
 RU Biochim. Biophys. Acta 704:385-388 (1982).  
 RN (3)  
 RP SEQUENCE OF 111-138 AND 270-280.  
 RA MEDLINE=81114230; PubMed=6780352;  
 RA Hofsteenge J., Vereijken J.M., Weijer W.J., Beintema J.J.,  
 RA Wieringa R.K., Drenth J.;  
 RT "Primary and tertiary structure studies of p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. Isolation and alignment of the cDNA peptides; interactions of the protein with flavin adenine dinucleotide.";  
 RU Eur. J. Biochem. 113:141-150 (1980).  
 RN (4)  
 RP SEQUENCE OF 1-52; 53-65 AND 66-110.  
 RA MEDLINE=81114232; PubMed=6780353;  
 RA Vereijken J.M., Hofsteenge J., Bak H.J., Beintema J.J.;  
 RT "The amino-acid sequence of the three smallest cDNA peptides from p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens.";  
 RU Eur. J. Biochem. 113:151-157 (1980).  
 RN (5)  
 RP SEQUENCE OF CNR PEPTIDES AND TERTIARY STRUCTURE.  
 RA MEDLINE=83209654; PubMed=6406229;  
 RA Hofsteenge J., Weijer W.J., Jekel P.A., Beintema J.J.;  
 RT "p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. 1. Completion of the elucidation of the primary structure.";  
 RU Eur. J. Biochem. 133:91-106 (1983).  
 RN (6)  
 RP SEQUENCE OF CNR PEPTIDES AND STRUCTURE OF ACTIVE SITE.  
 RA MEDLINE=83209623; PubMed=6406227;  
 RA Weijer W.J., Hofsteenge J., Beintema J.J., Wieringa R.K., Drenth J.;

RT "p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. 2. Flitting of the amino-acid sequence to the tertiary structure.";  
 RT Eur. J. Biochem. 133:109-118 (1983).  
 RN (7)  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RA MEDLINE=80029705; PubMed=40036;  
 RA Wieringa R.K., de Jong R.J., Kalk K.H., Hol W.G.J., Drenth J.;  
 RT "Crystal structure of p-hydroxybenzoate hydroxylase.";  
 RU J. Mol. Biol. 131:55-73 (1979).  
 RN (8)  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RA MEDLINE=88172509; PubMed=3351945;  
 RA Schreuder H.A., van der Laan J.M., Hol W.G.J., Drenth J.;  
 RT "Crystal structure of p-hydroxybenzoate hydroxylase complexed with its reaction product 3,4-dihydroxybenzoate.";  
 RU J. Mol. Biol. 199:637-648 (1988).  
 RN (9)  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF REDUCED FORM.  
 RA MEDLINE=93028353; PubMed=1409567;  
 RA Schreuder H.A., van der Laan J.M., Swarte M.B.A., Kalk K.H., Hol W.G.J., Drenth J.;  
 RT "Crystal structure of the reduced form of p-hydroxybenzoate hydroxylase refined at 2.3-A resolution.";  
 RU Proteins 14:178-190 (1992).  
 RN (10)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT LYS-44.  
 RA MEDLINE=95354684; PubMed=7628466;  
 RA Eppink M.H., Schreuder H.A., van Berkel M.J.;  
 RT "Structure and function of mutant Arg44Lys of 4-hydroxybenzoate hydroxylase implications for NADPH binding.";  
 RU Eur. J. Biochem. 231:157-165 (1995).  
 RN (11)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT LYS-42 AND SER-42.  
 RA MEDLINE=98237589; PubMed=9578477;  
 RA Eppink M.H., Schreuder H.A., van Berkel M.J.;  
 RT "Lys42 and Ser42 variants of p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens reveal that Arg42 is essential for NADPH binding.";  
 RU Eur. J. Biochem. 253:194-201 (1998).  
 RN (12)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANTS.  
 RA MEDLINE=99148809; PubMed=10025942;  
 RA Eppink M.H., Buntbol C., Schreuder H.A., van Berkel M.J.;  
 RT "Phe161 and Arg166 variants of p-hydroxybenzoate hydroxylase. Implications for NADPH recognition and structural stability.";  
 RU FEBS Lett. 443:251-255 (1999).  
 CC -1 CATALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) = p-hydroxybenzoate + NADP(+) + H(2)O.  
 CC -1 COFACTOR: FAD.  
 CC -1 PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COA.  
 CC -1 SUBUNIT: Homodimer.  
 CC -1 SIMILARITY: TO E. COLI UBIH/VISB AND VISB.  
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 CC -----  
 DR EMBL: X68438; CAA8483.1; .  
 DR PIR: A90643; WHPSEF.  
 DR PDB: 1PHH; 15-JAN-93.  
 DR PDB: 2PHH; 15-APR-92.  
 DR PDB: 1PBB; 30-SEP-94.  
 DR PDB: 1PBC; 30-SEP-94.  
 DR PDB: 1PBD; 30-SEP-94.  
 DR PDB: 1PBE; 30-SEP-94.  
 DR PDB: 1PBF; 30-SEP-94.  
 DR PDB: 1PDH; 31-MAR-95.  
 DR PDB: 1PFI; 12-AUG-98.  
 DR PDB: 1BGI; 12-AUG-98.

DR PDB; 18GN; 12-AUG-98.  
 DR PDB; 18W; 22-JUL-98.  
 DR PDB; 1CC4; 12-MAR-99.  
 DR PDB; 1CC6; 12-MAR-99.  
 DR PDB; 1CC2; 30-APR-99.  
 DR PDB; 1CC3; 30-APR-99.  
 DR PDB; 1CC4; 30-APR-99.  
 DR InterPro; IPR00733; Flav\_monoxygenase.  
 DR InterPro; IPR002938; Moxv\_FAD\_binding.  
 DR InterPro; IPR003042; Rng\_moxxygenase.  
 DR Pfam; PF01494; FAD\_binding\_3; 1.  
 DR Pfam; PF01360; Monoxygenase; 1.  
 DR PRINTS; PR00420; RINGMOXGNASE.  
 KM Aromatic hydrocarbons catabolism; Oxidoreductase; Monoxygenase;  
 FM Flavoprotein; FAD; NADP; 3D-structure.  
 FT NP\_BIND 4 33 FAD (POTENTIAL).  
 FT CONFLICT 276 286 FAD (POTENTIAL).  
 FT STRAND 344 344 W -> Y (IN REF. 2).  
 FT STRAND 2 2  
 FT STRAND 5 8  
 FT HELIX 12 23  
 FT TURN 24 31  
 FT STRAND 28 35  
 FT HELIX 36 40  
 FT TURN 41 41  
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 FT HELIX 50 58  
 FT TURN 59 60  
 FT HELIX 63 68  
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 FT TURN 125 130  
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 FT TURN 144 145  
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 FT TURN 168 168  
 FT HELIX 171 173  
 FT STRAND 175 190  
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 FT HELIX 322 327  
 FT HELIX 328 350  
 FT HELIX 358 371  
 FT TURN 372 373

Query Match 63.8%; Score 37; DB 1; Length 394;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YGNSPKGFA 9  
 DB 201 YANHRGFA 209  
 RESULT 6  
 RNTL DROME STANDARD; FRT; 1180 AA.  
 AC OYVRS3; Q25R93;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Regulator of nonsense transcripts 1 homolog.  
 GN UPF1 OR CG1559.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OK NCBI\_taxid=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celtnker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Borchan M.R., Bouch J., Brokstein P., Brotter P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lai X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pecleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,  
 RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.",  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.B.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN  
 RN (3)  
 RN SQUENCE FROM N.A.  
 RC STRAIN=Berkeley; TISSUE=Embryo;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,  
 RA Chame M., Chavez C., Dorsett V., Farfan D., Frise E., George R.A.,  
 RA Gonzalez M., Guarin H., Li P.W., Liao G., Miranda A., Mungall C.J.,  
 RA Munoz J., Paclet J.M., Paragas V., Park S., Phouamvong S.,  
 RA Man K.H., Yu C., Lewis S.E., Rubin G.M., Celinker S.E.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBS databases.  
 CC -1- FUNCTION: Eliminates the production of nonsense-containing  
 CC RNAs (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.  
 CC  
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 CC  
 CC EMBL: A8003487; AAF48115.2; -;  
 DR EMBL: A7061379; AAL28927.1; -;  
 DR  
 KW Hydrolase; Fggn0030354; Upt1.  
 KM Hydrophobic protein; Hydrolyase; Helicase; ATP-binding; Zinc-finger.  
 FT ZN FING 108 136 CCH2-TYPE (ATYPICAL) (POTENTIAL).  
 FT ZN FING 160 190 CA-TYPE (POTENTIAL).  
 FT NP BIND 473 480 ATP (POTENTIAL).  
 FT DOMAIN 931 1105 GLY-RICH  
 SQ SEQUENCE 1180 AA; 129912 MW; 150BA970D22100E CRC64;  
 Query Match 63.8%; Score 37; DB 1; Length 1180;  
 Best Local Similarity 75.0%; Pred. No. 66;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YGNSPKGF 8  
 DB 957 YGNSPKGF 964  
 RESULT 7  
 ID HOS2 YEAST STANDARD; PRT; 452 AA.  
 AC PS3056;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Probable histone deacetylase HOS2.  
 GN HOS2 OR YGL194C OR G1330.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxId=4932;  
 OK  
 RN (1)  
 RN SQUENCE FROM N.A.  
 RC STRAIN=S288c; FY1679;  
 RX MEDLINE=97197971; Pubmed=9046087;  
 RA Cogillevina M., Klima R., Bertani I., Delneri D., Zaccaria P.,  
 RA Brusch C.V., Klima R., Bertani I., Delneri D., Zaccaria P.,  
 RT "Sequencing of a 40.5 kb fragment located on the left arm of  
 RT chromosome VII from *Saccharomyces cerevisiae*.";  
 RL Yeast 13:55-64(1997).  
 RL (2)  
 RX GENE NAME.  
 RX MEDLINE=97121415; Pubmed=8962081;

RA Rundlett S.E., Cammen A.A., Kobayashi R., Baykin S., Turner B.M.,  
 RA Grunstein M.;  
 RT "HDA1 and RPD3 are members of distinct yeast histone deacetylase  
 RT complexes that regulate silencing and transcription";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).  
 RN  
 RN (3)  
 RN IDENTIFICATION IN A COMPLEX WITH SET3, HST1, SNT1, SIF2, CPR1 AND  
 RP YIL112W.  
 RX PubMed=11711434;  
 RA Pijnappel W.W.M.P., Schaft D., Roguev A., Shevchenko A., Tekotte H.,  
 RA Wilm M., Rigaut G., Seraphin B., Aasland R., Stewart A.F.;  
 RT "The *S. cerevisiae* SET3 complex includes two histone deacetylases,  
 RT Hst2 and Hst1, and is a meiotic-specific repressor of the sporulation  
 RT gene program";  
 RL Gene Dev. 15:2991-3004(2001).  
 RN  
 RN (4)  
 RN FUNCTION, AND MUTAGENESIS OF 195-HIS-196.  
 RX PubMed=12434058;  
 RA Wang A., Kurdiatani S.K., Grunstein M.;  
 RT "Requirement of Hst2 histone deacetylase for gene activity in yeast";  
 RL Science 298:1412-1414(2002).  
 CC -1- FUNCTION: Responsible for the deacetylation of lysine residues on  
 CC the N-terminal part of the core histones (H2A, H2B, H3 and H4). In  
 CC contrast to other histone deacetylase proteins, which give a tag  
 CC for epigenetic repression, it is apparently involved in  
 CC transcriptional activation.  
 CC -1- SUBUNIT: Identified in a Set3C complex with SET3, HST1, SNT1,  
 CC SIF2, CPR1 and HOS4/YIL112W.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA  
 CC FAMILY. HD SUBFAMILY 1.  
 CC  
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 CC  
 CC EMBL: Z72716; CAA96906.1; -;  
 DR EMBL: X91837; CAA62950.1; -;  
 DR PIR: S64211; S64211.  
 DR  
 DR SGD; S00003162; HOS2.  
 DR GO; GO:0000118; C:histone deacetylase complex; IPT.  
 DR GO; GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.  
 DR GO; GO:0045129; F:NAD-independent histone deacetylase activity; IDA.  
 DR GO; GO:0016575; P:histone deacetylation; IDA.  
 DR GO; GO:0045835; P:negative regulation of meiosis; IMP.  
 DR InterPro: IPR000286; His deacetylase.  
 DR Pfam: PF00850; Hist deacetylase.  
 DR PRINTS; PRO1270; HDA5UPER.  
 DR KMW Hydrolyase; Nuclear protein; Chromatin regulator;  
 KW Transcription regulation; Activator.  
 FT DOMAIN 26 340 HISTONE DEACETYLASE.  
 FT ACT SITE 197 197 BY SIMILARITY.  
 FT MUTAGEN 196 197 HH->AA: LEADS TO HYPERACETYLATION.  
 FT CONFLICT 352 364 PRDSGSGDYSLY -> HSGHSGGIHIFI (IN REF.  
 FT  
 SQ SEQUENCE 452 AA; 51455 MW; 024E8BA04445A08 CRC64;  
 Query Match 62.1%; Score 36; DB 1; Length 452;  
 Best Local Similarity 75.0%; Pred. No. 39;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 NSPKGFAY 10  
 DB 163 NSPKGFAY 170  
 RESULT 8  
 ID LYP1 YEAST STANDARD; PRT; 611 AA.  
 RX LYP1 YEAST

AC P32487;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Lysine-specific permease.  
 OS *Yeast* OR YNL268W OR N0790.  
 GN *Saccharomyces cerevisiae* (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OK NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 28583 / FL100;  
 RX MEDLINE=93377414; PubMed=8368011;  
 RA Sychrova H., Chevallier M.R.;  
 RT "Cloning and sequencing of the *Saccharomyces cerevisiae* gene *LYP1*  
 RL coding for a lysine-specific permease.";  
 RL Yeast 9:771-782(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / FY1679;  
 RX MEDLINE=96310631; PubMed=8740425;  
 RA Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann U.H.;  
 RT "The sequence of a 24,152 bp segment from the left arm of chromosome  
 RT XIV from *Saccharomyces cerevisiae* between the *ENI1* and the *POL2*  
 RT genes.";  
 RL Yeast 12:505-514(1996).  
 RN [3]  
 RP FUNCTION.  
 RX PubMed=10654085;  
 RA Regenbergh B., Durig-Olsen L., Kjelland-Brandt M.C., Holmberg S.;  
 RT "Substrate specificity and gene expression of the amino-acid permeases  
 RT in *Saccharomyces cerevisiae*.";  
 RL Curr. Genet. 36:317-328(1999).  
 CC -1- FUNCTION: High-affinity permease for lysine.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the amino acid permease family.  
 CC  
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 CC  
 CC EMBL; X67315; CAA47729.1; -;  
 CC EMBL; X92494; CAA63230.1; -;  
 CC EMBL; Z71544; CAA96175.1; -;  
 CC PIR; S60914; S60914.  
 CC SGD; S0005212; LYP1.  
 CC GO; GO:0015174; P:basic amino acid transporter activity; IDA.  
 CC GO; GO:0015802; P:basic amino acid transport; IDA.  
 CC InterPro; IPR002293; AA/rel\_permease.  
 CC InterPro; IPR004840; AAC\_permease.  
 CC InterPro; IPR004841; Permease.  
 CC InterPro; IPR004762; Yeast AA perm.  
 CC Pfam; PF00324; aa\_permeases; 1.  
 CC TIGRFAMs; TIGR00913; 2A0310; 1.  
 CC PROSITE; P500218; AMINO\_ACID\_PERMEASE\_1; 1.  
 CC Transport; Amino-acid transport; Transmembrane.  
 CC FT TRANSMEM 116 136  
 CC FT TRANSMEM 142 162 POTENTIAL.  
 CC FT TRANSMEM 186 205 POTENTIAL.  
 CC FT TRANSMEM 224 243 POTENTIAL.  
 CC FT TRANSMEM 257 274 POTENTIAL.  
 CC FT TRANSMEM 304 321 POTENTIAL.  
 CC FT TRANSMEM 345 365 POTENTIAL.  
 CC FT TRANSMEM 399 418 POTENTIAL.  
 CC FT TRANSMEM 446 464 POTENTIAL.  
 CC FT TRANSMEM 474 494 POTENTIAL.  
 CC FT TRANSMEM 514 532 POTENTIAL.  
 CC FT TRANSMEM 548 566 POTENTIAL.

FT CONFLICT 90 90 T -> P (IN REF. 1).  
 FT CONFLICT 93 93 N -> D (IN REF. 1).  
 FT CONFLICT 561 561 V -> M (IN REF. 1).  
 SQ SEQUENCE 611 AA; 68089 MW; 4E7AF6F7P5F1461B CRC64;  
 Query Match 62.1%; Score 36; DB 1; Length 611;  
 Best Local Similarity 62.7%; Pred. No. 52;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GNSPKGPRAY 10  
 DB 430 GNAKQFGY 438  
 RESULT 9  
 ID YK69 YEAST STANDARD; PRT; 910 AA.  
 AC P36165;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Hypothetical 102.7 kDa protein in PRP16-GRP40 intergenic region.  
 GN YK089C OR YK0409.  
 OS *Saccharomyces cerevisiae* (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OK NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94262327; PubMed=8203164;  
 RA Garcia-Cantalejo V., Baladron V., Esteban P.F., Santos M.A., Bou G.,  
 RA Ramacha M.A., Revuelta J.L., Ballesla J.P.G., Jimenez A., del Rey F.;  
 RT "The complete sequence of an 18,002 bp segment of *Saccharomyces*  
 RT cerevisiae chromosome XI contains the *HBS1*, *MRP-L20* and *PRP16* genes,  
 RT and six new open reading frames.";  
 RL Yeast 10:231-245(1994).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: TO YEAST YMR313C AND S.POMBE SPCL1450.16C.  
 CC  
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 CC  
 CC EMBL; Z27116; CAA81640.1; -;  
 CC EMBL; Z28314; CAA82168.1; -;  
 CC PIR; S38167; S38167.  
 CC SGD; S0001797; YKR089C.  
 CC InterPro; IPR002641; Patatin.  
 CC Pfam; PF01734; Patatin; 1.  
 CC Hypothetical protein; Transmembrane.  
 CC FT TRANSMEM 282 302 POTENTIAL.  
 CC FT TRANSMEM 310 326 POTENTIAL.  
 CC FT TRANSMEM 426 442 POTENTIAL.  
 CC SQ SEQUENCE 910 AA; 102716 MW; 1CC0C0CA46B64B9C CRC64;  
 Query Match 62.1%; Score 36; DB 1; Length 910;  
 Best Local Similarity 75.0%; Pred. No. 77;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YGNSPKGF 8  
 DB 710 YGNSPKGF 717  
 RESULT 10  
 ID LPH RAT STANDARD; PRT; 1928 AA.  
 AC 002401; 063712; 063719;  
 DT 01-JUL-1993 (Rel. 26, Created)



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RESULT 12
BHCL_RHOCO STANDARD; PRT; 291 AA.
ID BHCL_RHOCO
AC P47231;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Biphenyl-2,3-diol 1,2-dioxygenase I (EC 1.13.11.39) (33OHBP
  dioxygenase I) (2,3-dihydroxybiphenyl dioxygenase I) (DHBD I).
GN BHCL.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pe;
RX MEDLINE=94171820; PubMed=8126007;
RA Asturias J.A., Ellis L.D., Prucha M., Timmis K.N.;
RT "Analysis of three 2,3-dihydroxybiphenyl 1,2-dioxygenases found in
  Rhodococcus globerulus Pe. Identification of a new family of
  extradiol dioxygenases."
  J. Biol. Chem. 269:7807-7815 (1994)
CC -1- CATALYTIC ACTIVITY: Biphenyl-2,3-diol + O(2) = 2-hydroxy-6-oxo-6-
  phenylhexa-2,4-dienoate + H(2)O.
CC -1- COFACTOR: FERROUS ION.
CC -1- PATHWAY: DEGRADATION OF BI-PHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
  BENZOIC ACID AND CHLOROBENZOIC ACIDS.
CC -1- SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
  FAMILY.
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CC -----
CC EMBL; X75633; CAA53297.1; -
CC PIR; B53419; B53419.
CC HSSP; P47228; 1HAN.
CC InterPro; IPR004360; Gly_bleo_diox.
CC InterPro; IPR000466; Xdiol_dioxygen.
CC Pfam; PF00903; Glyoxalase_1.
CC ProDom; PD000977; Xdiol_dioxygenase; 1.
CC PROSITE; P500082; EXTRADIOL_DIOXYGENAS; 1.
CC OXidoreductase; Dioxygenase; Aromatic hydrocarbons catabolism; Iron.
  FT METAL 146 146 IRON (BY SIMILARITY).
  FT METAL 210 210 IRON (BY SIMILARITY).
  FT METAL 260 260 IRON (BY SIMILARITY).
SQ SEQUENCE 291 AA; 32081 MW; 104F189FBE1EDDA6A CRC64;

Query Match 60.3%; Score 35; DB 1; Length 291;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 YGNSPKGFA 9
Db 250 YGATPSGFA 258

RESULT 13
C1C3_CAVPO STANDARD; PRT; 332 AA.
ID C1C3_CAVPO
AC Q902T6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD13 precursor (CD1-c3 antigen).
GN CD13.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia; Butheria; Rodentia; Hystriognathi; Cavidae; Cavia.
CC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; and NIH 2; TISSUE=Thymus;
RX MEDLINE=20021845; PubMed=10553074;
RA Dacher C.C., Hiramatsu K., Naylor J.W., Brauer P.P., Brown K.A.,
  Storey J.R., Behar S.M., Kawasaki E.S., Porcelli S.A., Brenner M.B.,
  Lectar K.P.;
RT "Conservation of a CDI multigene family in the guinea pig."
  J. Immunol. 163:5478-5488 (1999).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
  SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
CC EMBL; AF145489; AAF12744.1; -
CC HSSP; P11609; 1CDL.
CC InterPro; IPR007110; Ig_1Ike.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00447; Ig_1.
CC SMART; SM00407; Icd1; 1.
CC PROSITE; P550835; IG_LIKE; 1.
CC KIM Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;
  KW Multigene family.
  FT SIGNAL 1 17
  FT CHAIN 18 332
  FT DOMAIN 18 300
  FT TRANSLEM 301 321
  FT DOMAIN 322 332
  FT DOMAIN 205 292
  FT DISULFID 120 184
  FT DISULFID 224 279
  FT CARBOHYD 25 25
  FT CARBOHYD 38 38
  FT CARBOHYD 75 75
  FT CARBOHYD 146 146
SQ SEQUENCE 332 AA; 37437 MW; 19DA52B30CC05DFC CRC64;

Query Match 60.3%; Score 35; DB 1; Length 332;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 2 GNSPKGFAY 10
Db 125 GSPKGFILY 133

RESULT 14
KNPD_PASMTU STANDARD; PRT; 349 AA.
ID KNPD_PASMTU
AC Q9CNP3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Electron transport complex protein rmd.
GN KNPD OR PM0384.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.

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RK STRAIN-Pm70;  
 RA MEDLINE=21145866; PubMed=11248100;  
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.,  
 RT "Complete genomic sequence of *Pasteurella multocida* Pm70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
 CC -1- FUNCTION: May be part of a membrane complex involved in electron  
 CC transport (By similarity).  
 CC -1- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC,  
 CC rnfD, rnfE and rnfG (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (potential).  
 CC -1- SIMILARITY: BELONGS TO THE NQR3/RNFD FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB06074; AK02468.1; -.  
 DR HAMAP; MF\_00462; -; 1. NQR3\_RNFD\_RNFD.  
 DR InterPro; IPR004338; NQR3\_RNFD\_RNFD; 1.  
 DR Pfam; PF03116; NQR3\_RNFD\_RNFD; 1.  
 KW Electron transport; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 21 38 POTENTIAL.  
 FT TRANSMEM 42 64 POTENTIAL.  
 FT TRANSMEM 69 88 POTENTIAL.  
 FT TRANSMEM 98 118 POTENTIAL.  
 FT TRANSMEM 125 145 POTENTIAL.  
 FT TRANSMEM 214 234 POTENTIAL.  
 FT TRANSMEM 237 257 POTENTIAL.  
 FT TRANSMEM 269 289 POTENTIAL.  
 FT TRANSMEM 299 319 POTENTIAL.  
 FT TRANSMEM 320 340 POTENTIAL.  
 SQ SEQUENCE 349 AA; 38470 MW; DE45D63370FC6BE CRC64;  
 Query Match 60.3%; Score 35; DB 1; Length 349;  
 Best Local Similarity 60.0%; Pred. No. 46;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YGNSPKGFAY 10  
 DB 315 YGNYPDGVAF 324  
 RESULT 15  
 NLDP\_SALTI  
 ID NLDP\_SALTI STANDARD; PRT; 373 AA.  
 AC Q56131;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Lipoprotein nlpd precursor.  
 GN NLDP OR STY3050 OR T2826.  
 OS *Salmonella typhi*.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; *Salmonella*.  
 CC NCBI\_Taxid=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RA MEDLINE=21534947; PubMed=11677608;  
 RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Cornerton F.,  
 RA Cronin A., Davis A., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagers K.,  
 RA Kitchin A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*

RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ty2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;  
 RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2  
 RT and CT18.";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 RN [3]  
 RP SEQUENCE OF 255-373 FROM N.A.  
 RC STRAIN=Ty2a;  
 RX MEDLINE=95220644; PubMed=7705608;  
 RA Robbe-Saule V., Coyanuit C., Norel F.;  
 RT "The live oral typhoid vaccine Ty2a is a rps mutant and is  
 RT susceptible to various environmental stressors.";  
 RL FEWS Microbiol. Lett. 170:141-143(1999).  
 RN [4]  
 RP SEQUENCE OF 269-373 FROM N.A.  
 RC STRAIN=Ty2 / ATCC 700931.  
 RX MEDLINE=99118315; PubMed=9919662;  
 RA Robbe-Saule V., Norel F.;  
 RT "The rps mutant allele of *Salmonella typhi* Ty2 is identical to that  
 RT of the live typhoid vaccine Ty2a.";  
 RL FEWS Microbiol. Lett. 170:141-143(1999).  
 CC -1- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid  
 CC anchor (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE E. COLI NLDP / HAMOPHILUS LPPB FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AL627276; CAD06031.1; -.  
 DR EMBL; AB016843; AA070383.1; -.  
 DR EMBL; X81641; CA57297.1; -.  
 DR EMBL; Y17610; CA76806.1; -.  
 DR MEROPS; M37.UFW; -.  
 DR InterPro; IPR002482; LysM.  
 DR InterPro; IPR002886; Peptidase\_M37.  
 DR Pfam; PF01476; LysM; 1.  
 DR Pfam; PF01551; Peptidase\_M37; 1.  
 DR SMART; SM00257; LysM; 1.  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 DR Inner membrane; Lipoprotein; Repeat; Signal; Complete proteome.  
 KW SIGNAL  
 FT CHAIN 25  
 FT SIGNAL 1 25  
 FT CHAIN 26 373  
 FT LIPID 26 26  
 FT DOMAIN 199 246  
 FT REPEAT 199 205  
 FT REPEAT 221 227  
 FT REPEAT 233 239  
 FT REPEAT 240 246  
 SQ SEQUENCE 373 AA; 39183 MW; DD075BB440098PF7 CRC64;  
 Query Match 60.3%; Score 35; DB 1; Length 373;  
 Best Local Similarity 85.7%; Pred. No. 49;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YGNSPKG 7  
 DB 103 YGNIPIKG 109  
 Search completed: November 7, 2003, 07:28:04  
 Job time : 2.72096 secs

Fri Nov 7 09:40:11 2003

us-09-661-992b-5.rsp

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 3.29773 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-5

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

SPRMBL.23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.9	120	11 Q920E8	Q920E8 mus musculus
2	43	74.1	294	16 Q8XN61	Q8XN61 clostridium
3	42	72.4	160	3 Q8UTU1	Q8UTU1 schizosacch
4	42	72.4	833	3 Q13620	Q13620 schizosacch
5	41	70.7	389	8 Q98R27	Q98R27 guillardi
6	41	70.7	453	16 P7A064	P7A064 synchocyst
7	40	69.0	291	5 Q9VTH9	Q9VTH9 drosophila
8	40	69.0	1312	16 Q9XNH6	Q9XNH6 drosophila
9	39	67.2	401	16 Q9XK6	Q9XK6 rhizobium
10	39	67.2	491	4 Q98ZB7	Q98ZB7 vibrio chol
11	39	67.2	559	13 Q9YGA5	Q9YGA5 homo sapien
12	39	67.2	559	13 Q9YGA5	Q9YGA5 brachydanio
13	39	67.2	559	13 Q9YGA5	Q9YGA5 carassius a
14	39	67.2	561	11 P70166	P70166 mus musculu
15	39	67.2	566	4 Q9BZB8	Q9BZB8 homo sapien
16	39	67.2	568	13 Q91572	Q91572 xenopus lae

17	Q9386	09386 brachydanio
18	Q99R88	Q99R88 straphylococ
19	Q8NV56	Q8NV56 straphylococ
20	Q2LNK1	Q2LNK1 arabidopsis
21	Q827V6	Q827V6 salmoneilla
22	Q82622	Q82622 salmoneilla
23	Q92SK5	Q92SK5 mycobacteri
24	Q9P982	Q9P982 leishmania e
25	Q93233	Q93233 caenorhabdi
26	Q9P4V6	Q9P4V6 candida boi
27	Q9W086	Q9W086 drosophila
28	Q8C6S6	Q8C6S6 mus musculu
29	Q35935	Q35935 mus musculu
30	Q43484	Q43484 homo sapien
31	Q28165	Q28165 bos taurus
32	Q9LPA0	Q9LPA0 arabidopsis
33	Q9LPA0	Q9LPA0 arabidopsis
34	Q9LPA0	Q9LPA0 arabidopsis
35	Q927L6	Q927L6 rhizobium
36	Q8U7H0	Q8U7H0 agrobacteri
37	Q97KK5	Q97KK5 clostridium
38	Q8KG23	Q8KG23 chlorobium
39	Q8CF51	Q8CF51 mus musculu
40	Q215X3	Q215X3 pseudomonas
41	Q96G09	Q96G09 homo sapien
42	Q9FX45	Q9FX45 arabidopsis
43	Q60572	Q60572 homo sapien
44	Q9ROT9	Q9ROT9 mus musculu
45	Q70307	Q70307 mus musculu

## ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	120 AA.
Q920E8			
AC Q920E8	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RF	SEQUENCE FROM N.A.		
RA	Atkin J.D., Tape A., Jennings I.G., Horvath O., Cotton R.G.H.;		
RT	Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.		
KL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF307936; AAL09420.1; .		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_V.		
DR	Pfam; PF00047; IG_1.		
DR	SMART; SM00406; IGV_1.		
DR	PROSITE; PS0835; IG_LIKE; 1.		
FT	NON TER		
FT	NON TER		
FT	NON TER		
SQ	SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56FC CRC64;		
Query Match	75.9%;	Score 44;	DB 11; Length 120;
Best Local Similarity	80.0%;	Pred. No. 1.4;	
Matches	8;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 YGNSPKGFAY 10		
Db	101 YGNSPKGFAY 110		

## RESULT 2

Q8XN61 PRELIMINARY; PRT; 294 AA.  
 AC Q8XN61; 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Probable beta-glycosyltransferase.  
 GN CPE0477,  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX PubMed=11792842;  
 RA Shima T., Ohnishi K., Hirakawa H., Ohshima K., Yamashita A.,  
 Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 flesh-eater";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL; AF003186; BAB80183.1; -  
 DR InterPro; IPR001173; Glyco\_transf\_2.  
 DR Pfam; PF00535; Glycos\_transf\_2; 1.  
 KM Transferrase; Complete proteome.  
 SQ SEQUENCE 294 AA; 34356 MW; 390BFS93B712CA35 CRC64;

Query Match 74.1%; Score 43; DB 16; Length 294;  
 Best Local Similarity 70.0%; Pred. No. 5.8;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 Db 222 YKNPKGFAY 231

## RESULT 3

Q90TU1 PRELIMINARY; PRT; 160 AA.  
 AC Q90TU1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Hypothetical 18.1 kDa protein (Fragment).  
 GN 2257512,  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=968 H90;  
 RX MEDLINE=20232868; PubMed=10759889;  
 RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,  
 Hirakawa Y.;  
 RT "Large-scale screening of intracellular protein localization in living  
 fission yeast cells by the use of a GFP-fusion genomic DNA library";  
 RL Genes Cells 5:169-190(2000).  
 DR EMBL; AB028003; BAA87307.1; -  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rtm; 1.  
 DR SMART; SMO0360; RRM; 1.  
 DR PROSITE; PS0102; RRM; 1.  
 DR PROSITE; PS0030; RRM\_FNP\_1; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT 160  
 SQ SEQUENCE 160 AA; 18116 MW; 168A1FIDS5A94FS CRC64;

Query Match 72.4%; Score 42; DB 3; Length 160;  
 Best Local Similarity 87.5%; Pred. No. 4.6;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSPKGFAY 10  
 Db 58 NNPKGFAV 65

## RESULT 4

O13620 PRELIMINARY; PRT; 833 AA.  
 AC O13620;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Hypothetical 93.7 kDa protein (RNA binding protein, 5 RRM RNA  
 recognition motifs).  
 GN P1029 OR SPB22H7.02C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972 H-;  
 RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Hatakeyama J.,  
 Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,  
 Ogura K., Otsuka R., Kudoh Y., Yangida M., Machida M., Zhang M.Q.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972h-;  
 RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB004535; BAA21408.1; -  
 DR EMBL; AL590883; CAC37370.1; -  
 DR GeneDB; Spombe; SPB22H7.02C; -  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rtm; 5.  
 DR SMART; SMO0360; RRM; 5.  
 DR PROSITE; PS0102; RRM; 5.  
 DR PROSITE; PS0030; RRM\_FNP\_1; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 833 AA; 93676 MW; 64FE767D43B02FE4 CRC64;

Query Match 72.4%; Score 42; DB 3; Length 833;  
 Best Local Similarity 87.5%; Pred. No. 29;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSPKGFAY 10  
 Db 361 NNPKGFAV 368

## RESULT 5

Q98RZ7 PRELIMINARY; PRT; 389 AA.  
 AC Q98RZ7; 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Polyadenylate-binding protein.  
 GN PAB1.  
 OS Giardia theta (Cryptomonas phi).  
 OC Nucleomorph.  
 CC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 OX NCBI\_TaxID=55529;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21223349; PubMed=11333671;  
 RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,  
 Mu X., Reith M., Cavalier-Smith T., Møller U.G.;  
 RT "The highly reduced genome of an enslaved algal nucleus";

RL Nature 410:1091-1096(2001).  
 DR EMBL: AF165818; AAK39803.1; -  
 DR InterPro: IPR000504; PNA\_rec\_moc.  
 DR Pfam: PF00076; rrm; 3.  
 DR SMART: SM00360; RRM; 3.  
 DR PROSITE: PSS0102; RRM; 3.  
 DR PROSITE: PSS0030; RRM\_RNP\_1; 1.  
 SQ SEQUENCE 389 AA; 45171 MW; 72145033D37FE40D CRC64;

Query Match 70.7%; Score 41; DB 6; Length 389;  
 Best Local Similarity 70.0%; Pred. No. 19;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
 DB 222 YGNSPKGFAY 231

## RESULT 6

ID P74064 PRELIMINARY; PRT; 453 AA.  
 AC P74064;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical protein s110804.  
 GN S110804.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Baceteria; Cyanobacteria; Chroococcales; Synecocystis.  
 NCBI\_TaxId=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Aamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugita M., Saezoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90911; BAA18140.1; -  
 DR InterPro: IPR005225; Small\_GTP.  
 DR TrEMBL: TIGR00231; small\_GTP; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 453 AA; 49154 MW; 4CFDPAD77536F59 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7  
 DB 224 YGNSPKG 230

## RESULT 7

ID Q9W2J8 PRELIMINARY; PRT; 2515 AA.  
 AC Q9W2J8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE TUD protein.  
 GN TUD OR CG9450.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;  
 MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,  
 RA Jirli J.P., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burling K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Hartveit D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter R., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Waeasman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AEO03453; AAF46693.1; -  
 DR HSSP: Q16637; 1GSV.  
 DR FlyBase: FBgn0003691; tud.  
 DR InterPro: IPR001097; Maternal\_tudor.  
 DR TrEMBL: TIGR002999; Tudor.  
 DR Pfam: PF00567; TUDOR; 10.  
 DR SMART: SM00333; TUDOR; 9.  
 DR PROSITE: PSS0304; TUDOR; 9.  
 SQ SEQUENCE 2515 AA; 285264 MW; 1218700174D6701 CRC64;

Query Match 70.7%; Score 41; DB 5; Length 2515;  
 Best Local Similarity 87.5%; Pred. No. 15e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8  
 DB 2171 YGNSPKSF 2178

## RESULT 8

ID Q9VTH9 PRELIMINARY; PRT; 291 AA.  
 AC Q9VTH9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CG11726 protein.  
 GN CG11726.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed:10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratilake P.G., Scherer S.E., Li P.W., Houshens R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blaze R.G., Chape M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Bailly R.M., Basu A., Bakendahl J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fierliera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo W., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
DR EMBL: AEO03545; AAF50069.1; -.
DR FlyBase: FBgn0036156; CG11726.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; Rrm_1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS0102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 291 AA; 32307 MW; 65A1F6D3407AA699 CRC64;

Query Match 69.0%; Score 40; DB 5; Length 291;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GNSPKGFAY 10
Db 119 GRRPKGFAY 127

RESULT 9
ID Q98NH6 PRELIMINARY; PRT; 1312 AA.
AC Q98NH6;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
DE Ribonucleotide reductase.
GN MLE0136.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxId=381;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed:11214968;
RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Matsubara A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Nochiyuki Y., Nakayama S., Nakazaki N., Shiino S., Sugimoto M.,
RA Takenuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: APO02994; BAB47785.1; -.
DR InterPro: IPR000788; Ribonucleo red.
DR Pfam: PF02867; ribonuc_red_1gc; 1.
DR PRINTS: PR01183; RIBORDTASEM1.
KW Complete proteome.
SQ SEQUENCE 1312 AA; 143398 MW; 409464CB9F709F38 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 1312;
Best Local Similarity 87.5%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GNSPKGFA 9
Db 1183 GNSPKGFA 1190

RESULT 10
ID Q9KRK6 PRELIMINARY; PRT; 401 AA.
AC Q9KRK6;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Multidrug resistance protein.
GN VCI1634.
OS Vibrrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16361 / Serotype O1;
RX MEDLINE=20406833; PubMed:10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gmin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uitterlind T., Fleischmann R.D., Niemann W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RT Nature 406:477-483(2000).
RL EMBL: AEO04241; AAF94785.1; -.
DR TIGR: VCI1634; -.
DR InterPro: IPR004812; Efflux_Bcr_CFLA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR005828; Sub_transporter.
DR Pfam: PF00083; sugat_tr; 1.
DR TIGRFAMs: TIGR00710; efflux_Bcr_CFLA; 1.
DR PROSITE: PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 401 AA; 42914 MW; 814CD7A2A86E3BDB CRC64;

Query Match 67.2%; Score 39; DB 16; Length 401;
Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 YGNSPKGFAY 10
Db 251 YGVSPDGFAY 260

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## RESULT 11

Q9B2B7 PRELIMINARY; PRT; 491 AA.  
 ID Q9B2B7; (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Cytoplasmic polyadenylation element-binding protein short form.  
 GN CPB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary, and Brain;  
 RX MEDLINE=2112522; PubMed=1123249;  
 RA Halk J.F., Charlesworth A., Smith G.D., Macnicol A.M.;  
 RT Identification and characterization of the gene encoding human  
 cytoplasmic polyadenylation element binding protein.";  
 RL Gene 263:113-121 (2001).  
 DR EMBL; AF329403; AK01240.1; -  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 2  
 DR PROSITE; PS50102; RRM; 2  
 SQ SEQUENCE 491 AA; 54162 MW; 561A40FBD482262 CRC64;

Query Match 67.2%; Score 39; DB 4; Length 491;  
 Best Local Similarity 66.7%; Pred. No. 59;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
 DB 280 GNMFKGYV 288

## RESULT 12

Q9YXG5 PRELIMINARY; PRT; 559 AA.  
 ID Q9YXG5; (TREMBLrel. 10, Created)  
 AC Q9YXG5; (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ZOR-1.  
 GN ZOR1 OR ZOR-1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suzuki H., Maegawa S., Murakawa M., Hoshijima K., Shimura Y.,  
 RA Yasuda K., Inoue K.;  
 RT Identification of zebrafish maternal RNA-binding proteins, ZOR-1 and  
 RT -2."  
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AB011680; BA875637.1; -  
 DR EMBL; AB011680; BA875637.1; -  
 DR ZFIN; ZDB-GENE-990927-1; ZDBA.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS50102; RRM; 1.  
 SQ SEQUENCE 559 AA; 62255 MW; 36CF42E1AC70A377 CRC64;

Query Match 67.2%; Score 39; DB 13; Length 559;  
 Best Local Similarity 66.7%; Pred. No. 68;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
 DB 348 GNMFKGYV 356

## RESULT 13

Q9DEDS PRELIMINARY; PRT; 559 AA.  
 ID Q9DEDS; (TREMBLrel. 16, Created)  
 AC Q9DEDS; (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Cytoplasmic polyadenylation element binding protein.  
 GN CPB.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OC NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Katsu Y., Yamashita M., Ogawa K., Nagahama Y.;  
 RT Goldfish cytoplasmic polyadenylation element binding protein  
 (CPB): its interaction with CPB of cyclin B mRNA and phosphorylation  
 by cdk and Egg2 protein kinases."  
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AB044534; BAB19051.1; -  
 DR EMBL; AB044534; BAB19051.1; -  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS50102; RRM; 1.  
 SQ SEQUENCE 559 AA; 62122 MW; 05507CE5D1568144 CRC64;

Query Match 67.2%; Score 39; DB 13; Length 559;  
 Best Local Similarity 66.7%; Pred. No. 68;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
 DB 348 GNMFKGYV 356

## RESULT 14

P70166 PRELIMINARY; PRT; 561 AA.  
 ID P70166; (TREMBLrel. 02, Created)  
 AC P70166; (TREMBLrel. 02, Last sequence update)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Cytoplasmic polyadenylation element-binding protein (CPB).  
 GN CPB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Ovary;  
 RX MEDLINE=97121433; PubMed=8962099;  
 RA Gebauer F., Richter J.D.;  
 RT "Mouse cytoplasmic polyadenylation element binding protein: An  
 RT evolutionarily conserved protein that interacts with the cytoplasmic  
 RT polyadenylation elements of c-mos mRNA."  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607 (1996).  
 RL EMBL; Y08260; CAA69588.1; -  
 DR EMBL; Y08260; CAA69588.1; -  
 DR MGD; MGI:108442; Cpab.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS50102; RRM; 2.  
 SQ SEQUENCE 561 AA; 61917 MW; CB795885AB13FF6 CRC64;

Query Match 67.2%; Score 39; DB 11; Length 561;  
 Best Local Similarity 66.7%; Pred. No. 69;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
 DB 354 GNMFKGYV 362

## RESULT 15

Q9BZB8 PRELIMINARY; PRT; 566 AA.  
 ID Q9BZB8  
 AC Q9BZB8;  
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Cytoplasmic polyadenylation element-binding protein long form.  
 GN CPEB1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary, and Brain;  
 RX MEDLINE=2113222; PubMed=11223249;  
 RA Weik J.F., Charlesworth A., Smith G.D., MacNicol A.M.;  
 RT "Identification and characterization of the gene encoding human  
 cytoplasmic polyadenylation element binding protein.";  
 RU Gene 263:113-121 (2001).  
 DR EMBL; AF329402; AA01239.1; ".  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR PROSITE; PS50102; RRM; 2\_  
 SQ SEQUENCE 566 AA; 62594 MW; 9E41B5B0EC69DA87 CRC64;

Query Match 67.2%; Score 39; DB 4; Length 566;  
 Best Local Similarity 66.7%; Pred. No. 69;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GNSPKGFAY 10  
 Db 355 GNMFKGYV 363

Search completed: November 7, 2003, 07:34:27  
 Job time: 6.39773 secs



PT increasing amidolytic activity of factor IXa, and for treating blood  
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
XX  
Claim 7; Page 74; 138pp; English.  
PS  
VZ

The present sequence is that of complementarity determining region 3 (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma 13J3/MD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor IX (FIIa) activity. It is an example of anti-FIX/FIIa antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CDR3 peptide) have Factor VIIa (FVIIa) cofactor activity or FIIa activating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FIIa, even in the presence of FVIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVII or FVIIa, and in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.

[illegible]

QY	1	YGNSPKGPAY	10
Db	1	YGNSPKGPAY	10

RESULT 2
AAB20444
ID AAB20444 standard; Peptide; 16 AA

DT	21-JUN-2001	(first entry)
XX		
DE	Anti-FIX/FIXa antibody CDR3.	
DE		

XX  
KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant  
KW Factor VIII cofactor; blood coagulation disorder; haemophi  
KM haemorrhagic diathesis; haemostatic; amydolytic; therapy  
KN complementarily determining region; CDR.

Mus musculus.

FH	Key	Location/Qualifiers

FT	/note= "any amino acid"
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      /note= "any amino acid"
FT

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11000 DIFFERENCE AT
11001 /note= "any amino acid"
11002 FT

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FT      /note= "any amino acid"
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WO200119992-A2

AA PD 22-MAR-2001

13-SEP-2000: 2000WO-EP08936.

XX 14-SEP-1999: 99AT-0001576

XX  
PA (BAXT ) BAXTER AG  

PI Scheifflinger F Kerschbaum B Fajner B Dornier E  
XX

XX: WPT: 2001-290358/30

XX

PT New factor IX/factor IXa antibodies and their derivatives useful for  
PT increasing amolytic activity of factor IXa, and for treating blood  
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis -  
XX  
PS  
XX Claim 7; Page 74; 138pp; English.

CC The present sequence is that of complementarity determining  
CC region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or  
CC anti-activated Factor IX (FIXa) activity. Such antibodies  
CC and their derivatives (including those that comprise the present  
CC CDR3 peptide) have Factor VIIa (FVIIa) cofactor activity or FIXa  
CC activating activity. Administration of the antibodies or their  
CC derivatives leads to an increase in the procoagulant activity of  
CC FIXa, even in the presence of FVIIa inhibitors. This allows for  
CC rapid blood coagulation even in the absence of FVII or FVIIa, and  
CC in the case of FVII inhibitor patients. The antibodies or their  
CC derivatives are used in a claimed pharmaceutical composition for  
CC treating patients with blood coagulation disorders, especially  
CC haemophilia A and haemorrhagic diathesis.

**SD Sequence 16 AA;**

Query Match	100.0%	Score 58	DB 22	Length 16
Best Local Similarity	100.0%	Pred. No. 0.002		
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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QY      1 YGNSPKGFAY  10  
        |||||  
Db      4 YGNSPKGFAY  13
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RESULT 3  
AAB20433  
ID AAB20433 standard; Protein; 242 AA

DT	21-JUN-2001	(first entry)
XX		
DE	Anti-PIX/FIXa antibody 193/AD3 scFv	

KM Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;  
 KW Factor VII cofactor; blood coagulation disorder; haemophilia A  
 KW haemorrhagic diathesis; haemostatic; antidolytic; therapy; mouse

OS Chimeric - *Mus musculus*.

11

FT	protein	1.119
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FT	Region	98..108
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FT	Peptide	
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FT	Protein	135..242
1	Protein	135..242

FT	Region	223..231
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f1
xx
/label=CDK:

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7W-766TT0070M  
XX NF

FD-22-MAR-2001  
XX

13-SEP-2000; 2000MC-EP08936

PR 14-SEP-1999; 99AT-0001576.  
XX

PA (BAXT ) BAXTER AG.  
XX

PI Schefflinger F, Kerschbaum R, Falkner F, Dorner F;  
XX

DR WPT; 2001-290358/30.

DR N-PSDB; AAF30723.

XX New factor IX/factor IXa antibodies and their derivatives useful for  
PT increasing amidolytic activity of factor IXa, and for treating blood  
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
PS Claim 8; Fig 14; 138pp; English.

CC The present sequence is that of a single chain Fv (scFv) derivative  
CC of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain  
CC variable regions of 193/AD3 joined by an artificial, flexible linker  
CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
CC 193/AD3 VH and VL regions and cloning in vector pDAP2. 193/AD3 is  
CC an example of the invention. Anti-FIX/FIXa and their derivatives,  
CC including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor  
CC activity or FIXa activating activity. Administration leads to an  
CC increase in the procoagulant activity of FIXa, even in the presence  
CC of FVIIa inhibitors. This allows for rapid blood coagulation even  
CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
CC inhibitor patients. The antibodies and derivatives are used in a  
CC claimed pharmaceutical composition for treating patients with blood  
CC coagulation disorders, especially haemophilia A and haemorrhagic  
CC diathesis.

SQ Sequence 242 AA;

Query Match 100.0%; Score 58; DB 22; Length 242;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
|||  
Db 99 YGNSPKGFAY 108

#### RESULT 4

AB66460 standard; Protein; 626 AA.

XX AAB66460;

DT 09-APR-2001 (first entry)

XX Protein encoded by *Mycobacterium tuberculosis fad26* (RV2930) gene.

KM *Mycobacterium tuberculosis*; attenuated microorganism; fad26; RV2930;

KW signature tagged transposon mutant; mutant library;

KW mycobacterial infection; actinomycetales; antibacterial; immunostimulant;  
vaccine.

XX *Mycobacterium tuberculosis*.

OS MO200102555-A1.

PD 11-JAN-2001.

PF 06-JUL-2000; 2000MO-IB00950.

PR 06-JUL-1999; 99US-0142882.

PR 08-JUL-1999; 99US-0142833.

PA (INSP) INST PASTEUR.

PI Glacquel B, Guilhot C, Camacho L;

DR WPI; 2001-091804/10.

DR N-PSDB; AAF31627.

XX Screening a mutant library for mutants unable to grow under specific  
PT conditions and for identifying loci involved in pathogenicity,  
PT comprises using signature tagged transposon mutagenesis -

PS Example 8; Fig 5A; 159pp; English.

CC The present sequence is given in a specification relating to a method for  
CC screening a library of mutants. The method comprises constructing a  
CC library with insertions in genes and/or regulatory regions of the  
CC organisms of interest, where the insertion contains a tag and/or a  
CC transposon associated with a tag. The mutants are identified by  
CC hybridisation of the tags to known sequences. The method is useful for  
CC treating an individual suffering from a mycobacterial infection,  
CC suspected of being infected with a *Mycobacterium*, or having been  
CC exposed to an infectious *Mycobacterium*. It is also useful for  
CC identifying and isolating mutants of actinomycetales and for identifying  
CC compounds that have antibiotic activity. The method is used to identify  
CC mutants of microorganisms, preferably an actinomycetales, such as  
CC *M. tuberculosis*, *M. bovis*, *M. leprae*, *M. avium*, *M. intracellulare* and  
CC *M. paratuberculosis*, that is unable to grow under specific conditions.  
CC It is especially useful for identifying loci involved in pathogenicity.  
CC It is useful in constructing vaccines. The method can be used to screen  
CC multiple libraries concurrently. It can screen libraries of different  
CC organisms or different strains of the same organism. The present  
CC protein is encoded by a gene which is disrupted by the insertion of  
CC the IS 1096 transposon to produce an attenuated mutant of *Mycobacterium*  
CC tuberculosis.

SQ Sequence 626 AA;

Query Match 72.4%; Score 42; DB 22; Length 626;  
Best Local Similarity 77.8%; Pred. No. 60;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 9  
|||  
Db 73 YGSDPKGFAY 81

#### RESULT 5

AB66427 standard; Protein; 2515 AA.

XX AAB66427;

DT 26-MAR-2002 (first entry)

XX *Drosophila melanogaster* polypeptide SEQ ID NO 20073.

KM *Drosophila*; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS *Drosophila melanogaster*.

PN MO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001MO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PERK) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL08530.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
PT interactions -

PS Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (ABBS7737-ABR72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 2515 AA;

Query Match 70.7%; Score 41; DB 22; Length 2515;  
Best Local Similarity 87.5%; Pred. No. 3.9e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSEPKGF 8  
|||  
DB 2171 YGNSEPKGF 2178

RESULT 6  
ID ABB63366  
AC ABB63366 standard; Protein; 291 AA.

XX ABB63366;

DT 26-MAR-2002 (first entry)

DE *Drosophila melanogaster* polypeptide SEQ ID NO 16890.

KW *Drosophila*; developmental biology; cell signalling; insecticide; pharmaceutical.

OS *Drosophila melanogaster*.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li FWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07469.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

XX Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (ABBS7737-ABR72072).

XX The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

XX Sequence 291 AA;

Query Match 69.0%; Score 40; DB 22; Length 291;  
Best Local Similarity 77.8%; Pred. No. 59;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
|||  
DB 119 GNSPKGFAY 127

RESULT 7  
ID ABB08836  
AC ABB08836 standard; Protein; 116 AA.

XX ABB08836;

DT 25-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:17654.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;  
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
XX hypertension; hypothyroidism; cholesterol ester storage disease;  
XX immune deficiency; immune disorder; infectious disease;  
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
XX myasthenia gravis.

OS Homo sapiens.

PN WO200192523-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US10836.

PR 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

DR WPI; 2002-106308/14.

DR N-PSDB; ABB24588.

XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -

XX Disclosure; SEQ ID 17654; 1037pp; English.

XX The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABB15763 to ABB27252 encode the human ORFX proteins given in ABB00010 to ABB11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated syndrome in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from

CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WtO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC

XX Sequence 116 AA;

Query Match 67.2%; Score 39; DB 23; Length 116;  
 Best Local Similarity 77.8%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGNSPKGFA 9  
 DB 65 YGNSPDGFA 73

RESULT 8

AA43866  
 ID AA43866 standard; Peptide; 129 AA.

XX AA43866;

DT 11-FEB-2000 (first entry)

XX Heavy chain (VH) gene sequence of Bacillus anthracis antibody 7-1.

XX Heavy chain; VH; IGG; monoclonal antibody; spore; Bacillus;  
 XX VH gene usage; anthrax.

OS Mus sp.

XX WO9955842-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US09122.

XX 29-APR-1998; 98US-0069628.

XX (UABR-) UAB RES FOUND.

XX Kearney JF;

XX WPI; 2000-013435/01.

XX Monoclonal antibody specific for Bacillus spores, used to detect

XX anthrax -

XX Example 13; Page 53-54; 64pp; English.

XX AA43862-75 represent the amino acid sequences of the heavy chain  
 CC (VH) gene sequences from antibodies against Bacillus anthracis  
 CC spores. The antibodies are produced by different hybridomas. The  
 CC specification describes monoclonal antibodies (especially Igg  
 CC antibodies) which are highly specific and can discriminate between the  
 CC spores of the Bacillus family. The antibodies are produced by exposing  
 CC mice to Bacillus spores. The humoral immune response to Bacillus spores  
 CC shows a conservation of VH gene usage which is distinct for each spore.  
 CC Peptide fragments derived from the antibodies are also capable of  
 CC binding spores. The monoclonal antibody, and peptide fragments of it, can  
 CC be used to detect Bacillus spores in a field sample. It is particularly  
 CC uses for detecting anthrax in a field sample.

XX Sequence 129 AA;

Query Match 65.5%; Score 38; DB 21; Length 129;  
 Best Local Similarity 70.0%; Pred. No. 56;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 YGNSPKGFA 10  
 DB 77 YGNYPAWFA 86

RESULT 9  
 AB01013  
 ID AB01013 standard; Protein; 151 AA.

XX AB01013;

DT 05-SEP-2002 (first entry)

XX Human breast specific protein SEQ ID NO: 96.

XX Human, breast specific gene; breast cancer; gene therapy; breast disease;  
 XX cytoskeletal.

XX Homo sapiens.

XX WO00240672-A2.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-US45079.

XX 20-NOV-2000; 2000US-249998P.

XX 22-NOV-2000; 2000US-252563P.

XX (DIAD-) DIADEXUS INC.

XX Salceda S, Macina RA, Reclon H, Cafferkey R, Sun Y, Liu C;

XX WPI; 2002-500220/53.

XX Novel breast-specific polypeptides and polynucleotides encoding

XX polypeptide, useful for identifying, diagnosing, monitoring, staging,

XX imaging and treating breast cancer and non-cancerous disease states in

XX breast -

XX Claim 11; Page 219; 243pp; English.

XX The present invention provides human breast specific coding sequences and

XX CC proteins. These are useful for detecting breast tissue and for detecting

XX CC and treating breast cancer and other breast diseases. The present

XX CC sequence is a breast specific polypeptide of the invention.

XX Sequence 151 AA;

Query Match 63.8%; Score 37; DB 23; Length 151;  
 Best Local Similarity 75.0%; Pred. No. 99;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GNSPKGFA 9  
 DB 6 GNGPRGFA 13

XX ABB68781;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 33135.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

Pf	23-MAR-2001; 2001WO-US09231.
Xx	
Pt	23-MAR-2000; 2000US-191637P.
Dk	11-JUL-2000; 2000US-0614150.
Xx	
Xx	(PEKE ) PE CORP NY.
Pa	
Xx	
Pi	Venter JC, Adams M, Li PWD, Myers BW;
Xx	
Dr	WPI; 2001-656860/75.
Nr	N-PSDB; ABL12884.
Xx	
Pt	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
Pn	
Xx	
Ps	Disclosure; SEQ ID NO 31315; 21bp + Sequence Listing; English.
Xx	
Cc	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABSL01840-ABSL61175) and the encoded proteins (ABBS7737-ABB72072).
Cc	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Cc	
Cc	
Sq	Sequence    258 AA;
Xx	
Qy	Query Match                  63.8%; Score 37; DB 22; Length 258; Best Local Similarity        75.0%; Pred.No.1,7e+02; Matches     6; Conservative     1; Mismatches    1; Indels     0; Gaps     0;  1 YGNSPKGF 8    :-    7 -:-
Db	188 YGNAPVGF 195
Xx	
Result 11	
AAM59884	
ID	AAM59884 standard; Protein; 365 AA.
XX	
AC	AAM59884;
XX	
DT	20-NOV-1998 (first entry)
XX	
DE	Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX	
KW	Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
OS	Homo sapiens.
XX	
PN	MO9831800-A2.
XX	
PD	23-JUL-1998.
XX	
PF	21-JAN-1998; 98WO-US00960.
XX	
PR	21-JAN-1997; 97US-0034205.
XX	
PA	21-JAN-1997; 97US-0034204.
XX	
PA	(AUCC-) AUCKLAND UNISERVICES LTD.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
Pi	Feng P, Gentz RL, Kristiansen GW, Ni J, Rosen CA;
Xi	Su JY;
XX	
NR	WPI; 1998-414099/35.
NR	N-PSDB; AAV41925.

XX	New isolated polynucleotides and encoded polypeptides - used to
PT	develop products for treating e.g. inflammatory diseases,
PT	infections, immunological disorders, autoimmune diseases, allergies
XX	or tumours
PS	
XX	Claim 1; Fig 12A-12D; 120pp; English.
CC	
CC	This is the amino acid sequence of the cDNA clone Bcl-1ike (HAICH29),
CC	used in the method of the invention. The products of the clone can be
CC	used for treating conditions associated with abnormal expression of
CC	the polypeptides. They can be used for e.g. treating chronic
CC	inflammatory diseases, immunological disorders, autoimmune diseases,
CC	infectious diseases, various allergies, and as anti-infectious agents.
CC	The products can also be used for detection and diagnosis.
XX	
XX	Sequence 365 AA;
Query Match	63.8%; Score 37; DB 19; Length 365;
Best Local Similarity	60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 YGNSPKGFAY 10
Db	267 FSGHPKGFAY 276
RESULT 12	
ABG95556	
ID	ABG95556 standard; Protein; 365 AA.
XX	ABG95556;
XX	
DT	15-JAN-2003 (first entry)
XX	
DE	Human novel secreted protein gene 120 polypeptide #1.
XX	
KM	Human; secreted protein; autoimmune disease; Chemotaxis;
KM	Rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KM	liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KM	cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KM	nervous system disorders; Alzheimer's disease; infection; tissue regeneration;
KM	ocular disorder; corneal infection; wound healing; tissue regeneration;
KM	epithelial cell proliferation; organ transplantation; food additive;
KM	preservative; nutritional.
XX	
OS	Homo sapiens.
XX	
XX	US6420526-B1.
XX	
PN	16-JUL-2002.
DD	
XX	
PF	08-SEP-1998; 98US-0149476.
XX	
PR	07-MAR-1997; 97US-038621P.
PR	07-MAR-1997; 97US-040161P.
PR	07-MAR-1997; 97US-040162P.
PR	07-MAR-1997; 97US-040163P.
PR	07-MAR-1997; 97US-040331P.
PR	07-MAR-1997; 97US-040334P.
PR	07-MAR-1997; 97US-040336P.
PR	07-MAR-1997; 97US-040626P.
PR	11-APR-1997; 97US-043311P.
PR	11-APR-1997; 97US-043312P.
PR	11-APR-1997; 97US-043313P.
PR	11-APR-1997; 97US-043314P.
PR	11-APR-1997; 97US-043315P.
PR	11-APR-1997; 97US-043568P.
PR	11-APR-1997; 97US-043569P.
PR	11-APR-1997; 97US-043576P.
PR	11-APR-1997; 97US-043578P.
PR	11-APR-1997; 97US-043580P.
PR	11-APR-1997; 97US-043669P.

PR	22-AUG-1997;	97US-056909P.
PR	22-AUG-1997;	97US-056910P.
PR	22-AUG-1997;	97US-056911P.
PR	22-AUG-1997;	97US-057610P.
PR	05-SEP-1997;	97US-057650P.
PR	05-SEP-1997;	97US-057659P.
PR	12-SEP-1997;	97US-058785P.
PR	02-OCT-1997;	97US-061060P.
PR	06-MAR-1998;	98MO-US04493.
XX		
PA	(HUMA-) HUMAN GENOME SCT INC.	
XX		
PI	Ruben SM, Rosen GA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;	
PI	Endress GA, Yu G, Ni Y, Feng P, Young PE, Greene JM, Ferrie AM;	
PI	Duan R, Hu J, Florence KA, Olsen HS, Ehner R, Brewer LA;	
PI	Moore PA, Shi Y, Iafleur DM, Li Y, Zeng Z, Kyaw H,	
DR	WPI; 2002-634796/68.	
XX		
PT	New isolated human secreted protein for diagnosing, preventing,	
PT	treating or ameliorating medical conditions and used as a food additive	
PT	or preservative -	
XX		
PS	Disclosure; Column 103; 129p; English.	
XX		
CC	The invention relates to an isolated protein that is one of 186 human	
CC	secreted proteins, given in the specification, encoded by one of	
CC	309 cDNA sequences also given in the specification. The protein is used	
CC	in a pharmaceutical composition used to prevent, treat or ameliorate a	
CC	medical condition in e.g. humans, mice, rabbits, goats, horses, cats,	
CC	dogs, chickens or sheep. Disorders which are diagnosed or treated include	
CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative	
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders	
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,	
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,	
CC	infections caused by bacteria, viruses and fungi and ocular disorders	
CC	e.g. corneal infection. The polypeptides can also be used to aid wound	
CC	healing and epithelial cell proliferation, to prevent skin aging due to	
CC	sunburn, to maintain organs before transplantation, for supporting cell	
CC	culture of primary tissues, to regenerate tissues and in chemotaxis. The	
CC	polypeptides can also be used as a food additive or preservative to	
CC	increase or decrease storage capabilities, fat content, lipid, protein,	
CC	carbohydrate, vitamins, minerals, cofactors and other nutritional	
CC	components. The present sequence represents one of the novel human	
CC	secreted proteins of the invention.	
XX		
SQ	Sequence 365 AA;	
	Query Match 63.8%; Score 37; DB 23; Length 365;	
	Best Local Similarity 60.0%; Pred. No. 2.5e+02;	
	Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
OY	1 YGNSPKGPAY 10	
	:	
Db	267 FSGHPKGPAY 276	
RESULT 13		
ID	AAG02102	
XX	AAG02102 standard; Protein; 92 AA.	
AC	AAG02102;	
DT	06-OCT-2000 (first entry)	
DE	Human secreted protein, SEQ ID NO: 6183.	
KW	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;	
XX	gene therapy; chromosome mapping.	
OS	Homo sapiens.	
XX		
NN	EP1033401-A2.	

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PD XX      06-SEP-2000.
PF XX      21-FEB-2000; 200DEP-0200610.
PR XX      26-FEB-1999; 99US-0122487.
PA XX      (GEST ) GENSET.
PI XX      Dumas Milne Edwards J, Duclert A, Giordano J,
XX      WPJ; 2000-500381/45.
DR XX      N-PEDB; AAC02108.
PT XX      New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX      obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX      diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX      Claim 13; SEQ ID 6183; 71pp + CD-ROM; English.
XX
XX      The present sequence is a polypeptide encoded by one of a large number
XX      of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX      were prepared from total human RNAs or polyA+ RNAs derived from 30
XX      different tissues. EST sequences usually correspond mainly to the 3'
XX      untranslated region (UTR) of the mRNA because they are often obtained
XX      from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX      isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX      those cases where longer cDNA sequences have been obtained, the full 5'
XX      UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX      ends and can therefore be used to obtain full length cDNAs and genomic
XX      DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX      chromosome mapping procedures. They are used to obtain upstream
XX      regulatory sequences and to design expression and secretion vectors.
XX
SQ      Sequence    92 AA;

Query Match       62.1%; Score 36; DB 21; Length 92;
Best Local Similarity 60.0%; Pred. NO. 88;
Matches     6; Conservative   1; Mismatches     3; Indels    0; Gaps    0.

QY      1 YGNSPKGFAY 10
        | | | | |
Db      46 YTRRRGRFAY 55

RESULT 14
ID ABP03818
ABP03818 standard; Protein; 117 AA.
XX
XX ABP03818;
XX
XX 24-JUN-2002 (First entry)
XX
XX Human ORFX protein sequence SEQ ID NO:7618.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX      hyperproliferative disorder; peritiasis; benign tumour; hemorrhage;
XX      degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX      cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX      hypertension; hypothyroidism; cholesterol ester storage disease;
XX      immune deficiency; immune disorder; infectious disease;
XX      autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX      myasthenia gravis.
XX
XX Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001MO-US10836.
XX
XX 30-MAY-2000; 2000US-206132P.

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PR	29-NOV-2000; 2000US-228716P.
XX	(CIPA-) CURAGEN CORP.
PA	Shimkels PA, Leach MD;
P1	MPI: 2002-106308/14.
DR	N-PDSB; ABN19570.
XX	Novel human polypeptides and polynucleotides useful for diagnosing,
PT	preventing and treating cardiovascular disease, neurodegenerative,
PR	hyperproliferative disorders and autoimmune disorders -
PS	Disclosure; SEQ ID 7618; 1037bp; English.
CC	The present invention describes substantially purified human proteins
CC	(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC	in the specification)). ABN15762 to ABN27252 encode the human ORFX
CC	proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC	treating or preventing a pathology associated with an ORFX-associated
CC	disorder in humans, and in the manufacture of a medicament for treating a
CC	syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC	sequences can be used in gene therapy. ORFX sequences can be used in the
CC	treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC	psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC	osteoarthritis, neurodegenerative disorders, disorders related to organ
CC	transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC	lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC	storage disease, various immune deficiencies and disorders, infectious
CC	diseases, autoimmune thyroiditis such as multiple sclerosis, rheumatoid
CC	arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC	disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC	useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC	bone degenerative disorders, or periodontal disease, and for gut
CC	protection or regeneration and treatment of lung or liver fibrosis,
CC	reflexion injury in various tissues and conditions resulting from
CC	systemic cytokine damage.
CC	N.B. The sequence date for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 117 AA;
SQ	
Dd	Query Match 62.1%; Score 36; DB 23; Length 117;
CY	Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Db	Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	1 YGNSPKGF 8
	43 YGNSPSGF 50
RESULT 15	
ID	ABG00681
AB	ABG00681 standard; Protein; 118 AA.
XX	ABG00681;
AC	
DT	13-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #672.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder.
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
FE	30-MAR-2001; 2001MO-US08631.
XX	

PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.

PA (HSEB-) HSEB INC.

PI Drmanac RT, Liu C, Tang YT;

XX MPI: 2001-639362/73.

DR N-PDB: AAG64868.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

XX Claim 20; SEQ ID No 31040; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAG00010-AB030377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 118 AA;

Query Match 62.1%; Score 36; DB 22; Length 118;

Best Local Similarity 60.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10

DB 46 YTRRRPGFAY 55

Search completed: November 7, 2003, 07:26:56  
Job time : 5.31242 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 8.7717 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992b-5

Perfect score: 58

Sequence: 1 YGNSPKGFAY 10

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\*

Listing first 45 summaries

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Published Applications NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	63.8	151	US-10-001-887-96	Sequence 96, Appl
2	37	63.8	249	US-10-153-668-118	Sequence 118, Appl
3	37	63.8	306	US-10-153-668-120	Sequence 118, Appl
4	37	63.8	365	US-09-809-391-696	Sequence 696, Appl
5	37	63.8	365	US-09-882-171-696	Sequence 696, Appl
6	36	62.1	373	US-10-219-220-285	Sequence 285, Appl
7	36	62.1	396	US-10-219-220-153	Sequence 153, Appl
8	35	62.1	1038	US-10-156-761-1315	Sequence 1315, A
9	35	60.3	524	US-10-032-585-7154	Sequence 7154, A
10	35	60.3	1197	US-10-884-668-12	Sequence 12, Appl
11	35	60.3	1257	US-09-738-626-4750	Sequence 4750, A
12	34	58.6	9	US-09-852-870A-12	Sequence 12, Appl
13	34	58.6	200	US-09-764-864-953	Sequence 953, Appl
14	34	58.6	284	US-09-769-787-40	Sequence 40, Appl
15	34	58.6	324	US-10-272-419-18	Sequence 18, Appl

16	34	58.6	443	US-09-801-368-174	Sequence 174, Appl
17	34	58.6	839	US-10-231-035-6	Sequence 6, Appl
18	34	58.6	929	US-10-156-761-14135	Sequence 14135, A
19	33	56.9	128	US-09-530-139-16	Sequence 16, Appl
20	33	56.9	144	US-09-886-429-4	Sequence 4, Appl
21	33	56.9	144	US-10-041-406-5	Sequence 5, Appl
22	33	56.9	144	US-10-162-435-23	Sequence 23, Appl
23	33	56.9	144	US-10-162-435-30	Sequence 30, Appl
24	33	56.9	222	US-09-728-914-16	Sequence 16, Appl
25	33	56.9	222	US-09-530-139-46	Sequence 36, Appl
26	33	56.9	238	US-09-530-139-36	Sequence 40, Appl
27	33	56.9	239	US-09-530-139-40	Sequence 44, Appl
28	33	56.9	250	US-09-530-139-44	Sequence 11743, A
29	33	56.9	340	US-09-815-242-11743	Sequence 7314, A
30	33	56.9	748	US-10-032-585-7314	Sequence 11464, A
31	33	56.9	855	US-10-156-761-11464	Sequence 7923, A
32	33	56.9	927	US-10-032-585-7923	Sequence 5207, A
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35	32	55.2	238	US-10-195-117-3	Sequence 1383, A
36	32	55.2	238	US-10-195-117-4	Sequence 8843, A
37	32	55.2	243	US-10-156-761-9592	Sequence 138, Appl
38	32	55.2	297	US-10-238-075-1383	Sequence 11430, A
39	32	55.2	388	US-10-156-761-8843	Sequence 11585, A
40	32	55.2	394	US-09-853-386-33	Sequence 16, Appl
41	32	55.2	396	US-09-801-368-138	
42	32	55.2	420	US-09-815-242-11430	
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44	32	55.2	438	US-10-121-032-16	
45	32	55.2	438	US-10-093-037-16	

## ALIGNMENTS

RESULT 1  
US-10-001-887-96  
; Sequence 96, Application US/10001887  
; Publication No. US2002015546A1  
; GENERAL INFORMATION:  
; APPLICANT: Salceda, Susana  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Heirve  
; APPLICANT: Cafferkey, Robert  
; APPLICANT: Sun, Yongming  
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Gen  
; FILE REFERENCE: DEX-0269  
; CURRENT APPLICATION NUMBER: US/10/001,887  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/249,998  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/252,563  
; PRIOR FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 96  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-001-887-96

Query Match  
Best Local Similarity 63.8%; Score 37; DB 14; Length 151;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFA 9  
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Db 6 GNSPKGFA 13

RESULT 2  
US-10-153-668-118

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; Sequence 118, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-118
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Query Match          63.8%; Score 37; DB 15; Length 249;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      1 YGNSPKGFAY 10
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Db      151 FSGHPKGFAY 160
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US-10-153-668-120
; Sequence 120, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-120
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Best Local Similarity 60.0%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Db      208 FSGHPKGFAY 217
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US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
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; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696
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Query Match          63.8%; Score 37; DB 11; Length 365;
Best Local Similarity 60.0%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Db      267 FSGHPKGFAY 276
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US-09-882-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
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; PRIOR FILING DATE: 1997-03-07
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
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53	PRIOR APPLICATION NUMBER: 60/048, 974
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PRIOR FILING DATE:	1997-08-22

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PRIOR FILING DATE: 1997-08-22  
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PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,875  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,862  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,887  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,908  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/048,964  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/057,650  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/056,884  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/057,669  
PRIOR FILING DATE: 1997-09-05

Query Match 63.8%; Score 37; DB 12; Length 365;  
Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
DB 267 FSGHPKGFAY 276

RESULT 6  
US-10-219-220-285  
Sequence 285, Application US/10219220  
Publication No. US20030082724A1  
GENERAL INFORMATION:  
APPLICANT: Flynn, Barry  
TITLE OF INVENTION: Compositions affecting programmed cell  
TITLE OF INVENTION: death and their use in the modification of plant development  
FILE REFERENCE: 11000.1022c1  
CURRENT APPLICATION NUMBER: US/10/219,220  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 285  
LENGTH: 373  
TYPE: PRT  
ORGANISM: Pinus radiata  
US-10-219-220-285

Query Match 62.1%; Score 36; DB 15; Length 373;  
Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
DB 305 YGKSPGEGIN 314

RESULT 7  
US-10-219-220-153  
Sequence 153, Application US/10219220  
Publication No. US20030082724A1  
GENERAL INFORMATION:  
APPLICANT: Flynn, Barry  
TITLE OF INVENTION: Compositions affecting programmed cell  
TITLE OF INVENTION: death and their use in the modification of plant development  
FILE REFERENCE: 11000.1022c1  
CURRENT APPLICATION NUMBER: US/10/219,220  
CURRENT FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 153  
LENGTH: 396  
TYPE: PRT  
ORGANISM: Pinus radiata  
US-10-219-220-153

Query Match 62.1%; Score 36; DB 15; Length 396;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
DB 328 YGKSPGEGIN 337

RESULT 8  
US-10-156-761-13515  
Sequence 13515, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272657  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 13515  
LENGTH: 1038  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-13515

Query Match 62.1%; Score 36; DB 15; Length 1038;  
Best Local Similarity 75.0%; Pred. No. 5.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8  
DB 254 YGHPKGF 261

RESULT 9  
US-10-032-585-7154  
Sequence 7154, Application US/10032585  
Publication No. US20030180953A1  
GENERAL INFORMATION:  
APPLICANT: Terry, Roemer D.  
APPLICANT: Bo, Jiang  
APPLICANT: Charles, Boone  
APPLICANT: Howard, Bussey  
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
FILE REFERENCE: 10182-005-999  
CURRENT APPLICATION NUMBER: US/10/032,585  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 8000  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7154  
LENGTH: 521  
TYPE: PRT

ORGANISM: Candida albicans  
US-10-032-585-7154

Query Match 60.3%; Score 35; DB 12; Length 521;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8  
DB 225 YGESPPGF 232

RESULT 10  
US-10-284-668-12

Sequence 12, Application US/10284668  
Publication No. US20030106100A1

GENERAL INFORMATION:

APPLICANT: Kossmann, Jens  
Springer, Franziska

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/284,668

FILING DATE: 29-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-JUL-1997

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995

APPLICATION NUMBER: DE P 44 41 408.0

FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: Agrevo-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9000

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1197 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-284-668-12

Query Match 60.3%; Score 35; DB 15; Length 1197;

Best Local Similarity 85.7%; Pred. No. 9e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8  
DB 45 GSSPKGF 51

RESULT 11

US-09-738-626-4750  
Sequence 4750, Application US/09738626  
Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO

APPLICANT: HAYASHI, MIKIO

APPLICANT: OCHIAI, KEIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: TATEISHI, NAOKO

APPLICANT: SENOH, AKIHIRO

APPLICANT: IKEDA, MASATO

APPLICANT: OKAZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7053

SOFTWARE: Patentin ver. 3.0

SEQ ID NO 4750

LENGTH: 1257

TYPE: PRT

ORGANISM: Corynebacterium glutamicum

US-09-738-626-4750

Query Match 60.3%; Score 35; DB 10; Length 1257;

Best Local Similarity 50.0%; Pred. No. 9.5e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGF 10  
DB 883 FANTPEGFNY 892

RESULT 12

US-09-852-870A-12

Sequence 12, Application US/09852870A

Patent No. US20020165132A1

GENERAL INFORMATION:

APPLICANT: Goodman, Murray

APPLICANT: Osapay, George

TITLE OF INVENTION: Lanthionin Bridged Proteins

FILE REFERENCE: LKR 9122-D

CURRENT APPLICATION NUMBER: US/09/852,870A

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: US 09/384,601

PRIOR FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Cys-Ser Lanthionine bridge

US-09-852-870A-12

Query Match 58.6%; Score 34; DB 10; Length 9;

Best Local Similarity 71.4%; Pred. No. 5.8e+05;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7  
DB 3 FGNSPKG 9

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RESULT 13
US-09-764-864-953
; Sequence 953, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 953
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-953

Query Match
Best Local Similarity 58.6%; Score 34; DB 10; Length 200;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSPKGF 8
Db 34 NSPKGF 39

RESULT 14
US-09-769-787-40
; Sequence 40, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PNC/P21129MO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-40

Query Match
Best Local Similarity 58.6%; Score 34; DB 11; Length 284;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
Db 42 GDTVKGFAF 50

RESULT 15
US-10-272-419-18
; Sequence 18, Application US/10272419
; Publication No. US20030087403A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419

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; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-18

Query Match
Best Local Similarity 58.6%; Score 34; DB 15; Length 324;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
Db 31 FSNTPKGF 38

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 Job time: 10.7717 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 1.46862 Seconds  
(without alignments)

288.098 Million cell updates/sec

Title: US-09-661-992B-5

Perfect score: 58

Sequence: 1 YGNSEKGPAY 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/aa/6A.COMB.pdb:\*  
4: /cgn2\_6/ptodata/1/aa/6B.COMB.pdb:\*  
5: /cgn2\_6/ptodata/1/aa/PCITUS.COMB.pdb:\*  
6: /cgn2\_6/ptodata/1/aa/backfilest.pdb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	63.8	365	4	US-09-149-476-696
2	37	63.8	426	4	US-09-252-991A-32215
3	36	62.1	149	4	US-09-252-991A-19973
4	36	62.1	396	4	US-09-325-932A-153
5	35	62.1	484	4	US-09-134-001C-5402
6	35	60.3	474	4	US-09-252-991A-29381
7	35	60.3	1197	3	US-08-836-567-12
8	35	60.3	1197	4	US-09-606-304-12
9	35	60.3	1230	2	US-08-968-542C-35
10	35	60.3	1257	2	US-08-750-152A-2
11	34	58.6	9	3	US-08-467-472C-12
12	34	58.6	9	3	US-09-384-064-12
13	34	58.6	111	4	US-08-858-207A-64
14	34	58.6	263	5	PCT-US94-00844-11
15	34	58.6	324	4	US-09-648-004-18
16	34	58.6	334	4	US-09-107-532A-6336
17	34	58.6	402	4	US-09-134-001C-1138
18	33	56.9	410	4	US-09-252-991A-11004
19	33	56.9	434	4	US-09-198-452A-118
20	33	56.9	34	3	US-08-441-507-27
21	32	55.2	34	4	US-07-969-875A-17
22	32	55.2	74	3	US-08-441-507-11
23	32	55.2	74	4	US-07-969-875A-11
24	32	55.2	78	3	US-08-441-507-13
25	32	55.2	78	3	US-08-441-507-14
26	32	55.2	78	4	US-07-969-875A-13
27	32	55.2	78	4	US-07-969-875A-14

#### ALIGNMENTS

RESULT 1	US-09-149-476-696	Sequence 696, App	Sequence 15, App1
Sequence 696, Application US/09149476	Patent No. 6420526	Sequence 3215, A	Sequence 31838, A
GENERAL INFORMATION:	APPLICANT: Rosen et al.	Sequence 19973, A	Sequence 57, App1
TITLE OF INVENTION: 186 Human Secreted proteins	FILE REFERENCE: P2002P1	Sequence 153, App	Sequence 3702, App1
CURRENT APPLICATION NUMBER: US/09/149, 476	EARLIER FILING DATE: 1997-03-07	Sequence 5402, App	Sequence 30103, A
EARLIER APPLICATION NUMBER: PCT/US98/04493	EARLIER FILING DATE: 1997-03-07	Sequence 29391, A	Sequence 21, App1
EARLIER FILING DATE: 1997-03-06	EARLIER APPLICATION NUMBER: 60/040, 162	Sequence 12, App1	Sequence 32, App1
EARLIER APPLICATION NUMBER: 60/040, 162	EARLIER FILING DATE: 1997-03-07	Sequence 35, App1	Sequence 5008, App
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/040, 333	Sequence 12, App1	Sequence 15, App1
EARLIER APPLICATION NUMBER: 60/038, 621	EARLIER FILING DATE: 1997-03-07	Sequence 12, App1	Sequence 26771, A
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/040, 626	Sequence 35, App1	Sequence 2, App1
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/040, 334	Sequence 12, App1	Sequence 16, App1
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/040, 336	Sequence 12, App1	Sequence 5048, App
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/040, 163	Sequence 12, App1	Sequence 2, App1
EARLIER FILING DATE: 1997-03-07	EARLIER APPLICATION NUMBER: 60/047, 600	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 615	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 597	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 502	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 633	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 583	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 617	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 618	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 503	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 592	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 581	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 584	Sequence 12, App1	
EARLIER FILING DATE: 1997-05-23			

Fri Nov 7 09:40:10 2003

us-09-661-992b-5.ral

Page 2

1	EARLIER	APPLICATION NUMBER: 60/04/7,500
2	EARLIER	FILING DATE: 1997-05-23
3	EARLIER	APPLICATION NUMBER: 60/04/7,588
4	EARLIER	FILING DATE: 1997-05-23
5	EARLIER	APPLICATION NUMBER: 60/04/7,492
6	EARLIER	FILING DATE: 1997-05-23
7	EARLIER	APPLICATION NUMBER: 60/04/7,598
8	EARLIER	FILING DATE: 1997-05-23
9	EARLIER	APPLICATION NUMBER: 60/04/7,613
10	EARLIER	FILING DATE: 1997-05-23
11	EARLIER	APPLICATION NUMBER: 60/04/7,582
12	EARLIER	FILING DATE: 1997-05-23
13	EARLIER	APPLICATION NUMBER: 60/04/7,596
14	EARLIER	FILING DATE: 1997-05-23
15	EARLIER	APPLICATION NUMBER: 60/04/7,612
16	EARLIER	FILING DATE: 1997-05-23
17	EARLIER	APPLICATION NUMBER: 60/04/7,632
18	EARLIER	FILING DATE: 1997-05-23
19	EARLIER	APPLICATION NUMBER: 60/04/7,601
20	EARLIER	FILING DATE: 1997-05-23
21	EARLIER	APPLICATION NUMBER: 60/04/7,580
22	EARLIER	FILING DATE: 1997-04-11
23	EARLIER	APPLICATION NUMBER: 60/04/7,568
24	EARLIER	FILING DATE: 1997-04-11
25	EARLIER	APPLICATION NUMBER: 60/04/7,314
26	EARLIER	FILING DATE: 1997-04-11
27	EARLIER	APPLICATION NUMBER: 60/04/7,565
28	EARLIER	FILING DATE: 1997-04-11
29	EARLIER	APPLICATION NUMBER: 60/04/7,311
30	EARLIER	FILING DATE: 1997-04-11
31	EARLIER	APPLICATION NUMBER: 60/04/7,611
32	EARLIER	FILING DATE: 1997-04-11
33	EARLIER	APPLICATION NUMBER: 60/04/7,674
34	EARLIER	FILING DATE: 1997-04-11
35	EARLIER	APPLICATION NUMBER: 60/04/7,669
36	EARLIER	FILING DATE: 1997-04-11
37	EARLIER	APPLICATION NUMBER: 60/04/7,312
38	EARLIER	FILING DATE: 1997-04-11
39	EARLIER	APPLICATION NUMBER: 60/04/7,313
40	EARLIER	FILING DATE: 1997-04-11
41	EARLIER	APPLICATION NUMBER: 60/04/7,672
42	EARLIER	FILING DATE: 1997-04-11
43	EARLIER	APPLICATION NUMBER: 60/04/7,315
44	EARLIER	FILING DATE: 1997-04-11
45	EARLIER	APPLICATION NUMBER: 60/04/7,974
46	EARLIER	FILING DATE: 1997-06-06
47	EARLIER	APPLICATION NUMBER: 60/05/7,866
48	EARLIER	FILING DATE: 1997-08-22
49	EARLIER	APPLICATION NUMBER: 60/05/7,877
50	EARLIER	FILING DATE: 1997-08-22
51	EARLIER	APPLICATION NUMBER: 60/05/7,889
52	EARLIER	FILING DATE: 1997-08-22
53	EARLIER	APPLICATION NUMBER: 60/05/7,893
54	EARLIER	FILING DATE: 1997-08-22
55	EARLIER	APPLICATION NUMBER: 60/05/7,630
56	EARLIER	FILING DATE: 1997-08-22
57	EARLIER	APPLICATION NUMBER: 60/05/7,878
58	EARLIER	FILING DATE: 1997-08-22
59	EARLIER	APPLICATION NUMBER: 60/05/7,662
60	EARLIER	FILING DATE: 1997-08-22
61	EARLIER	APPLICATION NUMBER: 60/05/7,872
62	EARLIER	FILING DATE: 1997-08-22
63	EARLIER	APPLICATION NUMBER: 60/05/7,888
64	EARLIER	FILING DATE: 1997-08-22
65	EARLIER	APPLICATION NUMBER: 60/05/7,879
66	EARLIER	FILING DATE: 1997-08-22
67	EARLIER	APPLICATION NUMBER: 60/05/7,880

[illegible]

EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 63.8%; Score 37; DB 4; Length 365;  
Best Local Similarity 60.0%; Pred. No. 51;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
DB 267 FSGHPKGFAY 276

RESULT 2  
US-09-252-991A-32215  
Sequence 32215, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 32215  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32215

Query Match 63.8%; Score 37; DB 4; Length 426;  
Best Local Similarity 66.7%; Pred. No. 60;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9  
DB 233 YANHPRGFA 241

RESULT 3  
US-09-252-991A-19973

Sequence 19973, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 19973  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19973

Query Match 62.1%; Score 36; DB 4; Length 149;  
Best Local Similarity 66.7%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9  
DB 141 YGONPKGIA 149

RESULT 4  
US-09-325-932A-153

Sequence 153, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:

APPLICANT: Flinn, Barry  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 153  
LENGTH: 396  
TYPE: PRT  
ORGANISM: Pinus radiata  
US-09-325-932A-153

Query Match 62.1%; Score 36; DB 4; Length 396;  
Best Local Similarity 60.0%; Pred. No. 83;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10  
DB 328 YGKSPGGINY 337

RESULT 5  
US-09-134-001C-5402

Sequence 5402, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5402  
LENGTH: 484  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5402

Query Match 62.1%; Score 36; DB 4; Length 484;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9  
DB 353 FGNPSGIA 361

RESULT 6  
US-09-252-991A-29391

Sequence 29391, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDO  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 29391  
LENGTH: 474  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29391

Query Match 60.3%; Score 35; DB 4; Length 474;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSPKGFA 9  
Db 245 NAKGFA 251

## RESULT 7

US-08-836-567-12  
Sequence 12, Application US/08836567  
Patent No. 6130367  
GENERAL INFORMATION:  
APPLICANT: Kossmann, Jens  
APPLICANT: Springer, Franziska  
APPLICANT: Abel, Gernot  
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,567  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04415  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: Agrevo-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-567-12

Query Match 60.3%; Score 35; DB 3; Length 1197;

Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8  
Db 45 GSSPKGF 51

## RESULT 8

US-09-606-304-12  
Sequence 12, Application US/09606304  
Patent No. 6483010  
GENERAL INFORMATION:  
APPLICANT: Kossmann, Jens  
APPLICANT: Springer, Franziska  
APPLICANT: Abel, Gernot  
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRAN  
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/606,304  
FILING DATE: 28-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,567  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: Agrevo-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-606-304-12

Query Match 60.3%; Score 35; DB 4; Length 1197;  
Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8  
Db 45 GSSPKGF 51

## RESULT 9

US-08-968-542C-35  
Sequence 35, Application US/08968542C  
Patent No. 5981728  
GENERAL INFORMATION:  
APPLICANT: Myers, et al.  
TITLE OF INVENTION: dulla Codes For A No. 5981728el Starch

```

; TITLE OF INVENTION: Synthase
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 6.0.1 for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,542C
; FILING DATE: No. 5981728member 12, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D6036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1230 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: amino acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; US-08-968-542C-35

Query Match      60.3%; Score 35; DB 2; Length 1230;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GNSPKGF 8
Db      78 GSSPKGF 84

RESULT 10
US-08-750-152A-2
; Sequence 2, Application US/08750152A
; Patent No. 5977331
; GENERAL INFORMATION:
; APPLICANT: ASAKURA, YOKO
; APPLICANT: KIMURA, KICHIRO
; APPLICANT: ABE, CHIZU
; APPLICANT: KAWAHARA, YOSHIO
; APPLICANT: NAKAMATSU, TSUYOSHI
; TITLE OF INVENTION: ALPHA-KETOSULFURATE DEHYDROGENASE GENE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq Version 1.5
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,152A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-750-152A-2

Query Match      60.3%; Score 35; DB 2; Length 1257;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 YGNSPKGFAY 10
Db      883 YANTPEGFNY 892

RESULT 11
US-08-467-472C-12
; Sequence 12, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" floppy disc
; COMPUTER: COMPAC - IBM compatible
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LXR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
```

DESCRIPTION: PEPTIDE  
HYPOTHETICAL: N/A  
ANTI-SENSE: N/A  
FRAGMENT TYPE: INTERNAL  
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
ORIGINAL SOURCE: INC.,  
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104  
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE  
POSITION IN GENOME: N/A  
FEATURES:  
NAME/KEY: N/A  
LOCATION: N/A  
IDENTIFICATION METHOD: N/A  
OTHER INFORMATION: water is removed and  
OTHER INFORMATION: thereby  
OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
PUBLICATION INFORMATION:  
AUTHORS: JUNG, GUNTHER  
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
VOLUME: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 865 - 869  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: SHIBA, TETSUO  
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
JOURNAL: BIOPOLYMERS  
VOLUME: JOHN WILEY AND SONS, INC.  
ISSUE: SUPPLEMENTARY  
PAGES: 511 - 519  
DATE: 1986  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: BEAN, MARK F.  
TITLE: IDENTIFICATION OF A THIOETHER  
TITLE: BY-PRODUCT  
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
TITLE: BY  
TITLE: TANDEM MASS SPECTROMETRY  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
VOLUME: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 443 - 445  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
US-08-467-472C-12

Query Match 58.6%; Score 34; DB 3; Length 9;  
Best Local Similarity 71.4%; Pred. No. 2.5e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNSPRG 7  
DB 3 FNSPRG 9

RESULT 12

US-09-384-061-12  
Sequence 12, Application US/09384061  
Patent No. 6268339  
GENERAL INFORMATION:  
APPLICANT: GOODMAN, MURRAY  
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BROOKS HAIDT HAFNER & DELAUNTY  
STREET: 99 PARK AVENUE  
CITY: NEW YORK  
STATE: NY  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" FLOPPY DISC  
COMPUTER: COMPAQ - IBM COMPATIBLE  
OPERATING SYSTEM: MS-DOS Version 6.2  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/384,061  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,472  
FILING DATE:  
APPLICATION NUMBER: US 08/021,606  
FILING DATE: 28-JANUARY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINSON, WILLIAM R.  
REGISTRATION NUMBER: 27,224  
REFERENCE/DOCKET NUMBER: LKR-9122B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 697-3355  
TELEFAX: (212) 557-5635  
TELEX: NONE  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
HYPOTHETICAL: N/A  
ANTI-SENSE: N/A  
FRAGMENT TYPE: INTERNAL  
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
ORIGINAL SOURCE: INC.,  
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104  
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY: N/A  
LOCATION: N/A  
IDENTIFICATION METHOD: N/A  
OTHER INFORMATION: water is removed and  
OTHER INFORMATION: thereby  
OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
PUBLICATION INFORMATION:  
AUTHORS: JUNG, GUNTHER  
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
VOLUME: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 865 - 869  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
PUBLICATION INFORMATION:

AUTHORS: SHIBA, TETSUO  
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
JOURNAL: BIOPOLYMERS  
VOLUME: JOHN WILEY AND SONS, INC.  
ISSUE: SUPPLEMENTARY  
PAGES: 511 - 519  
DATE: 1986  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: BEAN, MARK F.  
TITLE: IDENTIFICATION OF A THIOETHER  
TITLE: BY-PRODUCT  
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
TITLE: BY  
JOURNAL: TANDEN MASS SPECTROMETRY  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
JOURNAL: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 443 - 445  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER  
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
US-09-384-061-12

Query Match 58.6%; Score 34; DB 3; Length 9;  
Best Local Similarity 71.4%; Pred. No. 2.5e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7  
Db 3 FGNSPRG 9

RESULT 13  
US-08-858-207A-464  
Sequence 464, Application US/08858207A  
Patent No. 6348328  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Nicholas, Richard  
APPLICANT: Stodola, Robert  
TITLE OF INVENTION: No. 6348328e1 Compounds  
NUMBER OF SEQUENCES: 552  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SmitKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A  
FILING DATE: 09-May-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-May-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 464:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6348328e  
US-08-858-207A-464

Query Match 58.6%; Score 34; DB 4; Length 111;  
Best Local Similarity 66.7%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10  
Db 42 GDTYKGFAY 50

RESULT 14  
PCT-US94-00844-11  
Sequence 11, Application PC/TUS9400844  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method of Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
PATENTIN Release #1.0, Version #1.25 (EPO)  
APPLICATION NUMBER: PCT/US94/00844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/010403  
FILING DATE: 29-JAN-1993  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-00844-11

Query Match 58.6%; Score 34; DB 5; Length 263;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGF 8  
Db 69 GNSPKGF 75

RESULT 15  
US-09-648-004-18  
Sequence 18, Application US/09648004  
Patent No. 6498242  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
FILE REFERENCE: CL-1341-A  
CURRENT APPLICATION NUMBER: US/09/648,004

; CURRENT FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/252,553  
 ; PRIOR FILING DATE: 1999-02-19  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO: 18  
 ; LENGTH: 324  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter sp.  
 US-09-648-004-18

Query Match 58.6%; Score 34; DB 4; Length 324;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 YGNSPKGF 8  
 : |||||  
 Db 31 PSNTPKGF 38

Search completed: November 7, 2003, 07:30:05  
 Job time : 2.46862 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 1.55407 Seconds

(without alignment)  
742.581 Million cell updates/sec

Title: US-09-661-992B-6  
Perfect score: 72  
Sequence: 1 DGHGYSFPDY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	69.4	173	TS1469	glycine/proline-ri
2	47	65.3	205	F87623	hypothetical prote
3	44	61.1	456	D95384	protein (imported
4	44	61.1	475	C64757	probable iron-sulf
5	44	61.1	475	A90672	hypothetical prote
6	44	61.1	475	E85522	hypothetical prote
7	43	59.7	35	E83824	hypothetical prote
8	43	59.7	215	T17207	hypothetical prote
9	43	59.7	235	T33380	hypothetical prote
10	43	59.7	304	T02651	lysophospholipase
11	42	58.3	390	T48524	lysophospholipase
12	42	58.3	1163	T28808	hypothetical prote
13	41	56.9	492	A84863	probable carboxyph
14	41	56.9	702	S40904	FUN2 protein - yea
15	40	55.6	25	PH1733	Ig heavy chain V r
16	40	55.6	33	PH1738	Ig heavy chain V r
17	40	55.6	33	PH1742	Ig heavy chain V r
18	40	55.6	33	PH1739	Ig heavy chain V r
19	40	55.6	80	B45466	glycine/tyrosine-r
20	40	55.6	83	A45466	glycine/tyrosine-r
21	40	55.6	109	PH0973	Ig heavy chain V r
22	40	55.6	126	G1HUKL	Ig heavy chain V r
23	40	55.6	137	H32513	Ig heavy chain pre
24	40	55.6	139	T04310	strong gravity str
25	40	55.6	157	G01859	RNA binding motif
26	40	55.6	286	A45350	matrix protein M1
27	40	55.6	289	F96770	protein RNA-bindin
28	40	55.6	290	C27115	k-kininogen, LMM p
29	40	55.6	315	A27115	major acute phase

30	40	55.6	328	2	H87535	hypothetical prote
31	40	55.6	373	2	E84647	hypothetical prote
32	40	55.6	378	2	T49164	zinc transporter-1
33	40	55.6	404	2	B84745	probable RNA-bindi
34	40	55.6	405	2	T49963	hypothetical prote
35	39	54.2	1227	2	D69798	conserved hypochet
36	39	54.2	94	2	S06612	chorion protein s1
37	39	54.2	111	2	S25047	Ig heavy chain V r
38	39	54.2	211	2	E71334	hypothetical prote
39	39	54.2	273	2	AH2432	hypothetical prote
40	39	54.2	313	2	A35699	synaptophysin - hu
41	39	54.2	321	2	AC0821	probable exported
42	39	54.2	353	1	S56750	single stranded D
43	39	54.2	385	2	D41732	heterogeneous nuc1
44	39	54.2	399	2	B83398	hypothetical prote
45	39	54.2	480	2	D83086	conserved hypochet

## ALIGNMENTS

RESULT 1  
TS1469  
glycine/proline-rich protein - Arabidopsis thaliana  
N: Alternate names: protein K10A8\_130  
C: Species: Arabidopsis thaliana (mouse-ear cress)  
C: Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C: Accession: TS1469  
R: Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asanuma, E.; Kotani, H.; Tabata  
submitted to the Protein Sequence Database, August 2000  
A: Reference number: Z25394  
A: Accession: TS1469  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-173 <SAT>  
A: Cross-references: EMBL:AL391151  
C: Genetics:  
A: Experimental source: cultivar Columbia; BAC clone K10A8  
A: Map position: 5  
A: Introns: 97/1  
A: Note: K10A8\_130

Query Match  
Best Local Similarity 69.4%; Score 50; DB 2; Length 173;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GHGYSFPDY 12  
Db 36 GHGYSFPDY 45

RESULT 2  
F87623  
hypothetical protein CC3024 (imported) - Caulobacter crescentus  
C: Species: Caulobacter crescentus  
C: Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C: Accession: F87623  
R: Heide, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heide  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A: Title: Complete Genome Sequence of Caulobacter crescentus.  
A: Reference number: A87249; MIMD:21173698; PMID:11259647  
A: Accession: F87623  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-205 <STO>  
A: Cross-references: GB:AB005673; NID:gl3424664; PIND:AAK24986.1; GSPDB:GN00148  
C: Genetics:  
A: Gene: CC3024

Query Match 65.3%; Score 47; DB 2; Length 205;  
Best Local Similarity 70.0%; Pred. No. 3;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 GGGYSSFDY 12  
 |||||:  
 Db 163 GGGYGYDY 172

## RESULT 3

D95384  
 protein [imported] - *Sinorhizobium meliloti* (strain 1021) magaplasmid pSyma  
 C:Species: *Sinorhizobium meliloti*  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: D95384  
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower, J.; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*  
 A:Reference number: A95262; MUID:21396509; PMID:11461432  
 A:Accession: D95384  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-456 <KDR>  
 A:Cross-references: GB:AE006469; PIDN:AA65638.1; PID:914524124; GSPDB:GN00165  
 A:Experimental source: strain 1021, megaplasmid pSyma  
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kise, B.; Komp, C.; Lelaur, P.; Vandenbol, M.; Vorpolder, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.  
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: SMA1776  
 A:Genome: plasmid

Query Match 61.1%; Score 44; DB 2; Length 456;  
 Best Local Similarity 87.5%; Pred. No. 20;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 HGGSSFD 11  
 |||||:  
 Db 188 HGGNSFD 195

## RESULT 4

C64757  
 Probable iron-sulfur protein ykgF - *Escherichia coli* (strain K-12)  
 C:Species: *Escherichia coli*  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: C64757  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. A.; Rose, D.J.; Mau, B.; Siao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of *Escherichia coli* K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: C64757  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-475 <BLAT>  
 A:Cross-references: GB:AE000137; GB:U00096; NID:92367108; PIDN:AACT3410.1; PID:91786438;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ykgF  
 C:Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2 [4Fe-4S] h

C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein  
 F:312,315,318,372/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
 F:322,362,365,368/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
 Query Match 61.1%; Score 44; DB 2; Length 475;  
 Best Local Similarity 77.8%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGYSSSF 10  
 |||||:  
 Db 329 GGGYGSIV 337

## RESULT 5

A90672  
 hypothetical protein Ecs0345 [imported] - *Escherichia coli* (strain O157:H7, sub  
 C:Species: *Escherichia coli*  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C:Accession: A90672  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;  
 Gaswara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: A90672  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-475 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA833768.1; PID:913359802; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: Ecs0345  
 C:Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2 [

Query Match 61.1%; Score 44; DB 2; Length 475;  
 Best Local Similarity 77.8%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGYSSSF 10  
 |||||:  
 Db 329 GGGYGSIV 337

## RESULT 6

E85522  
 hypothetical protein ykgF [imported] - *Escherichia coli* (strain O157:H7, substre  
 C:Species: *Escherichia coli*  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: E85522  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.  
 11er, L.; Grobeck, E.J.; Davis, N.W.; Linn, A.; Dimalanta, E.; Petcamousis, K.;  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A:Reference number: A85480; MUID:21074335; PMID:11206551  
 A:Accession: E85522  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-475 <STO>  
 A:Cross-references: GB:AE005174; NID:912513108; PIDN:AA654641.1; GSPDB:GN00145;  
 A:Experimental source: strain O157:H7, substrain EDD933  
 C:Genetics:  
 A:Gene: ykgF  
 C:Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2 [4

Query Match 61.1%; Score 44; DB 2; Length 475;  
 Best Local Similarity 77.8%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGYSSSF 10  
 |||||:  
 Db 329 GGGYGSIV 337

## RESULT 7

E83824  
 hypothetical protein EH1397 [imported] - *Bacillus halodurans* (strain C-125)  
 C:Species: *Bacillus halodurans*  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C:Accession: E83824  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii,

Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: B33824  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-35 <STO>  
 A:Cross-references: GB:AP001511, GB:BA000004, NID:G10173727, PIDN:BA05116.1, GSPDB:GN00  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH1397

Query Match 59.7%; Score 43; DB 2; Length 35;  
 Best Local Similarity 77.8%; Pred. No. 2.2;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHGGSSE 10  
 DB 6 GGHGGSSE 14

## RESULT 8

T17207  
 Hypothetical protein DKFZP586F022.1 - human

C:Species: Homo sapiens (man)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 R:Kocher, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18722  
 A:Accession: T17207  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-215 <KOB>  
 A:Cross-references: EMBL:AL117395  
 A:Experimental source: adult uterus; clone DKFZP586F022  
 C:Genetics:  
 A:Note: DKFZP586F022.1  
 C:Superfamily: glycine-rich cell wall structural protein 1

Query Match 59.7%; Score 43; DB 2; Length 215;  
 Best Local Similarity 70.0%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHGGSSE 11  
 DB 46 GGHGGSSE 55

## RESULT 9

T33380  
 Hypothetical protein H22K11.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
 R:Beck, C.; Wamaley, P.; Keppeler, N.  
 submitted to the EMBL Data Library, July 1998  
 A:Description: The sequence of *C. elegans* cosmid H22K11.  
 A:Reference number: Z21333  
 A:Accession: T33380  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-235 <BEC>  
 A:Cross-references: EMBL:AF077544; PIDN:AA64619.1; GSPDB:GN00028; CESP:H22K11.3  
 A:Experimental source: strain Bristol N2; clone H22K11  
 C:Genetics:  
 A:Gene: CESP:H22K11.3  
 A:Map position: X  
 A:Introns: 35/1; 79/1; 128/1

Query Match 59.7%; Score 43; DB 2; Length 235;  
 Best Local Similarity 77.8%; Pred. No. 15;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHGGSSE 10  
 DB 207 GGHGGSSE 215

## RESULT 10

T02661  
 Lysophospholipase homolog - rice

C:Species: *Oryza sativa* (rice)  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
 R:Kim, C.Y.; Cheon, S.Y.; Jeong, S.Y.; Cheong, Y.H.; Han, C.D.; Cho, M.J.  
 submitted to the EMBL Data Library, December 1997  
 A:Reference number: Z14689  
 A:Accession: T02661  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-304 <KIM>  
 A:Cross-references: EMBL:AF039531, NID:G2801535, PID:G2801536  
 C:Genetics:  
 A:Gene: LPL1

Query Match 59.7%; Score 43; DB 2; Length 304;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DGHGGSSE 12  
 DB 87 DGHGGSSE 98

## RESULT 11

T48524  
 Lysophospholipase-like protein - *Arabidopsis thaliana*

N:Alternate names: protein T22P22.40  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 R:Bevan, M.; Hilbert, H.; Braun, M.; Hölzer, E.; Brandt, A.; Duesterhoeft, A.;  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z24490  
 A:Accession: T48524  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-390 <BEV>  
 A:Cross-references: EMBL:AL163814  
 A:Experimental source: cultivar Columbia; BAC clone T22P22  
 C:Genetics:  
 A:Map position: 5  
 A:Introns: 127/2; 140/2; 164/1; 185/3; 215/3; 246/3  
 A:Note: T22P22.40

Query Match 58.3%; Score 42; DB 2; Length 390;  
 Best Local Similarity 66.7%; Pred. No. 36;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGHGGSSE 12  
 DB 169 DGHGGSSE 180

## RESULT 12

T28808  
 Hypothetical protein C54D1.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
 R:Min, M.  
 submitted to the EMBL Data Library, January 1996  
 A:Description: The sequence of *C. elegans* cosmid C54D1.  
 A:Reference number: Z20527  
 A:Accession: T28808

A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1163 <MIN>  
 A:Cross-references: EMBL:U46673; FIDN:AA048153.1; GSPDB:GN00028; CESP:CS4D1.3  
 A:Experimental source: strain Bristol N2; clone CS4D1  
 A:Genetics: CESP:CS4D1.3  
 A:Map position: X  
 A:Introns: 44/1; 121/3; 145/3; 191/3; 250/1; 291/2; 330/3; 393/2; 463/2; 557/2; 603/3; 6

Query Match 58.3%; Score 42; DB 2; Length 1163;  
 Best Local Similarity 72.7%; Pred. No. 1.1e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGHGYGSSFDY 12  
 DB 908 GGGHGYGSSFDY 918

## RESULT 13

A84863  
 Probable carboxyphosphoenolpyruvate mutase [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C/Accession: A84863

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.B.; Unayam, L.; Tallon, L.;  
 Weiss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84863  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-492 <STO>  
 A:Cross-references: GB:AE02093; NID:g3763927; FIDN:AA064307.1; GSPDB:GN00139  
 A:Genetics:  
 A:Map position: 2

Query Match 56.9%; Score 41; DB 2; Length 492;  
 Best Local Similarity 54.5%; Pred. No. 66;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
 DB 146 DGGHGYGSSFD 156

## RESULT 14

S40904

FUN2 protein - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: protein YAR014c

C/Species: Saccharomyces cerevisiae  
 C/Date: 13-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 19-Apr-2002  
 C/Accession: S40904; S20121

R.Clark, M.M.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; One  
 submitted to the EMBL Data Library, November 1993

A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the  
 A:Reference number: S40891  
 A:Accession: S40904

A:Molecule type: DNA  
 A:Residues: 1-702 <CLAY>  
 A:Cross-references: EMBL:L22015; NID:g1339990; FIDN:AA064962.1; PID:g349754; MIPS:YAR014  
 R.Davies, C.J.; Hutchison III, C.A.  
 Nucleic Acids Res. 19, 5731-5738, 1991

A>Title: A directed DNA sequencing strategy based upon Tn3 transposon mutagenesis: appli  
 A:Reference number: S20121; MUID:92051323; PMID:1658741

A:Accession: S20121  
 A:Molecule type: DNA

A:Residues: 1-142 <DAV>  
 A:Cross-references: EMBL:M67445  
 C/Genetics:

A:Gene: SGD:YAR014; FUN2  
 A:Cross-references: SGD:S0000069  
 A:Map position: 1R

Query Match 56.9%; Score 41; DB 2; Length 702;  
 Best Local Similarity 63.6%; Pred. No. 95;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
 DB 404 DGGHGYGSSFD 414

## RESULT 15

PH173

Ig heavy chain V region (clone GCC-13) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 17-Mar-1999  
 C/Accession: PH173

R.McKoyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.  
 J. Exp. Med. 178, 295-307, 1993  
 A>Title: Antigen-driven B cell differentiation in vivo.  
 A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH173  
 A:Molecule type: mRNA  
 A:Residues: 1-25 <MCH>  
 A:Experimental source: B cell  
 A>Note: the authors translated the codon ACA for residue 13 as Ala  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 55.6%; Score 40; DB 2; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YGSSFDY 12  
 DB 19 YGSSFDY 25

Search completed: November 7, 2003, 07:36:18  
 Job time: 4.65407 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 0.865154 Seconds  
(Without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-6  
Perfect score: 72  
Sequence: 1 DSGHGYSSEFDY 12

Scoring table: ELOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query	Length	ID	Description
1	44	61.1	475	1	YKGF_ECOLI
2	43	59.7	346	1	ROH3_HUMAN
3	41	56.9	702	1	YAL4_YEAST
4	40	55.6	79	1	KRIA_RABIT
5	40	55.6	82	1	KRIA_SHEEP
6	40	55.6	126	1	HVJK_HUMAN
7	40	55.6	139	1	GRAL_ORISA
8	40	55.6	153	1	REM3_MOUSE
9	40	55.6	157	1	REM3_MOUSE
10	40	55.6	286	1	Y359_TREPA
11	39	54.2	211	1	Y359_TREPA
12	39	54.2	313	1	SYPH_HUMAN
13	39	54.2	384	1	VPRP_PRIVA
14	39	54.2	385	1	REB7_DROME
15	39	54.2	510	1	DMPI_BOVIN
16	39	54.2	647	1	NANH_MICVI
17	39	54.2	657	1	YVXL_BACSV
18	39	54.2	873	1	RX_DROME
19	39	54.2	1133	1	EGF_RAT
20	38	52.8	63	1	YIMF_CABEL
21	38	52.8	138	1	CH16_DROME
22	38	52.8	183	1	GRP2_ORYSA
23	38	52.8	256	1	HISJ_CAME
24	38	52.8	266	1	Y209_METTA
25	38	52.8	307	1	SYPH_BOVIN
26	38	52.8	307	1	SYPH_RAT
27	38	52.8	308	1	SYPH_MOUSE
28	38	52.8	326	1	YB27_METTA
29	38	52.8	383	1	TRIS_STACH
30	38	52.8	815	1	PHSG_ECOLI
31	37.5	52.1	250	1	CHIT_DIOJA
32	37.5	52.1	817	1	PHK_STROO
33	37	51.4	160	1	YBIA_ECOLI

34	37	51.4	208	1	PSB2_DROME	Q9vge5 drosophila
35	37	51.4	251	1	YAK6_SCHPO	Q09918 schizosacch
36	37	51.4	306	1	CH38_DROME	P07183 drosophila
37	37	51.4	373	1	RO31_XENLA	P51968 xenopus lae
38	37	51.4	385	1	RO32_XENLA	P51992 xenopus lae
39	37	51.4	431	1	KICQ_HUMAN	Q04695 homo sapien
40	37	51.4	473	1	KNOB_PLAFA	P13817 plasmodium
41	37	51.4	526	1	KICJ_BOVIN	P06394 bos taurus
42	37	51.4	530	1	HLY HAL17	P29143 halophillic
43	37	51.4	587	1	PTCB_PSEBR	P42790 pseudomonas
44	37	51.4	593	1	KICU_HUMAN	P13645 homo sapien
45	37	51.4	595	1	VPL_BECBP	P19192 bacteriophan

## ALIGNMENTS

RESULT 1	YKGF_ECOLI	STANDARD	PRT	475 AA
AC	YKGF_ECOLI			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Putative electron transport protein ykGF.			
GN	YKGF OR B0307.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis M.N., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
RL	Science 277:1453-1474(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,			
RA	Federpiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,			
RA	Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;			
RL	-1. SIMILARITY: (NOV-1996) to the EMBL/GenBank/DBJ databases.			
CC	'BACTERIAL-TYPE' 4FE-4S PERRODOXINS.			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
DR	EMBL; AB000137; AAC73410.1; -			
DR	EMBL; U73857; AAB18034.1; -			
DR	PIR; G64757; G64757.			
DR	Ecogene; EG13583; YKGF.			
DR	InterPro; IPR001450; 4FE4s_ferredoxin.			
DR	InterPro; IPR004452; Fe_S_Binding.			
DR	PIfam; PF00037; Fe4; 2.			
DR	TIGRFAMs; TIGR00273; TIGR00273; 1.			
DR	PROSITE; PS00198; 4FE4s_PRREROXIN; 2.			
KW	Hypothetical protein; Electron transport; Iron-sulfur; 4FE-4S;			
FT	Complete proteome.			
FT	METAL	312		IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT	METAL	315		IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT	METAL	318		IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT	METAL	322		IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT	METAL	362		IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).



FT VARSPLIC 259 276 /FtId=VSP\_005842.  
 CHRYHELFNSTPTGGSGG -> RKMCIMHTLPEKREKIK  
 FT (in isoform 5 and isoform 6).  
 FT VARSPLIC 277 346 /FtId=VSP\_005843.  
 Missing (in isoform 5 and isoform 6).  
 FT CONFLICT 137 138 /FtId=VSP\_005844.  
 RR -> HE (in REF. 4).  
 SQ SEQUENCE 346 AA; 36926 MW; P7D1C2947930B9E CRC64;

Query Match 59.7%; Score 43; DB 1; Length 346;  
 Best Local Similarity 70.0%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGYSSFD 11  
 Db 177 GGGYGGAGD 186

## RESULT 3

YAI4\_YEAST STANDARD; PRT; 702 AA.

ID YAI4\_YEAST STANDARD; PRT; 702 AA.  
 AC P27637;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical 78.3 kDa protein in SEN34-ADRI intergenic region.  
 GN YAI014C OR FDN2.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CX NCBI\_TaxID=4932;

(1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=288C / AB972;  
 RX MEDLINE=95028152; PubMed=7941740;  
 RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
 RA Delaney S., Quelette B.F.F., Barton A.B., Kaback D.B., Bussey H.;  
 RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of  
 RT the 42 kbp SP07-CEN1-CDC15 region.";  
 RL Yeast 10:535-541(1994).  
 (2)

RP SEQUENCE OF 1-142 FROM N.A.  
 RX MEDLINE=92051323; PubMed=1658741;  
 RA Davies C.J., Hutchison C.A. III;  
 RT "A directed DNA sequencing strategy based upon Tn3 transposon  
 RT mutagenesis: application to the ADRI locus on Saccharomyces  
 RT cerevisiae chromosome I.";  
 RL Nucleic Acids Res. 19:5731-5738(1991).  
 CC -1- SIMILARITY: Contains 1 SH3 domain.

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DR EMBL: L22015; AAC04962.1; -;  
 DR EMBL: M67445; AA334397.1; -;  
 DR PIR: S40904; S40904.  
 DR SGD: S0000069; BDD14.  
 DR GO: GO:0005935; C:bud neck; IDA.  
 DR GO: GO:0005934; C:bud tip; IDA.  
 DR GO: GO:000131; C:incipient bud site; IDA.  
 DR GO: GO:0000282; P:bud site selection; IMP.  
 DR GO: GO:0030447; P:filamentous growth; IMP.  
 DR InterPro: IPR001452; SH3.  
 DR Pfam: PF00018; SH3; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR PROSITE: PS0002; SH3; 1.  
 KW Hypothetical protein; SH3 domain.  
 FT DOMAIN 259 320 SH3.

SQ SEQUENCE 702 AA; 78333 MW; 4F9423BE8FA0088B CRC64;

Query Match 56.9%; Score 41; DB 1; Length 702;  
 Best Local Similarity 63.6%; Pred. No. 57;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DGGYSSFD 11  
 Db 404 DGGYGGAGD 414

## RESULT 4

KRAH\_RABIT STANDARD; PRT; 79 AA.

ID KRAH\_RABIT STANDARD; PRT; 79 AA.  
 AC Q02957;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Keratin, glycine/tyrosine-rich of hair.  
 GN KAP6-1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CX NCBI\_TaxID=9986;  
 (1)

RP SEQUENCE FROM N.A.  
 RX MEDLINE=93179467; PubMed=7680040;  
 RA Fratini A., Powell B.C., Rogers G.E.;  
 RT "Sequence, expression, and evolutionary conservation of a gene  
 RT encoding a glycine/tyrosine-rich keratin-associated protein of  
 RT hair.";  
 RL J. Biol. Chem. 268:4511-4518(1993).

CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES  
 CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID  
 CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-  
 CC SULFUR AND GLYCINE/TYROSINE-RICH PROTEINS, HAVING MOLECULAR  
 CC WEIGHTS OF 6-20 kDa WHEREAS THE MICROFIBRILS CONTAIN THE LARGER,  
 CC LOW-SULFUR PROTEINS (40-56 kDa).  
 CC -1- DEVELOPMENTAL STAGE: KAP6 PROTEINS ARE FIRST EXPRESSED IN  
 CC ABOVE THE PROLIFERATIVE ZONE OF THE FOLLICLE BULB.  
 CC -1- SIMILARITY: BELONGS TO THE KAP6 GLYCINE/TYROSINE-RICH TYPE II  
 CC PROTEIN FAMILY.

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DR EMBL: M95718; AA31379.1; -;  
 DR PIR: B45466; B45466.  
 KW Keratin; Multigene family; Acetylation.

FT INIT MET 0  
 FT MOD RES 1 1 ACETYLATION.  
 SQ SEQUENCE 79 AA; 8143 MW; 3A45A75B029E0F4 CRC64;

Query Match 55.6%; Score 40; DB 1; Length 79;  
 Best Local Similarity 70.0%; Pred. No. 8.7;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGGYSSFD 12  
 Db 68 GGGYGGAGD 77

## RESULT 5

KRAH\_SHEEP STANDARD; PRT; 82 AA.

ID KRAH\_SHEEP STANDARD; PRT; 82 AA.  
 AC Q02958;  
 DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, last sequence update)  
 DT 28-SEP-2003 (Rel. 41, last annotation update)  
 DE Keratin, glycine/tyrosine-rich of hair.  
 GN KAP6-1.  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 OK NCBI\_TaxID=9940;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Merino X Dorset horn; TISSUE=Wool follicles;  
 RX MEDLINE=93179467; PubMed=7680040;  
 RA Frattini A., Powell B.C., Rogers G.E.;  
 RT "Sequence, expression, and evolutionary conservation of a gene  
 encoding a glycine/tyrosine-rich keratin-associated protein of  
 hair";  
 RL J. Biol. Chem. 268:4511-4518(1993).  
 RN [2]  
 RP SEQUENCE OF 16-82.  
 RX MEDLINE=92231328; PubMed=1809119;  
 RA Rogers G.E., Fietz M.J., Frattini A.;  
 RT "Trichohyalin and matrix proteins";  
 RL Ann. N.Y. Acad. Sci. 642:64-81(1991).  
 CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES  
 CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-  
 CC SULFUR AND GLYCINE/TYROSINE-RICH PROTEINS, HAVING MOLECULAR  
 CC WEIGHTS OF 6-20 kDa WHEREAS THE MICROFILBRILS CONTAIN THE LARGER,  
 CC LOW-SULFUR PROTEINS (40-56 kDa).  
 CC -1- DEVELOPMENTAL STAGE: THE KAP6 PROTEINS ARE FIRST EXPRESSED IN  
 CC DIFFERENTIATING HAIR SHAFT KERATINOCYTES, A CONSIDERABLE DISTANCE  
 CC ABOVE THE PROLIFERATIVE ZONE OF THE FOLLICLE BULB.  
 CC -1- SIMILARITY: BELONGS TO THE KAP6 GLYCINE/TYROSINE-RICH TYPE II  
 CC PROTEIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M95719; AAA31554.1; -.  
 DR PIR; A45466; A45466.  
 KM Keratin; Multigene family; Repeat; Acetylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1  
 FT REPEAT 8  
 FT REPEAT 14  
 FT REPEAT 24  
 FT REPEAT 43  
 FT REPEAT 54  
 FT REPEAT 55  
 FT REPEAT 66  
 FT CONFLICT 16  
 FT CONFLICT 16  
 SQ SEQUENCE 82 AA; 8236 MW; 2B4EFBCD3FCF9267 CRC64;  
 QY Query Match 55.6%; Score 40; DB 1; Length 82;  
 DB Best Local Similarity 70.0%; Pred. No. 9;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 GGGGSGGSGFY 12  
 DB 71 GGGGSGGSGFY 80  
 RESULT 6  
 HV3K\_HUMAN STANDARD; PRT; 126 AA.  
 AC P01772;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region KOL.

OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE AND DISULFIDE BONDS.  
 RX MEDLINE=81072295; PubMed=6884994;  
 RA Schmidt W.R., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=81072295; PubMed=7441755;  
 RA Marguier M., Deisenhofer J., Huber R., Palm W.;  
 RT "Crystallographic refinement and atomic models of the intact  
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
 RT and 1.0-A resolution";  
 RL J. Mol. Biol. 141:369-391(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02055; G1HUKL.  
 DR PDB; 2PB4; 12-JUL-89.  
 DR GO; GO:000576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; 3D-structure; Pyroglutamate carboxylic acid.  
 FT FT DOMAIN 1 112  
 FT MOD\_RES 1  
 FT DISULFID 22 96  
 FT DISULFID 105 110  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT STRAND 14 15  
 FT STRAND 18 25  
 FT STRAND 29 31  
 FT STRAND 34 39  
 FT STRAND 41 42  
 FT STRAND 45 51  
 FT STRAND 51 51  
 FT STRAND 53 54  
 FT STRAND 58 60  
 FT STRAND 60 64  
 FT STRAND 64 64  
 FT HELIX 65 65  
 FT STRAND 66 67  
 FT TURN 68 73  
 FT TURN 74 77  
 FT STRAND 78 83  
 FT STRAND 88 90  
 FT STRAND 92 99  
 FT STRAND 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 FT NON\_TER 126  
 SQ SEQUENCE 126 AA; 13718 MW; EAD71852B16F8776 CRC64;  
 QY Query Match 55.6%; Score 40; DB 1; Length 126;  
 DB Best Local Similarity 77.8%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DGGHGSSS 9  
 DB 99 DGGHGSSS 107  
 RESULT 7

GRAL\_ORYZA STANDARD; PRT; 139 AA.  
 ID GRAL\_ORYZA  
 AC Q07077;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DS Gravity specific protein GSC 233.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Euphorbiaceae; Oryzaeae; Oryza.  
 CC NCB1\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare; TISSUE=Callus;  
 RX MEDLINE=93199820; PubMed=1363521;  
 RA Kwon S., Kikuchi S., Ono K.,  
 RT "Molecular cloning and characterization of gravity specific cDNA in  
 RL rice (Oryza sativa L.) suspension callus.",  
 CC Jpn. J. Genet. 67:335-348(1992).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN CALLUS.  
 CC -1- INDUCTION: BY GRAVITY STRESS.  
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 CC -----  
 CC DR EMBL; D11137; BAA01911.1; -;  
 CC DR EMBL; S56877; BAB25853.1; -;  
 CC DR PIR; T04310; T04310.  
 CC DR GRENFE; Q07077; -;  
 CC SQ SEQUENCE 139 AA; 15563 MW; A1C302F1988AC864 CRC64;  
 QY Query Match 55.6%; Score 40; DB 1; Length 139;  
 Best Local Similarity 87.5%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 DB 130 DGGHSGS 137  
 QY 1 DGGHSGS 8  
 ID 130 DGGHSGS 137  
 AC 089056;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative RNA-binding protein 3 (RNA binding motif protein 3).  
 GN RBM3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCB1\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC Danno S., Matsuda T., Fujita J.,  
 CC "Isolation and characterization of mouse rbm3 cDNA.",  
 CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=ICR;  
 CC RX MEDLINE=21463050; PubMed=11470798;  
 CC RA Chapell S.A., Owens G.C., Mauro V.P.,  
 CC "A 5' leader of Rbm3, a cold stress-induced mRNA, mediates internal  
 CC initiation of translation with increased efficiency under conditions  
 CC of mild hypothermia.",  
 CC J. Biol. Chem. 276:36917-36922(2001).  
 CC [3]

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RNM) domain.  
 CC -----  
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 CC -----  
 CC DR EMBL; AB016424; BAA32060.1; -;  
 CC DR EMBL; AY052860; AAL10707.1; -;  
 CC DR HSSP; P09651; IHA1.  
 CC DR KCD; MG1:1099460; Rbm3.  
 CC DR InterPro; IPR00504; RNA\_rec\_mot.  
 CC DR Pfam; PF00076; xrm; 1.  
 CC DR SMART; SM00360; RRM; 1.  
 CC DR PROSITE; PS00102; RRM; 1.  
 CC DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
 CC KW RNA-binding.  
 CC FT DOMAIN 6 84 RNA-BINDING (RRM).  
 CC FT DOMAIN 88 145 GYR-RICH.  
 CC SQ SEQUENCE 153 AA; 16605 MW; C54R66A1A9B4FF3D CRC64;  
 QY Query Match 55.6%; Score 40; DB 1; Length 153;  
 Best Local Similarity 70.0%; Pred. No. 17;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 DB 123 GYGGRSRDY 132  
 QY 3 GYGGRSRDY 12  
 ID 123 GYGGRSRDY 132  
 AC P98179;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Putative RNA-binding protein 3 (RNA binding motif protein 3) (RNPL).  
 GN RBM3 OR RNPL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCB1\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC RX MEDLINE=96177655; PubMed=8634703;  
 CC RA Derry J.M., Kerns J.A., Francke U.,  
 CC "RBM3, a novel human gene in Xp11.23 with a putative RNA-binding  
 CC domain.",  
 CC Hum. Mol. Genet. 4:2307-2311(1995).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U.,  
 CC Meindl A., Rosenthal A.,  
 CC Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC TISSUE=Placenta;  
 CC RX MEDLINE=22388257; PubMed=12477932;  
 CC STRAUBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 CC Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 CC Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,  
 CC Brownstein W.J., Ueda T.B., Toshiki S., Carninci P., Prange C.,  
 CC Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulys S.W.,  
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywnski M.I., Skalska U., Smalins D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -----
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CC -----
CC EMBL; U28686; AAB17212.1; -.
CC EMBL; AF196969; AAF06803.1; -.
CC EMBL; BC006825; AAB06825.1; -.
CC PIR; G01859; G01859.
CC HSSP; P09651; 1HA1.
CC GeneW; H88C:9900; RRM3.
CC MIM; 300027; -.
CC GO; GO:0003723; F:RNA binding activity; TAS.
CC GO; GO:0006396; P:RNA processing; TAS.
CC InterPro; IPR00504; RNA_rec_mot.
CC Pfam; PF00076; rrm; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS0102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC RNA-binding.
CC FT DOMAIN 6 84 RNA-BINDING (RRM).
CC FT 88 149 GLY-RICH.
CC SEQUENCE 157 AA; 17170 MW; 91C1E2A3E32CF84 CRC64;
SQ
Query Match 55.6%; Score 40; DB 1; Length 157;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGHGYSFPDY 12
Db 126 GYGGGRSDY 135
RESULT 10
RRP SYNVD STANDARD; PRT; 286 AA.
AC P2139;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nonstructural protein) (M1
DE phosphoprotein).
DE M1.
OS Sonchus yellow net virus (SYNV).
CC Viruses; ssRNA negative-strand viruses; Monomegavirales;
CC Rhabdoviridae; Nucleorhabdovirus.
CC NCBI_TaxID=11307;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=ATCC PV-263;
CC MEDLINE=91021022; PubMed=219720;
CC Hillman B.I., Heaton L.A., Hunter B.G., Modrell B., Jackson A.O.;
RT "Structure of the gene encoding the M1 protein of sonchus yellow net
RT virus."
CC Virology 179:201-207(1990).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).

```

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CC -----
CC EMBL; L32603; AAA50383.1; -.
CC EMBL; M35689; AAA47897.1; -.
CC PIR; A45350; A45350.
CC Transferrase; RNA-directed RNA polymerase; Phosphorylation;
CC Nonstructural protein.
CC SEQUENCE 286 AA; 31775 MW; 6B86F095788B6C98 CRC64;
SQ
Query Match 55.6%; Score 40; DB 1; Length 286;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DGCHGYG 7
Db 211 DGCHG 217
RESULT 11
Y359 TREPA STANDARD; PRT; 211 AA.
ID Y359 TREPA
AC O83378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0359.
GN TP0359.
OS Treponema pallidum.
CC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
CC NCBI_TaxID=160;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=Nichols;
CC MEDLINE=98332770; PubMed=9665876;
CC Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
CC Dodson R., Gwalt M., Hickey E.K., Clayton R., Ketchum K.A.,
CC Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
CC Khalak H., Richardson D., Howell J.K., Chidambaram M., Ureback T.,
CC McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
CC Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
CC Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RT Science 281:375-388(1998).
CC -----
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CC -----
CC EMBL; AE001215; AAC65354.1; -.
CC PIR; E71334; E71334.
CC TIGR; TP0359; -.
CC Hypothetical protein; Complete proteome.
CC SEQUENCE 211 AA; 23888 MW; 91FF8B824C630327 CRC64;
SQ
Query Match 54.2%; Score 39; DB 1; Length 211;
Best Local Similarity 54.2%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGHGYSFPDY 12
Db 114 GGHGHTSLDH 124

```

## RESULT 12

SYEP\_HUMAN STANDARD; PRT; 313 AA.  
 ID SYEP\_HUMAN  
 AC P08247;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN Synapophysin (Major synaptic vesicle protein P38).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90365048; PubMed=1975480;  
 RA Ozezcelik T., Lattemiere R.G., Archer B.T. III, Johnston P.A.,  
 RA Willard H.F., Franke U., Suedhof T.C.;  
 RA "Synapophysin: structure of the human gene and assignment to the X  
 RT chromosome in man and mouse."  
 RT Am. J. Hum. Genet. 47:551-561(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=88067787; PubMed=3120152;  
 RA Suedhof T.C., Lottspeich F., Greengard P., Wehl E., Jahn R.;  
 RA "The cDNA and derived amino acid sequences for rat and human  
 RT synapophysin."  
 RT Nucleic Acids Res. 15:9607-9607(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98008923; PubMed=9344658;  
 RA Fisher S.B., Ciccodicola A., Tanaka K., Curci A., Desicato S.,  
 RA D'Ursio M., Craig I.W.;  
 RA "Sequence-based exon prediction around the synapophysin locus  
 RT reveals a gene-rich area containing novel genes in human proximal  
 RT Xp."  
 RT Genomics 45:340-347(1997).  
 CC -1- FUNCTION: POSSIBLY INVOLVED IN STRUCTURAL FUNCTIONS AS ORGANIZING  
 CC OTHER MEMBRANE COMPONENTS OR IN TARGETING THE VESICLES TO THE  
 CC PLASMA MEMBRANE.  
 CC -1- SUBUNIT: HOMOHexamER OR HOMOTETRAMER.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic  
 CC vesicles.  
 CC -1- TISSUE SPECIFICITY: CHARACTERISTIC OF A TYPE OF SMALL (30-80 NM)  
 CC NEUROSECRETORY VESICLES, INCLUDING PRESYNAPTIC VESICLES, BUT ALSO  
 CC VESICLES OF VARIOUS NEUROENDOCRINE CELLS OF BOTH NEURONAL AND  
 CC EPITHELIAL PHENOTYPE.  
 CC -1- DOMAIN: THE CALCIUM-BINDING ACTIVITY IS THOUGHT TO BE LOCALIZED IN  
 CC THE CYTOPLASMIC TAIL OF THE PROTEIN.  
 CC -1- SIMILARITY: HIGHLY CONSERVED FROM CARTILAGINOUS FISH TO HUMANS;  
 CC NO HOMOLOGY IS FOUND TO OTHER KNOWN CALCIUM-BINDING PROTEINS. THE  
 CC GLYCINE-RICH DOMAIN SHOWS SIMILARITY TO TYPE I AND II CYTOSKELETAL  
 CC KERATIN AND BOVINE CARTILAGE ALPHA 1 (II) CHAIN.  
 CC -1- SIMILARITY: MEMBER OF THE SYNAPPOPHYSIN/SYNAPTOBREVIN CHANNEL  
 CC PROTEIN FAMILY.  
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 CC -----  
 DR EMBL: X06389; CAA29686.1; -;  
 DR EMBL: U93305; AAB92358.1; -;  
 DR PIR: A35689; A35699.  
 DR Genew; HGNC:11506; SIF.  
 DR MIM: 313475; -;  
 DR GO: GO:0030285; C: integral to synaptic vesicle membrane; NMS.  
 DR InterPro; IPR001285; synapophysin.

DR Pfam; PF01284; MARVEL; 1.  
 DR PRINTS; PRO0220; SYNAPPOPHYSN.  
 DR PROSITE; PS00604; SYNAPTOP; 1.  
 KW Calcium-binding; Synapse; Glycoprotein; Transmembrane;  
 KW Nerve; Synaptosome; Repeat.  
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 26 49 POTENTIAL.  
 FT DOMAIN 50 106 VESICULAR (POTENTIAL).  
 FT TRANSMEM 107 130 POTENTIAL.  
 FT DOMAIN 131 137 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 138 161 POTENTIAL.  
 FT DOMAIN 162 199 VESICULAR (POTENTIAL).  
 FT TRANSMEM 200 223 POTENTIAL.  
 FT DOMAIN 224 313 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 305 305 REPEATS, GLY-RICH.  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 313 AA; 33845 MW; 592289C43B12EFA7 CRC64;  
 Query Match 54.2%; Score 39; DB 1; Length 313;  
 Best Local Similarity 63.6%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GGGGGGSSFDY 12  
 DB 285 GGGGGGPGGDY 295

RESULT 13  
 VEPF\_PRIVKA STANDARD; PRT; 384 AA.  
 ID VEPF\_PRIVKA  
 AC P36702;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE DNA polymerase processivity factor (Polymerase accessory protein)  
 DE (PAP) (UL42 homolog).  
 OS Pseudorabies virus (strain Kaplan) (PRV).  
 CC Viruses; deDNA viruses; no RNA stage; Herpesviridae;  
 CC Alphaherpesvirinae; Varicelloviruses.  
 CC NCBI\_TaxID=33703;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9522727; PubMed=7707503;  
 RA Berthome H., Monahan S.J., Parrie D.S., Jacquemont B.,  
 RA Epstein A.L.;  
 RA "Cloning, sequencing, and functional characterization of the two  
 RT subunits of the pseudorabies virus DNA polymerase holoenzyme:  
 RT evidence for specificity of interaction."  
 RT J. Virol. 69:2811-2818(1995).  
 CC -1- FUNCTION: ACCESSORY SUBUNIT OF THE DNA POLYMERASE THAT ACTS TO  
 CC INCREASE THE PROCESSIVITY OF POLYMERIZATION (BY SIMILARITY).  
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES POLYMERASE ACCESSORY PROTEIN.  
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 CC -----  
 DR EMBL: M94355; AAB4384.1; -;  
 DR InterPro; IPR003202; UL42.  
 DR Pfam; PF02282; UL42; 2.  
 KW DNA-binding; DNA replication.  
 SQ SEQUENCE 384 AA; 40305 MW; FFA3CF0C1984936 CRC64;

Query Match 54.2%; Score 39; DB 1; Length 384;  
 Best Local Similarity 60.0%; Pred. No. 63;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DGGGGGSSGF 10  
 :||| | |

Db 375 BGGHAYGDLF 384

## RESULT 14

PB27 DROME STANDARD; PRT; 385 AA.

AC P48809;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Heterogeneous nuclear ribonucleoprotein 27C (hnRNP 48) (HRP48.1).

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephyridae; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S; TISSUE=Embryo;

RX MEDLINE=92112968; Pubmed=1730754;

RA Matunis B.L., Matunis M.J., Dreyfuss G.;

RT "Characterization of the major hnRNP proteins from Drosophila

RT melanogaster";

RT J. Cell Biol. 116:257-269 (1993).

CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE

CC NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING

CC MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.

CC -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.

CC -----

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CC -----

DR EMBL; X62639; CAA44505.1; -.

DR PIR; D41732; D41732.

DR HSSP; P09651; 1HA1.

DR FLYBase; FBgn0004838; Hrb27C.

DR GO; GO:0005654; C:nucleoplasm; IDA.

DR GO; GO:0030529; C:ribonucleoprotein complex; IDA.

DR InterPro; IPR000504; RNA\_rec\_mot.

DR Pfam; PF00076; rrm; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS00030; RRM\_RNP\_1; 2.

KW RNA-binding; Nuclear protein; Ribonucleoprotein; Repeat.

FT DOMAIN 7 88 RNA-BINDING (RRM) 1.

FT DOMAIN 96 173 RNA-BINDING (RRM) 2.

SQ SEQUENCE 385 AA; 41030 MW; 7543BE0FA96C9D4E CRC64;

Query Match 54.2%; Score 39; DB 1; Length 385;

Best Local Similarity: 75.0%; Pred. No. 63;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GYGSSFDY 12

DB 340 GYGSGDY 347

## RESULT 15

DMPL BOVIN

ID DMPL BOVIN STANDARD; PRT; 510 AA.

AC Q95120;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Dentin matrix acidic phosphoprotein 1 precursor (Dentin matrix

DE protein-1) (DMP-1).

GN DMPL.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxId=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tooth.

RX MEDLINE=97263952; Pubmed=9109824;

RA Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.;

RT "Cloning and expression analysis of the bovine dentin matrix acidic

RT phosphoprotein gene.";

RT J. Dent. Res. 76:754-760 (1997).

CC -!- FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION OF

CC EXTRACELLULAR MATRIX AND IN DENTINOGENESIS.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH

CC PARTICULARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED

CC IN LIVER AND SKIN.

CC -----

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CC -----

DR EMBL; U47636; AAB09412.1; -.

DR KX Extracellular matrix; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 510 DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1.

FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 427 427 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SITE 364 366 CELL ATTACHMENT SITE (POTENTIAL).

SQ SEQUENCE 510 AA; 55491 MW; 9BFA9A74F6450865 CRC64;

Query Match 54.2%; Score 39; DB 1; Length 510;

Best Local Similarity: 63.6%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11

DB 201 DSGHGDGSEFD 211

Search completed: November 7, 2003, 07:28:06  
Job time : 2.86515 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 3.95728 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-6

Sequence: 1 DGGHGYSSFDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	69.4	173	10 Q9LF59	Q9LF59 arabidopsis
2	47	65.3	205	16 Q9A419	Q9A419 caulobacter
3	47	65.3	1376	12 Q40925	Q40925 kaposi's sa
4	47	65.3	1376	12 P88917	P88917 kaposi's sa
5	47	65.3	1376	12 Q98139	Q98139 kaposi's sa
6	46	63.9	381	5 Q9GP09	Q9GP09 ixodes ric
7	46	63.9	1023	16 Q8XIH9	Q8XIH9 clostridium
8	45	62.5	348	10 Q8S651	Q8S651 oryza sativ
9	44	61.1	87	11 Q925H2	Q925H2 mus musculu
10	44	61.1	193	10 Q93W26	Q93W26 prunus pers
11	44	61.1	200	10 Q50000	Q50000 prunus pers
12	44	61.1	357	5 Q81DE1	Q81DE1 drosophila
13	44	61.1	456	16 Q92YV4	Q92YV4 rhizobium m
14	44	61.1	467	16 Q9CJY4	Q9CJY4 pasteurella
15	44	61.1	475	16 Q8XCE7	Q8XCE7 escherichia
16	44	61.1	475	16 Q8FKJ6	Q8FKJ6 escherichia

17	44	61.1	497	11 Q8C936	Q8C936 mus musculu
18	43	59.7	35	16 Q9KD22	Q9KD22 bacillus ha
19	43	59.7	59	11 Q925H5	Q925H5 mus musculu
20	43	59.7	87	11 Q925H6	Q925H6 mus musculu
21	43	59.7	88	4 Q81UB9	Q81UB9 mus musculu
22	43	59.7	141	11 Q925I0	Q925I0 homo sapien
23	43	59.7	235	5 Q76631	Q76631 mus musculu
24	43	59.7	340	3 Q8NK76	Q8NK76 caenorhabdi
25	43	59.7	304	10 Q49147	Q49147 oryza sativ
26	43	59.7	381	10 Q8LSP5	Q8LSP5 oryza sativ
27	42	58.3	339	10 Q941H8	Q941H8 oryza sativ
28	42	58.3	383	10 Q8LEB3	Q8LEB3 solanum tub
29	42	58.3	390	10 Q8LYG5	Q8LYG5 arabidopsis
30	42	58.3	395	10 Q8S2Q4	Q8S2Q4 oryza sativ
31	42	58.3	494	16 Q8EBA6	Q8EBA6 shewanella
32	42	58.3	1003	5 Q8MOL8	Q8MOL8 caenorhabdi
33	42	58.3	1080	5 Q18820	Q18820 caenorhabdi
34	41	56.9	177	11 Q925H9	Q925H9 mus musculu
35	41	56.9	113	5 Q9V5U5	Q9V5U5 mus musculu
36	41	56.9	119	5 Q9VPE3	Q9VPE3 drosophila
37	41	56.9	260	10 Q8H6Q2	Q8H6Q2 phytopthor
38	41	56.9	314	16 Q98PA9	Q98PA9 rhizobium l
39	41	56.9	479	10 Q8GYI4	Q8GYI4 arabidopsis
40	41	56.9	486	10 Q8S9J3	Q8S9J3 diospyros k
41	41	56.9	492	10 Q92W77	Q92W77 arabidopsis
42	41	56.9	617	2 Q8KJ49	Q8KJ49 rhizobium l
43	41	56.9	623	16 Q98AV1	Q98AV1 rhizobium l
44	41	56.9	781	2 Q9AN56	Q9AN56 bradyrhizob
45	41	56.9	902	6 Q9BDT9	Q9BDT9 echinops te

#### ALIGNMENTS

##### RESULT 1

Q9LF59 PRELIMINARY; PRT; 173 AA.

AC Q9LF59  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Glycine/proline-rich protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,  
 RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 RM [2]  
 RP SEQUENCE FROM N.A.  
 RA Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL391151; CA01909.1;  
 SQ SEQUENCE 173 AA; 18536 MW; E5310947AA98BC0A CRC64;

##### Query Match

Best Local Similarity 69.4%; Score 50; DB 10; Length 173;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGHGYSSFDY 12  
 |||||  
 Db 36 GGHGYSSFDY 45

##### RESULT 2

Q9A419 PRELIMINARY; PRT; 205 AA.  
 ID Q9A419  
 AC Q9A419;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Hypothetical protein CC3024.  
 GN CC3024.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
 OC Caulobacteraceae; Caulobacter.  
 NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=1259647;  
 RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohca N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn N.D., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,  
 RA Ueberback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AF005965; AK24986.1; -  
 DR TIGR; CC3024; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 205 AA; 22665 MW; C03B0E4FC08908E8 CRC64;

Query Match 65.3%; Score 47; DB 16; Length 205;  
 Best Local Similarity 70.0%; Pred. No. 6.9;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 GHGYSSTFDY 12  
 Db 163 GHGYSSTFDY 172

RESULT 3  
 ID 040925 PRELIMINARY; PRT; 1376 AA.  
 AC 040925;  
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
 DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE ORF 25.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 NCBI\_TaxID=37296;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97296220; PubMed=9151804;  
 RA Neipel F., Albrecht J.C., Fleckenstein B.;  
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus  
 human herpesvirus 8: determinants of its pathogenicity?";  
 RL J. Virol. 71:4187-4192(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,  
 RA Friedman-Kien A.E., Fleckenstein B.;  
 RT "The genome of human herpesvirus 8 cloned from Kaposi's sarcoma";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U93872; AB62606.1; -  
 DR InterPro; IPR000912; Herpes MCP.  
 DR InterPro; IPR003006; IG\_MHC\_  
 DR Pfam; PF01123; Herpes MCP.1.  
 DR PRINTS; PR00235; HSVCAPIIDMCP.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 SQ SEQUENCE 1376 AA; 153463 MW; F10B59E380745A49 CRC64;

Query Match 65.3%; Score 47; DB 12; Length 1376;  
 Best Local Similarity 63.6%; Pred. No. 63;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
 Db 476 DGGHGYGLRVE 486

RESULT 4  
 ID P88917 PRELIMINARY; PRT; 1376 AA.  
 AC P88917;  
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)  
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE ORF 25.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 NCBI\_TaxID=37296;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96099469; PubMed=8523568;  
 RA Moore P.S., Gao S.J., Dominguez G., Cesarman E., Lungu O.,  
 RA Knowles D.M., Garber R., Pellett P.E., McGeoch D.J., Chang Y.;  
 RT "Primary characterization of a herpesvirus agent associated with  
 Kaposi's sarcoma";  
 RL J. Virol. 70:549-558(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9704384; PubMed=8939871;  
 RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;  
 RT "Molecular mimicry of human cytokine and cytokine response pathway  
 genes by KSHV";  
 RL Science 274:1739-1744(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97121480; PubMed=8962146;  
 RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,  
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;  
 RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus  
 (HHV8).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,  
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;  
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U75698; AAC57106.1; -  
 DR InterPro; IPR000912; Herpes MCP.  
 DR InterPro; IPR003006; IG\_MHC\_  
 DR Pfam; PF01122; Herpes MCP.1.  
 DR PRINTS; PR00235; HSVCAPIIDMCP.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 SQ SEQUENCE 1376 AA; 153419 MW; 413E0CD4A7BB98D2 CRC64;

Query Match 65.3%; Score 47; DB 12; Length 1376;  
 Best Local Similarity 63.6%; Pred. No. 63;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
 Db 476 DGGHGYGLRVE 486

RESULT 5  
 ID Q98139 PRELIMINARY; PRT; 1376 AA.  
 AC Q98139;  
 DT 01-FEB-1997 (T-EMBLrel. 02, Created)  
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Major capsid protein.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.

OX NCBI\_TaxID=37296;  
 RN [1]  
 RP SEQUENCE OF 1175-1376 FROM N.A.  
 RX MEDLINE=5090463; PubMed=797879;  
 RA Chang Y., Cesarman E., Pessin M.S., Lee F., Culpepper J.,  
 RT Knowles D.M., Moore P.S.;  
 RT "Identification of herpesvirus-like DNA sequences in AIDS-associated  
 RT Kaposi's sarcoma.";  
 RL Science 266:1865-1869(1994).  
 RN [2]  
 RP SEQUENCE OF 1175-1376 FROM N.A.  
 RX MEDLINE=95214703; PubMed=7700310;  
 RA Moore P.S., Chang Y.;  
 RT "Detection of herpesvirus-like DNA sequences in Kaposi's sarcoma in  
 RT patients with and without HIV infection.";  
 RL N. Engl. J. Med. 332:1181-1185(1995).  
 RN [3]  
 RP SEQUENCE OF 1175-1376 FROM N.A.  
 RX MEDLINE=9539773; PubMed=7670109;  
 RA Cesarman E., Moore P.S., Rao P.H., Inghirami G., Knowles D.M.,  
 RA Chang Y.;  
 RT "In vitro establishment and characterization of two acquired  
 RT immunodeficiency syndrome-related lymphoma cell lines (BC-1 and BC-2)  
 RT containing Kaposi's sarcoma-associated herpesvirus-like (KSHV) DNA  
 RT sequences.";  
 RL Blood 86:2708-2714(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96099469; PubMed=8523568;  
 RA Moore P.S., Gao S.J., Dominguez G., Cesarman E., Lungu O.,  
 RA Knowles D.M., Gardner R., Pellett P.E., McGeoch D.J., Chang Y.;  
 RT "Primary characterization of a herpesvirus agent associated with  
 RT Kaposi's sarcoma.";  
 RL J. Virol. 70:549-558(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Moore P.S., Chang Y., Dominguez G., Pellett P.E.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U00377; AAB08392.1; -;  
 DR InterPro: IPR000912; Herpes\_MCP.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF03122; Herpes\_MCP; 1.  
 DR PRINTS: PR00235; HSVCAPIIDMCP.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 SQ SEQUENCE 1376 AA; 153401 MW; F2B7DF6F757C9215 CRC64;

Query Match 65.3%; Score 47; DB 12; Length 1376;  
 Best Local Similarity 63.6%; Pred. No. 63;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
 |||||  
 DB 476 DGGHGYGLRVE 486

## RESULT 6

Q9GP09 PRELIMINARY; PRT; 381 AA.  
 AC Q9GP09;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-JUN-2002 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Hypothetical 37.6 kDa protein.  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Ixodes.  
 OX NCBI\_TaxID=34613;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Salivary gland;  
 RA Iepoulle G., Rochez C., Louahed J., Rutti B., Brossard M.,  
 RA Godfroid E., Bollen A.;  
 RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors

RT Induced during the blood feeding process.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ300192; CAC20599.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 381 AA; 37570 MW; 0417F79C81EBBA1 CRC64;

Query Match 63.9%; Score 46; DB 5; Length 381;  
 Best Local Similarity 63.6%; Pred. No. 21;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGGHGYGSSFDY 12  
 |||||  
 DB 210 GGGYGGSGY 220

## RESULT 7

Q8XIH9 PRELIMINARY; PRT; 1023 AA.  
 AC Q8XIH9;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-JUN-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 21, Last annotation update)  
 DE Probable penicillin-binding protein 2.  
 OS CPZ140.  
 OC Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL: AP003193; BAB81846.1; -;  
 DR InterPro: IPR005311; PB2\_dimer.  
 DR InterPro: IPR001460; Transpeptidase.  
 DR Pfam: PF03717; PB2\_dimer; 1.  
 DR Pfam: PF00905; Transpeptidase; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1023 AA; 114912 MW; EBD302D9B3472CE3 CRC64;

Query Match 63.9%; Score 46; DB 16; Length 1023;  
 Best Local Similarity 80.0%; Pred. No. 65;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSP 10  
 |||||  
 DB 912 DGGHGYGSP 921

## RESULT 8

Q8S651 PRELIMINARY; PRT; 348 AA.  
 AC Q8S651;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Hypothetical protein.  
 OS OSNBA004A10.17 OR OSNMA0053D03.17.  
 OS Oryza sativa (Rice), and  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530; 39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=O. sativa; STRAIN=Nipponbare;  
 RA McComble W.R., de la Bastide M., Spiegel L., Nascimento L., Balija V.,

RA Zutaern T., Bell M., Preston R., Kirchoff K., Kuit K., Baker J.,  
 RA Santos L., Miller B., Cummins D.M., Katzenberger F., Muller S.,  
 RA Shah R., King L., Yang C., Dike S., O'Shaughnessy A., Palmer L.,  
 RA Dechia N.,  
 RT "Genomic sequence for *Oryza sativa*, Nipponbare strain, clone  
 RT OSJNBa0004A10, from chromosome 10, complete sequence.",  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*O. sativa* (japonica cultivar-group);  
 RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saeki C.,  
 RA Currie J., Collura K.,  
 RT "Rice Genomic Sequence.",  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC098682; AM01113.1; -  
 DR EMBL; AC131968; AA004952.1; -  
 DR Gramene; Q8651; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 348 AA; 35920 MW; F7E8ACE3AB599F9F CRC64;

Query Match 62.5%; Score 45; DB 10; Length 348;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCGSS 8  
 DB 224 GGGGCGSS 231

## RESULT 9

ID 0925H2 PRELIMINARY; PRT; 87 AA.  
 AC 0925H2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Keratin-associated protein 16.9.  
 GN KRTAP16-9 OR KRTAP16.9.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB;  
 RX MEDLINE=21185977; Pubmed=11280294;  
 RA Tratchenko A.V., Visconti R.P., Shang L., Papenbrock T., Pruett N.D.,  
 RA Ito T., Ogawa M., Anguilevitch A.,  
 RT "Overexpression of Hoxc13 in differentiating keratinocytes results in  
 RT downregulation of a novel hair keratin gene cluster and alopecia.",  
 RL Development 128:1547-1558(2001).  
 DR EMBL; AF345299; AA052897.1; -  
 DR MED; MGI:2157769; Krtap16-9.  
 SQ SEQUENCE 87 AA; 8849 MW; 93936AD6E617369 CRC64;

Query Match 61.1%; Score 44; DB 11; Length 87;  
 Best Local Similarity 77.8%; Pred. No. 7.9;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGCGSS 10  
 DB 57 GGGGCGSS 65

## RESULT 10

ID 093WZ6 PRELIMINARY; PRT; 193 AA.  
 AC 093WZ6;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Abscissic stress ripening-like protein.  
 OS Prunus persica (Peach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OC NCBI\_TaxID=3760;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Suncrest; TISSUE=Fruit;  
 RA Callahan A.M., Morgens P.H., Cohen R.A.,  
 RT "Isolation and initial characterization of cDNAs for mRNAs regulated  
 RT during peach fruit development.",  
 RL J. Am. Soc. Hortic. Sci. 118:531-537(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Suncrest; TISSUE=Fruit;  
 RA Callahan A.M., Morgens P.H., Cohen R.A., Scorza R.,  
 RT "Regulation of peach gene expression in a peach/almond hybrid.",  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF317062; AA126889.1; -  
 DR InterPro; IPR003496; ABA\_WDS.  
 DR Pfam; PF02496; ABA\_WDS; 1.  
 SQ SEQUENCE 193 AA; 20760 MW; D08C20DE062D719F CRC64;

Query Match 61.1%; Score 44; DB 10; Length 193;  
 Best Local Similarity 72.7%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGCGSS 12  
 DB 73 GGGGCGSS 83

## RESULT 11

ID 050000 PRELIMINARY; PRT; 200 AA.  
 AC 050000;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Abscissic stress ripening protein homolog.  
 DE Prunus armeniaca (Apricot).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OC NCBI\_TaxID=36596;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;  
 RA Mbegnie-A-Mbegnie D., Gomez R.-M., Fils-Lycaon B.,  
 RT "Molecular Cloning and Nucleotide Sequence of an Abscissic Acid-,  
 RT Stress-, Ripening-Induced (ASR)-Like Protein from Apricot Fruit  
 RT (Accession No. U93164). Gene Expression During Fruit Ripening. (PCR97-  
 RT 166)."  
 RL Plant Physiol. 115:1288-1288(1997).  
 DR EMBL; U93164; AA87140.1; -  
 DR InterPro; IPR003496; ABA\_WDS.  
 DR Pfam; PF02496; ABA\_WDS; 1.  
 SQ SEQUENCE 200 AA; 21240 MW; C145BA5B94C2D62 CRC64;

Query Match 61.1%; Score 44; DB 10; Length 200;  
 Best Local Similarity 72.7%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGCGSS 12  
 DB 80 GGGGCGSS 90

## RESULT 12

ID 0810E1 PRELIMINARY; PRT; 357 AA.  
 AC 0810E1;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

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DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE CG32065-PA.
GN CG32065.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neuroptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goecky J.D.,
RA Amaratunga P.G., Scherl S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abell J.F., Agbayan A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bencos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.N.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertile S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heitman T.J., Hernandez J.R., Houck J.,
RA Hosain D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jaiswal M., Kalish W., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mobergson C.,
RA Melnick G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weissbrock G.M., Weissbrock J.,
RA Williams S.M., Woodruff W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.H., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zhou S., Zhu X.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Celisner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Goecky J.D., Amaratunga P.G., Brandon R.C., Rogers Y.,
RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Bism D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Fafan D.,
RA Fertile S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Houston D., Howland T.J.,
RA Ibbesman C., Jalili M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phanavong S., Pittman G.S., Puri V., Richards S., Scheeler P.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise R., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,

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RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003548; AAN11915.1;
SQ SEQUENCE 357 AA; 40676 MW; 64F00379331EC7C8 CRC64;

Query Match 61.1%; Score 44; DB 5; Length 357;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGYGSSEFDY 12
DB 55 GGGYGSSEFDY 65

RESULT 13
ID Q92YV4 PRELIMINARY; PRT; 456 AA.
AC Q92YV4;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Hypothetical protein RA0980.
GN RA0980 OR SMA176.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Rhizobium meliloti (megaplasmid 1).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1021;
RC MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barlov-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kallan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federle N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
DR EMBL; AE007284; AAK5538.1;
DR InterPro; IPR000379; Ser_cetra_4ite.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 456 AA; 49502 MW; 8BA67515B59DA07A CRC64;

Query Match 61.1%; Score 44; DB 16; Length 456;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HGYGSSEFD 11
DB 188 HGYGSSEFD 195

RESULT 14
ID Q9CJY4 PRELIMINARY; PRT; 467 AA.
AC Q9CJY4;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Hypothetical protein PM1854.
GN PM1854.

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OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Pautian M.L., Whittem T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL: AE006223; AK03938.1;
DR InterPro: IPR001450; IPR0452; Fe_S_binding.
DR InterPro: IPR004452; Fe_S_binding.
DR TIGRFAMs: TIGR00273; TIGR00273; 1.
DR PROSITE: PS00198; 4FEAS_FERRDOXIN; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 467 AA; 51821 MW; D3DB3395B560A8B CRC64;

Query Match          61.1%; Score 44; DB 16; Length 467;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGHGYSSTF 10
Db 329 GGHGYSSTY 337

RESULT 15
ID 08X6E7 PRELIMINARY; PRT; 475 AA.
AC 08X6E7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Orf, hypothetical protein.
OS YKGF OR 20385 OR ECS0345.
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobleck E.J., Davis N.W., Lam A., Dimailanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tode T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shida T., Hatori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL: AE005208; ABG54541.1;
DR EMBL: AF002551; BAB33768.1;
DR InterPro: IPR001450; 4FEAS_FERRDOXIN.
DR InterPro: IPR004452; Fe_S_binding.
DR Pfam: PF00037; fer4; 2.
DR TIGRFAMs: TIGR00273; TIGR00273; 1.
DR PROSITE: PS00198; 4FEAS_FERRDOXIN; 2.
KW Complete proteome.

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SQ SEQUENCE 475 AA; 53000 MW; F81B64DD6A1C1B0E CRC64;
Query Match          61.1%; Score 44; DB 16; Length 475;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGHGYSSTF 10
Db 329 GGHGYSSTY 337

Search completed: November 7, 2003, 07:34:29
Job time : 6.05728 secs

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PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 XX  
 PS Claim 7; Page 74; 138pp; English.

CC The present sequence is that of complementarity determining region  
 CC 3 (CDR3) of the heavy chain of an antibody expressed by mouse  
 CC hybridoma 193/K2. This antibody has anti-Factor IX (FIX) or  
 CC anti-activated Factor IX (FIXa) activity. It is an example of  
 CC anti-FIX/FIXa antibodies of the invention. Such antibodies and  
 CC their derivatives (including those that comprise the present CDR3  
 CC peptide) have Factor VIIa (FVIIa) cofactor activity or FIXa  
 CC activating activity. Administration of the antibodies or their  
 CC derivatives leads to an increase in the procoagulant activity of  
 CC FIXa, even in the presence of FVIIa inhibitors. This allows for  
 CC rapid blood coagulation even in the absence of FVIII or FVIIa, and  
 CC in the case of FVIII inhibitor patients. The antibodies or their  
 CC derivatives are used in a claimed pharmaceutical composition for  
 CC treating patients with blood coagulation disorders, especially  
 CC haemophilia A and haemorrhagic diathesis.

CC Sequence 12 AA;

Query Match 100.0%; Score 72; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGGHGYGSSFDY 12  
 |||||  
 Db 1 DGGHGYGSSFDY 12

RESULT 2  
 AAB20434  
 ID AAB20434 standard; Protein; 249 AA.  
 XX  
 AC AAB20434;

DT 21-JUN-2001 (first entry)

XX Anti-FIX/FIXa antibody 193/K2 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;  
 KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.  
 XX  
 OS Chimeric - Mus musculus.

XX Chimeric - Synthetic.

XX Key Location/Qualifiers

FT Protein

FT Region

FT Peptide

FT Protein

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

DR WPI; 2001-290358/30.  
 DR N-PSDB; AAF30724.  
 XX  
 XX  
 PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 XX  
 PS Claim 10; Fig 15; 138pp; English.

CC The present sequence is that of a single chain Fv (scFv) derivative  
 CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain  
 CC variable regions of 193/K2 joined by an artificial, flexible linker  
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
 CC 193/K2 VH and VL regions and cloning in vector pDAP2. 193/K2 is  
 CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)  
 CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,  
 CC including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIIa inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis.

CC Sequence 249 AA;

Query Match 100.0%; Score 72; DB 22; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGGHGYGSSFDY 12  
 |||||  
 Db 99 DGGHGYGSSFDY 110

RESULT 3  
 AAR97835  
 ID AAR97835 standard; Protein; 1376 AA.  
 XX  
 AC AAR97835;

DT 11-SEP-1996 (first entry)

XX Kaposi's sarcoma associated herpesvirus ORF25 product.

KM Kaposi's sarcoma; gamma-2 herpesvirus; KSHV; therapy; diagnosis;  
 KM vaccine; diagnosis; AIDS.

XX Kaposi's sarcoma associated herpesvirus.

XX Key Location/Qualifiers

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

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FT Region

FT Region

FT Region

FT Region

FT Region

Herpes virus associated with Kaposi's sarcoma - also definitive DNA

PT sequences, useful for diagnosis of and to develop prods. for  
 PT treatment of Kaposi's sarcoma  
 XX  
 PS Claim 17; Page 175-180; 277pp; English.  
 CC  
 CC Lambda clone KS5 (AAT30681) is a fragment of a newly identified human  
 CC gamma-2 herpesvirus associated with Kaposi's sarcoma (KS). KS5 has  
 CC 17 open reading frames (AAT30682-98), 15 of which are complete,  
 CC including ORF25 (AAT30687). The protein products (AAR97830-46,  
 CC respectively) of the 17 ORFs can be expressed in eukaryotic or  
 CC bacterial host cells for use as vaccines, for KS diagnosis, or for  
 CC raising antibodies.  
 XX  
 SQ Sequence 1376 AA;  
 Query Match 65.3%; Score 47; DB 17; Length 1376;  
 Best Local Similarity 63.6%; Pred. No. 99;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DGGHGYGSSFD 11  
 DB 476 DGGHGYGLRYE 486  
 RESULT 4  
 AAR93601  
 ID AAR93601 standard; Protein; 1376 AA.  
 XX  
 AC AAR93601;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 13-AUG-1996 (first entry)  
 XX  
 DE Kaposi's sarcoma associated herpesvirus major capsid protein.  
 XX  
 KW Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;  
 KW capsid protein.  
 XX  
 OS Kaposi's sarcoma associated herpesvirus.  
 XX  
 PN MO9606159-A1.  
 PD 29-FEB-1996.  
 PF 11-AUG-1995; 95WO-US10194.  
 PR 18-AUG-1994; 94US-0292365.  
 PR 21-NOV-1994; 94US-0343101.  
 PR 11-APR-1995; 95US-0420235.  
 XX  
 PA (UYCO) UNIV COLUMBIA NEW YORK.  
 PA (GRAN/) GRANT D E.  
 PA (VIELE/) VIELE L.  
 PT Chang Y, Moore PS, Grant DE, Vele L,  
 XX WPI; 1996-151362/15.  
 DR N-PSDB; AAT16807.  
 XX  
 PT Herpesvirus DNA associated with Kaposi's sarcoma - also associated  
 PT vectors and proteins, used in detection and vaccination.  
 XX  
 PS Claim 17; Page 188-193; 305pp; English.  
 CC Kaposi's sarcoma associated herpes virus (KSHV) clone KS5 (AAT16806),  
 CC obtd. from a KS lesion genomic library, includes 15 complete ORFs and  
 CC 2 incomplete ORFs (AAT16807-23) named according to their herpesvirus  
 CC salmieri positional homologues. The major capsid protein (AAR93601)  
 CC is the product of ORF25 (AAT16807). KSHV proteins and peptides may be  
 CC obtd. by incorporating encoding sequences into a vector and expression  
 CC in host cells. They are useful in vaccines or for raising  
 CC antibodies of diagnostic or therapeutic value.  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX  
 SQ Sequence 1376 AA;  
 Query Match 65.3%; Score 47; DB 17; Length 1376;  
 Best Local Similarity 63.6%; Pred. No. 99;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DGGHGYGSSFD 11  
 DB 476 DGGHGYGLRYE 486  
 RESULT 5  
 AAG98933  
 ID AAG98933 standard; Protein; 475 AA.  
 XX  
 AC AAG98933;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE E. coli growth and proliferation related protein sequence SEQ ID NO:403.  
 XX  
 KW Escherichia coli; growth; proliferation; microbial; antimicrobial;  
 KW bacterial infection; microorganism.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO200134810-A2.  
 PD 17-MAY-2001.  
 PF 09-NOV-2000; 2000WO-US30950.  
 PR 09-NOV-1999; 99US-0164415.  
 PR 09-NOV-1999; 99US-0164415.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Forsyth RA, Ohlsen K, Zyskind J;  
 DR WPI; 2001-335933/35.  
 DR N-PSDB; AAH84604.  
 XX  
 PT Novel nucleic acids that inhibit Escherichia coli proliferation, useful  
 PT for screening for homologous genes and for designing expression vectors  
 PT -  
 XX  
 PS Claim 19; Page 467-468; 522pp; English.  
 CC AAH84373 to AAH84499 represent Escherichia coli growth and proliferation  
 CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli  
 CC growth and proliferation related proteins given in AAG99078 and AAG98830  
 CC to AAG98999. (I) can be used as potential targets for the generation of  
 CC new antimicrobial agents, and for identification of compounds which  
 CC interact with the gene products of (I). In addition the expression of  
 CC (I) and the purification of the proteins, the purified proteins can be  
 CC used to generate reagents and screen small molecule libraries or other  
 CC candidate compound libraries for compounds that can be further developed  
 CC to yield novel antimicrobial compounds. In addition, nucleic acid probes  
 CC complementary to (I) that are specific for particular species of  
 CC microorganisms can be used to identify particular microorganism species  
 CC in clinical specimens, therefore, providing a rapid and dependable  
 CC method by which to identify the causative agents of a bacterial  
 CC infection. Also, antibodies generated against proteins translated from  
 CC mRNA transcribed from proliferation-regulated sequences can also be used  
 CC to screen for specific microorganisms that produce such proteins in a  
 CC species-specific manner. AAH84371 and AAH84670 represent sequencing  
 CC primers used in the isolation of E. coli growth and proliferation  
 CC related sequence, which are used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 475 AA;  
 Query Match 61.1%; Score 44; DB 22; Length 475;

Best Local Similarity 77.8%; Pred. No. 99;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GGHGYGSSSF 10  
Db 329 GGHGYGSSIF 337

RESULT 6  
ABG27993  
ID ABG27993 standard; Protein; 81 AA.

AC ABG27993;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #27984.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSB-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS92180.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

PS Claim 20; SEQ ID NO 58352; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG0377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 81 AA;

Query Match 59.7%; Score 43; DB 22; Length 81;  
Best Local Similarity 77.8%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGHGYGSSSF 10  
Db 42 GGHGYGSSSF 50

RESULT 7  
ABP69638  
ID ABP69638 standard; Protein; 81 AA.

AC ABP69638;

DT 20-JAN-2003 (first entry)

DE Human polypeptide SEQ ID NO 1685.

KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoicide;  
KW antidiabetic.

OS Homo sapiens.

PN WO200270539-A2.

PD 12-SEP-2002.

PF 05-MAR-2002; 2002WO-US05095.

PR 05-MAR-2001; 2001US-0799451.

PA (HYSB-) HYSEQ INC.

PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

PI Wehrman T, Wang J, Wang D, Drmanac RT;

DR WPI; 2002-759812/82.

DR N-PSDB; ABZ11855.

PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
PT platelet or coagulation disorders

PS Claim 9; SEQ ID NO 1685; 1012pp + Sequence Listing; English.

CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences  
CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
CC coding protein or complementary sequences. The polynucleotides are useful  
CC for identifying expressed genes or for physical mapping of human genome.  
CC The encoded polypeptides (ABP68902-ABP68849) are useful as molecular  
CC weight markers, as a food supplement, for generating antibodies, in  
CC medical imaging, screening and diagnostic assays and for treating  
CC cell-proliferative disorders (cancer), neurodegenerative diseases  
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
CC disorders, platelet or coagulation disorders, wound, burns, incision,  
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
CC parasitic), arthritis, etc.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 81 AA;

Query Match 59.7%; Score 43; DB 23; Length 81;  
Best Local Similarity 77.8%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGHGXGSSF 10  
 ||:|||||  
 DB 42 GGYGSGSF 50

RESULT 8  
 ABG27994  
 ID ABG27994 standard; Protein, 139 AA.

XX AC ABG27994;

XX DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #27985.

XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW Food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS92181.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

PS Claim 20; SEQ ID No 58353; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations in  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 139 AA;

Query Match 59.7%; Score 43; DB 22; Length 139;  
 Best Local Similarity 77.8%; Pred. No. 42;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHGXGSSF 10  
 ||:|||||  
 DB 52 GGYGSGSF 60

RESULT 9  
 AAY76638  
 ID AAY76638 standard; Protein, 220 AA.

XX AC AAY76638;

XX DT 10-APR-2000 (first entry)

DE Human ovarian tumor EST fragment encoded protein 134.

XX KM Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
 XX KW gene therapy; treatment.

XX OS Homo sapiens.

XX PN DE19817557-A1.

XX PD 21-OCT-1999.

XX PF 09-APR-1998; 98DE-1017557.

XX PR 09-APR-1998; 98DE-1017557.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX DR WPI; 1999-591920/51.

XX DR N-PSDB; AAZ77506.

PT New nucleic acid sequences expressed in ovarian, and some other, cancer  
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
 PT identification of therapeutic agents

PS Claim 25; Page 299; 310bp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which  
 CC have anticancer activity and are highly expressed in ovarian tumor  
 CC tissue (and some also in testis and breast cancer tissue). The products  
 CC of the invention can be used for gene therapy. (A) are used (i) for  
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete  
 CC genes. (B) are used (i) to identify agents suitable for treatment of  
 CC ovarian cancer; (ii) directly for treating this form of cancer  
 CC (including expression from gene therapy vectors) and (iii) for generation  
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
 CC sequence tags) from a particular tissue type before comparison of  
 CC expression patterns. This allows a significantly longer fragment of the  
 CC gene to be revealed, so should reduce the number of failures associated  
 CC with the fact that ESTs from different libraries may represent different  
 CC parts of the same unknown gene, distorting the estimated frequency of  
 CC occurrence in a particular tissue. AAY75505-Y76638 represent protein  
 CC fragments encoded by the human ovarian tumor cDNA library derived EST  
 CC fragments represented in AAZ77450-Z77572.

XX Sequence 220 AA;

Query Match 59.7%; Score 43; DB 20; Length 220;  
 Best Local Similarity 70.0%; Pred. No. 66;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHGXGSSF 11  
 ||:|||||  
 DB 51 GGHGXGSGD 60

RESULT 10  
 AAE27023  
 ID AAE27023 standard; Protein, 223 AA.

XX AAE27023;  
 AC  
 XX  
 DT 13-DEC-2002 (first entry)  
 DE  
 XX Human gene 18 encoded secreted protein variant. SEQ ID NO:116.  
 DE  
 XX Human; immunodeficiency; X-linked agammaglobulinemia; septic shock;  
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW Grave's disease; diabetes mellitus; haematopoietic disorders; stroke;  
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;  
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;  
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;  
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;  
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;  
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;  
 KW endocrine disorder; Addison's disease; reproductive system disorder;  
 KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;  
 KW anti-HIV; tranquilliser; gout; antiparasitic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002077287-A1.  
 XX  
 PD 20-JUN-2002.  
 XX  
 XX 11-MAY-2001; 2001US-0852659.  
 PR  
 XX 11-SEP-1998; 98US-0152060.  
 PR  
 XX (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (LITY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 PA (FISC/) FISCHER C L.  
 PA (LIH/) LI H.  
 PA (SOP/) SOPPER D R.  
 PA (GENT/) GENTZ R L.  
 PA (WEI/) WEI Y.  
 XX  
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;  
 PI Sopper DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;  
 PI Ferrie AM;  
 XX  
 DR WPI; 2002-598780/64.  
 XX  
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,  
 PT preventing, treating immune, hyperproliferative, cardiovascular,  
 PT neurological, reproductive disorders and identifying modulators of  
 PT therapeutic use  
 XX  
 PS Disclosure; Page 205-206; 209pp; English.  
 XX  
 CC AAD4636-AAD4676 represent cDNAs corresponding to 28 human secreted  
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.  
 CC AAE27000-AAE27025 represent human secreted protein fragments or their  
 CC variants. The secreted proteins and genes are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Specific uses are described for each of the 28 genes, based  
 CC on the tissues in which they are most highly expressed and include  
 CC developing products for the diagnosis or treatment of immunodeficiencies,  
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe  
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus  
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune  
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,  
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions  
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel  
 CC disease, Crohn's disease, haematopoietic disorders, respiratory  
 CC disorders e.g., asthma and allergy, gastrointestinal disorders e.g.,  
 CC inflammatory bowel disease), cancers e.g., gastric, ovarian, lung,  
 CC liver, bladder and breast), central nervous system (CNS) disorders e.g.,  
 CC ischemic brain injury and/or stroke, neurodegenerative disorders e.g.,

CC Parkinson's disease and Alzheimer's disease, AIDS-related dementia and  
 CC prion disease, cardiovascular disorders e.g., atherosclerosis, arhythmias,  
 CC atherosclerosis, inflammatory disorders e.g., hepatitis, gout, trauma,  
 CC pancreatitis, sarcoidosis and allogeneic transplant rejection, blood-  
 CC related disorder (thrombosis, arterial thrombosis, atherosclerosis),  
 CC hyperproliferative disorders, respiratory disorders e.g., rhinitis,  
 CC sinusitis, tonsillitis, lung cancer, allergic disorders, pneumonitis,  
 CC renal disorders e.g., acute glomerulonephritis, neurological diseases,  
 CC liver disorders, endocrine disorders e.g., hyperthyroidism, Addison's  
 CC disease, hyperpituitarism, infectious diseases and reproductive system  
 CC disorders e.g., endometriosis. The present sequence represents a human  
 CC secreted protein variant of the invention.  
 XX  
 SQ Sequence 223 AA;  
 XX

Query Match 59.7%; Score 43; DB 23; Length 223;  
 Best Local Similarity 70.0%; Pred. No. 66;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GGHGYGSSPD 11  
 Db 162 GGHGYGAGD 171

RESULT 11  
 AAE27161  
 ID AAE27161 standard; Protein; 223 AA.  
 XX  
 AC AAE27161;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Human gene 18 encoded secreted protein fragment, SEQ ID NO:116.  
 DE  
 XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;  
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angioneu-  
 KW cerebral ischemia; cardiovascular disorder; nervous system disorder;  
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;  
 KW infection; corneal infection; skin aging; food additive; preservative;  
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;  
 KW cardiant; vasotropic; cerebroprotective; antiproliferative; cytostatic;  
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;  
 KW vulnery.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002076756-A1.  
 XX  
 PD 20-JUN-2002.  
 XX  
 XX 11-MAY-2001; 2001US-0853161.  
 PR  
 XX 02-FEB-2001; 2001US-265583P.  
 PR  
 XX (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (LITY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 PA (FISC/) FISCHER C L.  
 PA (LIH/) LI H.  
 PA (SOP/) SOPPER D R.  
 PA (GENT/) GENTZ R L.  
 PA (WEI/) WEI Y.  
 PA (MOOR/) MOORE P A.  
 PA (YOUNG/) YOUNG P E.  
 PA (GREEN/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 XX  
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;  
 PI Sopper DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;  
 PI Ferrie AM;  
 XX

DR WPI; 2002-574454/61.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful  
PT for diagnosing, preventing, treating or ameliorating medical conditions  
PT and as food additives or preservatives

XX Disclosure; Page 205-206; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted  
CC protein genes, and ABE27097-ABE27137 represent the proteins they encode.  
CC ABE27138-ABE27164 represent human secreted protein fragments. The genes  
CC and their corresponding secreted proteins are useful for preventing,  
CC treating or ameliorating medical conditions, e.g., by protein or gene  
CC therapy. Secreted protein sequences of the invention are useful for the  
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.,  
CC rheumatoid arthritis), hyperproliferative disorders (e.g., neoplasms of  
CC the breast or liver), cerebrovascular disorders (e.g., cerebral ischemia,  
CC angiodystrophies), cardiovascular disorders (e.g., cardiac arrest), nervous  
CC system disorders (e.g., Alzheimer's disease), infections caused by fungi,  
CC bacteria and viruses and ocular disorders (e.g., corneal infection). The  
CC polypeptides can also be used to aid wound healing and epithelial cell  
CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
CC before transplantation, for supporting cell culture of primary tissues,  
CC to regenerate tissues and in chemotaxis. They can also be used as food  
CC additives or preservatives to increase or decrease storage capabilities,  
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors  
CC and other nutritional components. The present sequence represents a human  
CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 223 AA;

Query Match 59.7%; Score 43; DB 23; Length 223;

Best Local Similarity 70.0%; Pred. No. 66;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGHGGSSPD 11  
|||  
162 GGGHGGCGAGD 171

RESULT 12  
ABU65034  
ID ABU65034 standard; Protein; 223 AA.

AC ABU65034;

DT 15-MAY-2003 (first entry)

DE Human secreted protein gene 18, protein #8.

XX Secreted protein; immunodeficiency; multiple sclerosis;  
XX severe combined immunodeficiency; autoimmune disorder; cancer;  
XX rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;  
XX inflammatory condition; septic shock; inflammatory bowel disease;  
XX Crohn's disease; respiratory disorder; asthma; allergy; stroke;  
XX gastrointestinal disorder; central nervous system disorder;  
XX ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;  
XX Alzheimer's disease; cardiovascular disorder; atherosclerosis;  
XX blood-related disorder; thrombosis; atherosclerosis; renal disorder;  
XX hyperproliferative disorder; acute glomerulonephritis; Addison's disease;  
XX endocrine disorder; liver disease; reproductive system disorder;  
XX endometriosis; infectious disease; pancreatic disorder; vaccine;  
XX wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;  
XX body height; hair colour; human.

XX Homo sapiens.

XX US2002172994-A1.

XX 21-NOV-2002.

XX 11-MAY-2001; 2001US-0852797.

PR 14-MAR-1997; 97US-040710B.  
PR 14-MAR-1997; 97US-040762B.  
PR 30-MAY-1997; 97US-048100B.  
PR 30-MAY-1997; 97US-048189B.  
PR 30-MAY-1997; 97US-048357B.  
PR 30-MAY-1997; 97US-050934B.  
PR 06-JUN-1997; 97US-048970B.  
PR 05-SEP-1997; 97US-057765B.  
PR 19-DEC-1997; 97US-068368B.  
PR 02-FEB-2001; 2001US-26583B.  
PR 12-MAR-1998; 98MO-US0486B.  
PR 11-SEP-1998; 98US-0152060.

XX (RUBEN/) RUBEN S M.  
XX (ROSE/) ROSEN C A.  
XX (LIYU/) LI Y.  
XX (ZENG/) ZENG Z.  
XX (KIM/) KIM H.  
XX (FISCH/) FISCHER C L.  
XX (LIH/) LI H.  
XX (SOPE/) SOPPE D R.  
XX (GENT/) GENTZ R L.  
XX (WEIY/) WEI Y.  
XX (MOOR/) MOORE P A.  
XX (YOUN/) YOUNG P E.  
XX (GREEN/) GREENE J M.  
XX (FERR/) FERRIE A M.

PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H,  
PI Soppe DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM,  
PI Ferrie AM;

XX WPI; 2003-310989/30.

XX New human secreted polypeptides and polynucleotides for diagnosing,  
PT prognosing, preventing and treating immune, hyperproliferative, liver,  
PT kidney, reproductive disorders and for identifying modulators of  
PT therapeutic use -

XX Disclosure; Page 13; 209pp; English.

XX The invention relates to an isolated polypeptide comprising an amino acid  
CC sequence at least 95% identical to sequence of 28 human secreted  
CC proteins, their fragment, polypeptide domain, epitope, secreted form,  
CC variant, allelic variant, or species homologue, or the encoded sequence  
CC included in ATCC 97921 and 97922. Also included are the encoding  
CC nucleic acids, recombinant vectors, host cells, antibodies, and genes.  
CC Treating, prognosing or ameliorating a medical condition e.g.,  
CC immunodeficiencies (e.g., X-linked agammaglobulinemia), B cell  
CC disorders (e.g., systemic erythematous, rheumatoid arthritis, multiple  
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,  
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),  
CC haematopoietic disorders, inflammatory conditions (e.g., septic shock),  
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),  
CC respiratory disorders (e.g., asthma and allergy), gastrointestinal  
CC disorders, cancers (e.g., gastric, ovarian, lung, bladder, liver and  
CC breast), central nervous system (CNS) disorders (e.g., ischemic brain  
CC injury and/or stroke, traumatic brain injury), neurodegenerative  
CC disorders (e.g., Parkinson's disease and Alzheimer's disease, AIDS-related  
CC dementia, and prion disease), cardiovascular disorders (e.g.,  
CC atherosclerosis, myocarditis, cardiomyopathy, heart failure, stroke,  
CC bypass complications), inflammation (e.g., hepatitis, gout, trauma,  
CC pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),  
CC blood-related disorders (thrombosis, arterial thrombosis),  
CC hyperproliferative disorders, renal disorders (e.g., acute  
CC glomerulonephritis), endocrine disorders (e.g., Addison's disease,  
CC hyperthyroidism, hyperparathyroidism), liver diseases and disorders,  
CC reproductive system disorders (e.g., endometriosis), infectious diseases,  
CC and pancreatic disorders. Many other diseases and disorders are listed in  
CC the specification. They also useful as a vaccine adjuvant. Further they  
CC are useful to enhance or inhibit complement mediated cell lysis, for

stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention.

Sequence 223 AA;

Query Match 59.7%; Score 43; DB 24; Length 223;

Best Local Similarity 70.0%; Pred. No. 66;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGHYGSSFPD 11  
|||  
DB 162 GGHYGGAGND 171

RESULT 13

AA678409  
ID AA678409 standard; protein; 248 AA.

AC AA678409;

DT 04-FEB-2002 (first entry)

DE Amino acid sequence of anti HSP90 antibody.

FW Fungal infection; beta glucan synthase inhibitor; antifungal;

KW anti HSP90 antibody; intensive care; non-albicans; Candida albicans;

KM amphoterin B; heat shock protein; echinocandin antifungal agent;

KX polyene antifungal agent.

OS Candida albicans.

OS Synthetic.

PN WO200176627-A1.

PD 18-OCT-2001.

PF 20-MAR-2001; 2001WO-GB01195.

PR 06-APR-2000; 2000GB-0008305.

PA (NEUT-) NEUTEC PHARMA PLC.

PI Burnie JP;

PP MPI; 2001-663017/76.

PT New composition useful in a composition for the treatment of fungal

PT infections comprises antibody comprising specified sequence

XX Claim 6; Page 46-47; 50pp; English.

This invention relates to an antibody or an antigen binding fragment specific for at least one epitope comprising a specified sequence. The applications of the anti HSP90 antibodies include fungal strain growth inhibitor, in the preparation of a diagnostic kit for diagnosing at least one fungal infection and also, in a composition for preparing and for treating fungal infections of human or animal body, caused due to a Candida Cryptococcus, Histoplasma, Aspergillus, Torulopsis, Mucormycosis, Blastomycosis, Cocciidiomycosis or Paracoccidiomycosis organism, resistant to the antifungal agent. The antibody may binds at least one epitope of a fungal

stresses protein and significantly enhances the efficacy of the antifungal agent against fungal infections, allowing for either lower treatment dosages or more effective treatment at the same dose, which allows for reduction of unwanted side-effects. This sequence represents the anti HSP90 antibody.

Sequence 248 AA;

Query Match 59.7%; Score 43; DB 22; Length 248;

Best Local Similarity 63.6%; Pred. No. 74;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGHYGSSFPDY 12  
|||  
DB 102 GGRDFGDSFPDY 112

RESULT 14

AA670222  
ID AAV70222 standard; Protein; 285 AA.

AC AAV70222;

DT 06-JUN-2000 (first entry)

DE Human RNA-associated protein-3 (RNAP-3).

FW RNA-associated protein; RNAP; human; clone 2263514; cytostatic;

KW immunosuppressive; antiinflammatory; keratolytic; neuroprotective;

KM antiarteriosclerotic; hepatotropic; antipsoriatic; virucide; anti-HIV;

KW antiallergic; antirheumatic; antiarthritic; ophthalmological; autoimmune;

KW antimicrobial; cell proliferative disorder; inflammation; cirrhosis;

KW actinic keratosis; bursitis; arteriosclerosis; artherosclerosis;

KW hepatitis; myelofibrosis; primary thrombocytopenia; psoriasis; cancer;

KW mixed connective tissue disease; MCTD; HIV; uveitis; Crohn's disease;

KX allergy; rheumatoid arthritis; parasitic infection.

OS Homo sapiens.

PN Key

FW Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Binding-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

Location/Qualifiers

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

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/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

/note= "Potential phosphorylation site"

Human RNA-associated proteins useful in diagnosing, treating and

preventing cell proliferative, autoimmune, inflammatory and infectious

disorders

Claim 1; Page 81; 123pp; English.

CC The present amino acid sequence is the human RNA-associated protein-3  
 CC (RNAP-3), identified in Incyte clone 2263514, derived from UTRN0702  
 CC library. It is expressed in reproductive, nervous and hematopoietic or  
 CC immune tissues. It has cytosolic, immunosuppressive, keratolytic,  
 CC antiinflammatory, antiarteriosclerotic, hepatotropic, virucide,  
 CC neuroprotective, antiparasitic, anti-HIV, antiallergic, antirheumatic,  
 CC antiarthritic, ophthalmological and antimicrobial activity.  
 CC RNAP antibodies are useful for diagnosis of diseases associated with  
 CC altered expression or activity of RNAP. It is used to treat cell  
 CC proliferative, autoimmune, inflammatory and infectious disorders, like  
 CC actinic keratosis, burns, arthritis, arteriosclerosis, atherosclerosis,  
 CC cirrhosis, hepatitis, myelofibrosis, mixed connective tissue disease  
 CC (MCTD), psoriasis, primary thrombocythemia and cancer, HIV, allergies,  
 CC rheumatoid arthritis, uveitis, Crohn's disease, and bacterial, viral and  
 CC parasitic infections.

XX  
 SQ Sequence 285 AA;

Query Match 59.7%; Score 43; DB 21; Length 285;  
 Best Local Similarity 70.0%; Pred. No. 85;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHGYGSSFD 11  
 ||||| :  
 Db 116 GGHGYGAGD 125

# RESULT 15

ABG02073  
 ID ABG02073 standard; Protein; 354 AA.

XX  
 AC ABG02073;

XX  
 DT 13-FEB-2002 (first entry)

XX  
 DE Novel human diagnostic protein #2064.

XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX  
 PN WO200175067-A2.

XX  
 PD 11-OCT-2001.

XX  
 PF 30-MAR-2001; 2001WO-US08631.

XX  
 PR 31-MAR-2000; 2000US-0540217.

XX  
 PR 23-AUG-2000; 2000US-0649167.

XX  
 PA (HYSE-) HYSEQ INC.

XX  
 PI Drmanac RT, Liu C, Tang YT;

XX  
 DR WPI; 2001-639362/73.

XX  
 DR N-PSDB; AAS66260.

XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

XX  
 PS Claim 20; SEQ ID No 32432; 103BP; English.

XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pat\_sequences.

XX  
 SQ Sequence 354 AA;

Query Match 59.7%; Score 43; DB 22; Length 354;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHGYGSSFD 11  
 ||||| :  
 Db 185 GGHGYGAGD 194

Search completed: November 7, 2003, 07:26:58  
 Job time : 7.1749 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 10.526 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992B-6

Perfect score: 72  
Sequence: 1 DGGHGYSSFPDY 12

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PC1\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44	61.1	102 12 US-10-029-386-28297	Sequence 28297, A
2	44	61.1	475 12 US-10-287-274-403	Sequence 403, App
3	43	59.7	223 9 US-09-853-161-116	Sequence 116, App
4	43	59.7	223 9 US-09-852-659A-116	Sequence 116, App
5	43	59.7	223 10 US-09-852-797-116	Sequence 116, App
6	43	59.7	248 12 US-10-240-819-2	Sequence 2, Appl
7	40	55.6	126 9 US-09-253-794-7	Sequence 7, Appl
8	40	55.6	126 9 US-09-229-200A-8	Sequence 8, Appl
9	40	55.6	126 9 US-09-229-200A-18	Sequence 10, Appl
10	40	55.6	126 11 US-09-795-515-10	Sequence 10, Appl
11	40	55.6	126 12 US-10-422-049-10	Sequence 10, Appl
12	40	55.6	126 15 US-10-267-286A-11	Sequence 11, Appl
13	40	55.6	159 9 US-09-925-302-630	Sequence 630, App
14	39	54.2	295 10 US-09-738-626-6160	Sequence 6160, App
15	39	54.2	657 9 US-09-950-368-1	Sequence 1, Appl

16	39	54.2	657 12 US-10-401-437-2	Sequence 2, Appl
17	39	54.2	657 12 US-10-402-312-2	Sequence 2, Appl
18	39	54.2	657 12 US-10-402-067-2	Sequence 2, Appl
19	39	54.2	657 12 US-10-401-436-2	Sequence 2, Appl
20	38.5	53.5	348 15 US-10-156-761-8089	Sequence 8089, App
21	38	52.8	307 10 US-09-036-613-7	Sequence 7, Appl
22	38	52.8	382 14 US-10-029-180-56	Sequence 56, Appl
23	38	52.8	428 14 US-10-062-254-372	Sequence 372, App
24	38	52.8	491 15 US-10-156-761-14939	Sequence 14939, A
25	38	52.8	558 10 US-09-770-517C-2	Sequence 2, Appl
26	38	52.8	582 15 US-10-156-761-11262	Sequence 11262, A
27	38	52.8	620 15 US-10-156-761-7979	Sequence 7979, App
28	38	52.8	1239 10 US-09-671-388-2	Sequence 2, Appl
29	37.5	52.1	286 12 US-10-374-534-2	Sequence 1872, App
30	37	51.4	10 11 US-09-572-404B-1872	Sequence 2864, App
31	37	51.4	10 11 US-09-572-404B-2864	Sequence 2864, App
32	37	51.4	10 11 US-09-572-404B-2874	Sequence 2874, App
33	37	51.4	195 12 US-10-425-586-5	Sequence 5, Appl
34	37	51.4	229 12 US-10-425-586-8	Sequence 8, Appl
35	37	51.4	246 12 US-10-425-586-6	Sequence 6, Appl
36	37	51.4	267 12 US-10-425-586-7	Sequence 7, Appl
37	37	51.4	279 15 US-10-204-887-138	Sequence 138, App
38	37	51.4	313 12 US-10-425-586-3	Sequence 3, Appl
39	37	51.4	432 10 US-09-919-172-9	Sequence 4, Appl
40	37	51.4	432 12 US-09-515-355-18	Sequence 9, Appl
41	37	51.4	432 12 US-10-156-761-13993	Sequence 18, Appl
42	37	51.4	446 15 US-10-102-806-469	Sequence 13993, A
43	37	51.4	459 15 US-10-102-806-469	Sequence 469, App
44	37	51.4	511 15 US-10-227-629-5	Sequence 5, Appl
45	37	51.4	519 9 US-09-815-242-11388	Sequence 11388, A

#### ALIGNMENTS

RESULT 1  
US-10-029-386-28297  
; Sequence 28297, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 28297  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR21, 50.0  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.4  
US-10-029-386-28297

Query Match 61.1%; Score 44; DB 12; Length 102;  
Best Local Similarity 80.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGHGYSSFPDY 12  
DB 91 GSGYSSFPDY 100  
RESULT 2  
US-10-287-274-403  
; Sequence 403, Application US/10287274  
; Publication No. US20030181408A1  
; GENERAL INFORMATION:

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; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELITRA 0089V1
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: RascSeq for Windows Version 4.0
; SEQ ID NO 403
; TYPE: PRT
; LENGTH: 475
; ORGANISM: Escherichia coli
US-10-287-274-403
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Query Match          61.1%; Score 44; DB 12; Length 475;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      2 GGHGSSSF 10
DB      329 GGHGSSIV 337
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RESULT 3
US-09-853-161-116
; Sequence 116: Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; TYPE: PRT
; LENGTH: 223
; ORGANISM: Homo sapiens
US-09-853-161-116
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Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      2 GGHGSSSFD 11
DB      162 GGHGSSGAGD 171
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RESULT 4
US-09-852-659A-116
; Sequence 116: Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; TYPE: PRT
; LENGTH: 223
; ORGANISM: Homo sapiens
US-09-852-659A-116
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Query Match          59.7%; Score 43; DB 9; Length 223;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      2 GGHGSSSFD 11
DB      162 GGHGSSGAGD 171
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RESULT 5
US-09-852-797-116
; Sequence 116: Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
```

PRIOR APPLICATION NUMBER: 60/040,762  
PRIOR FILING DATE: 1997-03-14  
PRIOR APPLICATION NUMBER: 60/040,710  
PRIOR FILING DATE: 1997-03-14  
PRIOR APPLICATION NUMBER: 60/050,934  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/048,100  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/048,357  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/048,189  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: 60/057,765  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/048,970  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/068,368  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 116  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-652-797-116

Query Match 59.7%; Score 43; DB 10; Length 223;  
Best Local Similarity 70.0%; Pred. No. 54;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGYGGSSFD 11  
Db 162 GGGYGGAGD 171

RESULT 6  
US-10-240-819-2  
Sequence 2, Application US/10240819  
Publication No. US20030180285A1  
GENERAL INFORMATION:  
APPLICANT: BURNIE, JAMES PETER  
TITLE OF INVENTION: TREATMENT OF FUNGAL INFECTIONS WITH POLYENE OR BETA GLUCAN  
TITLE OF INVENTION: SYNTHASE INHIBITOR ANTI-FUNGALS COMBINED WITH ANTI HSP90  
FILE REFERENCE: 050885/0232613  
CURRENT APPLICATION NUMBER: US/10/240,819  
CURRENT FILING DATE: 2002-10-07  
PRIOR APPLICATION NUMBER: PCT/GB01/01195  
PRIOR FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: GB 0008305.5  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic modified  
US-10-240-819-2

Query Match 59.7%; Score 43; DB 12; Length 248;  
Best Local Similarity 63.6%; Pred. No. 60;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGYGGSSFDY 12  
Db 102 GGGYGGSSFDY 112

RESULT 7  
US-09-253-794-7

Sequence 7, Application US/09253794  
Patent No. US20020018750A1  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
MOUSE MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-253-794-7

Query Match 55.6%; Score 40; DB 9; Length 126;  
Best Local Similarity 77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGYGGSS 9  
Db 99 DGGYGGSS 107

RESULT 8  
US-09-229-200A-8  
Sequence 8, Application US/09229200A  
Patent No. US20020099179A1  
GENERAL INFORMATION:  
APPLICANT: Jolliffe et al.  
TITLE OF INVENTION: CD4 Specific Recombinant Antibody  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Johnson & Johnson  
STREET: One Johnson & Johnson Plaza  
CITY: New Brunswick  
STATE: NJ  
COUNTRY: USA  
ZIP: 08933-7003  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS

SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,200A  
FILING DATE: 13-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Wallen, III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: ORT-948  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (858) 784-3239  
TELEFAX: (908) 524-2808  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-229-200A-8

Query Match 55.6%; Score 40; DB 9; Length 126;  
Best Local Similarity 77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

RESULT 9  
US-09-229-200A-18  
Sequence 18, Application US/09229200A  
Patent No. US20020099179A1  
GENERAL INFORMATION:  
APPLICANT: Jolliffe et al.  
TITLE OF INVENTION: CD4 Specific Recombinant Antibody  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESS: Johnson & Johnson  
STREET: One Johnson & Johnson Plaza  
CITY: New Brunswick  
STATE: NJ  
COUNTRY: USA  
ZIP: 08933-7003  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,200A  
FILING DATE: 13-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Wallen, III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: ORT-948  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (858) 784-3239  
TELEFAX: (908) 524-2808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-229-200A-18

Query Match 55.6%; Score 40; DB 9; Length 126;  
Best Local Similarity 77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DGGHGYGSS 9

DB 99 DGGHGYGSS 107

RESULT 10  
US-09-795-515-10  
Sequence 10, Application US/09795515  
Publication No. US20030039645A1  
GENERAL INFORMATION:  
APPLICANT: Adair, John R.  
APPLICANT: Atwal, Diljeet S.  
APPLICANT: Emtage, John S.  
TITLE OF INVENTION: Humanised Antibodies  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/795,515  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,658  
FILING DATE: 01-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Treviño, Doreen Yacko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-09-795-515-10

Query Match 55.6%; Score 40; DB 11; Length 126;  
Best Local Similarity 77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

RESULT 11  
US-10-422-049-10  
Sequence 10, Application US/10422049  
Publication No. US20030199679A1  
GENERAL INFORMATION:  
APPLICANT: Adair, John Robert  
APPLICANT: Atwal, Diljeet Singh  
APPLICANT: Emtage, John Spencer  
APPLICANT: Bodmer, Mark William  
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha  
FILE REFERENCE: CARP0063  
CURRENT APPLICATION NUMBER: US/10/422,049  
PRIOR FILING DATE: 2003-04-22  
CURRENT APPLICATION NUMBER: US/09/267,281  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 08/456,418

PRIOR FILING DATE: 1995-06-01  
PRIOR APPLICATION NUMBER: 08/373,882  
PRIOR FILING DATE: 1995-01-17  
PRIOR APPLICATION NUMBER: 07/920,378  
PRIOR FILING DATE: 1992-09-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 126  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-422-049-10

Query Match  
Best local Similarity 55.6%; Score 40; DB 12; Length 126;  
77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
|||:|  
Db 99 DGGHGYGSS 107

RESULT 12  
US-10-267-286A-11  
Sequence 11, Application US/10267286A  
Publication No. US20030108548A1  
GENERAL INFORMATION:  
APPLICANT: BLUESTONE, JEFFREY A.  
APPLICANT: ZIVIN, ROBERT A.  
APPLICANT: JOLIFFE, LINDA K.  
TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE  
TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL  
FILE REFERENCE: TOLT:004USC1  
CURRENT APPLICATION NUMBER: US/10/267,286A  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: 08/557,050  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: PCT/US94/06198  
PRIOR FILING DATE: 1994-06-01  
PRIOR APPLICATION NUMBER: 08/070,116  
PRIOR FILING DATE: 1993-06-01  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 11  
LENGTH: 126  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-267-286A-11

Query Match  
Best local Similarity 55.6%; Score 40; DB 15; Length 126;  
77.8%; Pred. No. 86;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
|||:|  
Db 99 DGGHGYGSS 107

RESULT 13  
US-09-925-302-630  
Sequence 630, Application US/09925302  
Patent No. US20020044941A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 630  
LENGTH: 159  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-302-630

Query Match  
Best local Similarity 55.6%; Score 40; DB 9; Length 159;  
70.0%; Pred. No. 1,1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNGYSSPDY 12  
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Db 128 GNGYSSPDY 137

RESULT 14  
US-09-738-626-6160  
Sequence 6160, Application US/09738626  
Publication No. US20020197603A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KETIRO  
APPLICANT: YOKOI, HARUHIRO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patentin ver. 3.0  
SEQ ID NO 6160  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6160

Query Match  
Best local Similarity 54.2%; Score 39; DB 10; Length 295;  
58.3%; Pred. No. 2.8e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGGHGYGSSPDY 12  
|||:|  
Db 282 DGGHGYGSSPDY 293

RESULT 15  
US-09-950-368-1  
Sequence 1, Application US/09950368  
Patent No. US20020061580A1  
GENERAL INFORMATION:  
APPLICANT: Genencor International, Inc.  
TITLE OF INVENTION: Alpha/Beta Hydrolyase-Fold Enzymes  
FILE REFERENCE: GC511-PCT  
CURRENT APPLICATION NUMBER: US/09/950,368  
CURRENT FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 09/355,166

; PRIOR FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 657  
; TYPE: PRT  
; ORGANISM: Bacillus  
US-09-950-368-1

Query Match 54.2%; Score 39; DB 9; Length 657;  
Best Local Similarity 66.7%; Pred. No. 6e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GSHGYGSSR 10  
| | | | |  
DB 469 GSHGYGQEF 477

Search completed: November 7, 2003, 08:16:50  
Job time : 11.526 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 : Search time 1.76235 Seconds  
(without alignments)  
288,098 Million cell updates/sec

Title: US-09-661-992B-6  
Perfect score: 72  
Sequence: 1 DQGHGYSFIDY 12

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued Patents AA:\*  
2: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	65.3	861	2 US-08-343-101A-18	Sequence 18, Appl
2	47	65.3	861	3 US-09-183-688-18	Sequence 18, Appl
3	47	65.3	861	4 US-09-519-489-18	Sequence 18, Appl
4	47	65.3	1376	1 US-08-420-235B-3	Sequence 3, Appl
5	47	65.3	1376	3 US-08-793-624-3	Sequence 3, Appl
6	47	65.3	1376	5 PCT-US95-10194-3	Sequence 3, Appl
7	43	59.7	223	4 US-09-152-060-16	Sequence 16, Appl
8	42	58.3	328	4 US-09-252-991A-19311	Sequence 19311, A
9	40	53.6	117	1 US-07-942-245-18	Sequence 18, Appl
10	40	53.6	125	1 US-07-942-245-33	Sequence 33, Appl
11	40	55.6	126	1 US-08-107-669D-8	Sequence 8, Appl
12	40	55.6	126	1 US-08-472-788A-8	Sequence 8, Appl
13	40	55.6	126	2 US-08-477-531B-8	Sequence 8, Appl
14	40	55.6	126	2 US-08-303-568B-10	Sequence 10, Appl
15	40	55.6	126	2 US-08-082-842A-8	Sequence 8, Appl
16	40	55.6	126	2 US-08-318-157B-7	Sequence 7, Appl
17	40	55.6	126	2 US-08-070-116A-11	Sequence 11, Appl
18	40	55.6	126	2 US-08-116-247-11	Sequence 11, Appl
19	40	55.6	126	2 US-08-557-050-11	Sequence 11, Appl
20	40	55.6	127	2 US-08-652-558-50	Sequence 50, Appl
21	39	54.2	296	2 US-08-700-637-4	Sequence 4, Appl
22	39	54.2	368	4 US-09-252-991A-19552	Sequence 19552, A
23	39	54.2	415	4 US-09-252-991A-31892	Sequence 31892, A
24	39	54.2	448	4 US-09-461-474-8	Sequence 8, Appl
25	39	54.2	626	6 5268290-2	Patent No. 5268290
26	39	54.2	632	4 US-09-252-991A-24590	Sequence 24590, A
27	39	54.2	657	4 US-09-355-166-1	Sequence 1, Appl

28	38	52.8	120	1 US-08-420-235B-29	Sequence 29, Appl
29	38	52.8	120	3 US-08-793-624-29	Sequence 29, Appl
30	38	52.8	120	5 PCT-US95-10194-29	Sequence 29, Appl
31	38	52.8	266	4 US-09-252-991A-20968	Sequence 20968, A
32	38	52.8	307	1 US-07-982-112-2	Sequence 2, Appl
33	38	52.8	328	4 US-09-215-694-2	Sequence 2, Appl
34	38	52.8	474	3 US-09-461-474-10	Sequence 10, Appl
35	38	52.8	537	1 US-08-173-508-2	Sequence 2, Appl
36	38	52.8	537	2 US-08-265-310-2	Sequence 2, Appl
37	38	52.8	537	3 US-08-951-742-2	Sequence 2, Appl
38	38	52.8	1239	2 US-08-937-931-2	Sequence 2, Appl
39	38	52.8	1239	3 US-09-285-502-2	Sequence 2, Appl
40	38	52.8	1239	4 US-09-709-126-2	Sequence 2, Appl
41	38	52.8	1239	4 US-09-871-385A-2	Sequence 2, Appl
42	37	51.4	139	2 US-08-894-922A-5	Sequence 5, Appl
43	37	51.4	252	2 US-08-894-922A-14	Sequence 14, Appl
44	37	51.4	271	2 US-08-894-922A-10	Sequence 10, Appl
45	37	51.4	432	2 US-08-705-660-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-08-343-101A-18  
Sequence 18, Application US/08343101A  
Patent No. 5830759  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma  
NUMBER OF INVENTION: Virus Sequences And Uses Thereof  
TITLE OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/343,101A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
FAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 861 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-861  
OTHER INFORMATION:  
US-08-343-101A-18  
Query Match 65.3%; Score 47; DB 2; Length 861;  
Best local Similarity 63.6%; Pred. No. 32;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYSSFD 11  
|||||  
: :  
Db 468 DGGHGYGLRYE 478

## RESULT 2

US-09-183-688-18  
Sequence 18, Application US/09183688  
Patent No. 6093550  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma  
TITLE OF INVENTION: Virus Sequences And Uses Thereof  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/183,688  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/343,101  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 861 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..861  
OTHER INFORMATION:

Query Match 65.3%; Score 47; DB 3; Length 861;  
Best Local Similarity 63.6%; Pred. No. 32;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYSSFD 11  
|||||  
: :  
Db 468 DGGHGYGLRYE 478

## RESULT 3

US-09-519-489-18  
Sequence 18, Application US/09519489  
Patent No. 6500663  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan

APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma  
TITLE OF INVENTION: Virus Sequences And Uses Thereof  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/519,489  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/343,101  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 861 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..861  
OTHER INFORMATION:

Query Match 65.3%; Score 47; DB 4; Length 861;  
Best Local Similarity 63.6%; Pred. No. 32;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYSSFD 11  
|||||  
: :  
Db 468 DGGHGYGLRYE 478

## RESULT 4

US-08-420-235B-3  
Sequence 3, Application US/08420235B  
Patent No. 5801042  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/420,235B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-420-235B-3

Query Match 65.3%; Score 47; DB 1; Length 1376;  
Best Local Similarity 63.6%; Pred. No. 50;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
|||||  
::  
Db 476 DGGHGYGLRYE 486

RESULT 5  
US-08-793-624-3  
Sequence 3, Application US/08793624C  
Patent No. 6150093  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And  
FILE REFERENCE: 45185-C-PCT-US/JPW  
CURRENT APPLICATION NUMBER: US/08/793,624C  
CURRENT FILING DATE: 1997-02-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1376  
TYPE: PRT  
ORGANISM: Kaposi's sarcoma-associated herpesvirus  
US-08-793-624-3

Query Match 65.3%; Score 47; DB 3; Length 1376;  
Best Local Similarity 63.6%; Pred. No. 50;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
|||||  
::  
Db 476 DGGHGYGLRYE 486

RESULT 6  
PCT-US95-10194-3  
Sequence 3, Application PC/TUS9510194  
GENERAL INFORMATION:  
APPLICANT: The Trustees of Columbia University in the City of New York  
APPLICANT: City  
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS  
TITLE OF INVENTION: SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10194  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/NSC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-10194-3

Query Match 65.3%; Score 47; DB 5; Length 1376;  
Best Local Similarity 63.6%; Pred. No. 50;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
|||||  
::  
Db 476 DGGHGYGLRYE 486

RESULT 7  
US-09-152-060-116  
Sequence 116, Application US/09152060  
Patent No. 6448230  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 28 Human Secreted Proteins  
FILE REFERENCE: P2003PI US  
CURRENT APPLICATION NUMBER: US/09/152,060  
CURRENT FILING DATE: 1998-09-11  
EARLIER APPLICATION NUMBER: PCT/US98/04858  
EARLIER FILING DATE: 1998-03-12  
EARLIER APPLICATION NUMBER: 60/040,762  
EARLIER FILING DATE: 1997-03-14  
EARLIER APPLICATION NUMBER: 60/040,710  
EARLIER FILING DATE: 1997-03-14  
EARLIER APPLICATION NUMBER: 60/050,934  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,100  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,357  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,189  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/057,765  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/068,368  
EARLIER FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 116  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-152-060-116

Query Match 59.7%; Score 43; DB 4; Length 223;  
Best Local Similarity 70.0%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHGYGSSFD 11  
DB 162 GGHGYGAGD 171

## RESULT 8

US-09-252-991A-19311  
Sequence 19311, Application US/09252991A  
Patent No. 6531795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 19311  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19311

Query Match 58.3%; Score 42; DB 4; Length 328;  
Best Local Similarity 63.6%; Pred. No. 65;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DGGHGYGSSFD 11  
DB 265 DGGHGYGCFD 275

## RESULT 9

US-07-942-245-18  
Sequence 18, Application US/07942245  
Patent No. 5639641  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Jan T.  
APPLICANT: SEARLE, Stephen M.J.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUILD, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sughrue, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 Workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: in house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860

TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-18

Query Match 55.6%; Score 40; DB 1; Length 117;  
Best Local Similarity 77.8%; Pred. No. 46;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

## RESULT 10

US-07-942-245-33  
Sequence 33, Application US/07942245  
Patent No. 5639641  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Jan T.  
APPLICANT: SEARLE, Stephen M.J.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUILD, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sughrue, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 Workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: in house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-33

Query Match 55.6%; Score 40; DB 1; Length 125;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

RESULT 11  
US-08-107-669D-8  
Sequence 8, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2540  
TELEFAX: 202/371-2600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-8

Query Match 55.6%; Score 40; DB 1; Length 126;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

RESULT 12  
US-08-472-788A-8  
Sequence 8, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-788A-8

Query Match 55.6%; Score 40; DB 1; Length 126;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
DB 99 DGGHGYGSS 107

RESULT 13  
US-08-477-531B-8  
Sequence 8, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-531B-8

Query Match 55.6%; Score 40; DB 2; Length 126;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
|||:|  
Db 99 DGGHGFCCS 107

RESULT 14  
US-08-303-569B-10  
; Sequence 10, Application US/08303569B  
; Patent No. 5859205  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, John R.  
; APPLICANT: Emtege, John S.  
; TITLE OF INVENTION: Humanised Antibodies  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205r1s  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/303,569B  
; FILING DATE: 07-SEP-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yacko  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3439  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-303-569B-10

Query Match 55.6%; Score 40; DB 2; Length 126;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
|||:|  
Db 99 DGGHGFCCS 107

RESULT 15  
US-08-082-842A-8  
; Sequence 8, Application US/08082842A  
; Patent No. 5863619  
; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,842A  
; FILING DATE: 23-JUN-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 0610.1000002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/371-2600  
; TELEFAX: 202/371-2540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-082-842A-8

Query Match 55.6%; Score 40; DB 2; Length 126;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGHGYGSS 9  
|||:|  
Db 99 DGGHGFCCS 107

Search completed: November 7, 2003, 07:30:06  
Job time: 2.76235 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 15.4112 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-82\_COPY\_1\_119

Sequence: 1 EVKLVSQPELKKRGETVKI.....CNSPKGFAYMGQGLTVNSA 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.5	84.1	120	B42848	I6 mab heavy chain
2	543.5	84.1	146	S33905	Ig heavy chain pre
3	535	82.8	119	A53285	Ig heavy chain V a
4	533	82.5	118	S19967	Ig heavy chain V r
5	529	81.9	117	S32190	Ig heavy chain V r
6	525.5	81.3	118	S37204	Ig heavy chain V r
7	523.5	81.0	109	S26325	Ig heavy chain V r
8	522	80.8	136	S35759	Ig heavy chain V r
9	514	79.6	113	B36259	BHDPD10 protein -
10	511	79.1	117	S33187	Ig heavy chain V r
11	508.5	78.7	115	S19968	Ig heavy chain V r
12	508	78.6	124	PH1404	Ig heavy chain V r
13	504.5	78.1	115	S19965	Ig heavy chain V r
14	504.5	78.1	139	PH1225	Ig heavy chain V r
15	504	78.0	119	H45722	Ig heavy chain pre
16	500.5	77.5	120	S19963	anti-glycoprotein
17	492.5	76.2	114	D32967	Ig heavy chain V r
18	492.5	76.2	118	A32530	Ig heavy chain V r
19	487.5	75.5	114	C32967	Ig heavy chain V r
20	484	74.9	105	S24765	Ig heavy chain V r
21	481	74.5	119	B32530	Ig heavy chain V r
22	472	73.1	105	S24764	Ig heavy chain V r
23	469.5	72.7	101	D24672	Ig heavy chain V r
24	466	72.1	114	P10256	Ig heavy chain V r
25	459	71.1	105	S24766	Ig heavy chain V r
26	452	70.0	99	S26326	Ig heavy chain V r
27	446.5	69.1	120	S26789	Ig heavy chain V r
28	445.5	68.0	93	C24672	Ig heavy chain V r
29	439	68.0	105	S24763	Ig heavy chain V r

30	435	67.3	131	2	S26792	Ig heavy chain V r
31	433	67.0	142	2	S19245	Ig heavy chain pre
32	423	65.5	134	2	S21916	Ig heavy chain V r
33	411	63.6	102	2	C32530	Ig heavy chain V r
34	400	61.9	117	2	S18554	Ig heavy chain V r
35	396	61.3	98	2	A49051	Ig heavy chain V r
36	393	60.8	98	2	S46460	Ig heavy chain V r
37	390	60.4	160	2	P10105	Ig heavy chain V r
38	386.5	59.8	135	2	S49530	anti-PR2 erythrocy
39	382.5	59.2	118	2	S36265	Ig heavy chain V r
40	382	59.1	98	2	H34964	Ig heavy chain V-I
41	377	58.4	122	2	S36271	Ig heavy chain V r
42	370.5	57.4	469	2	S37483	Ig heavy chain V r
43	367.5	56.9	136	2	S31600	Ig heavy chain V r
44	367	56.8	119	2	S20640	Ig heavy chain V r
45	367	56.8	126	2	I44151	Ig heavy chain V r

## ALIGNMENTS

### RESULT 1

B42848 I6 mab heavy chain V region - mouse (fragment)

C.Species: Mus musculus (house mouse)

C.Date: 27-Apr-1993 #sequence revision 18-Nov-1994 #text\_change 21-Jan-2000

C.Accession: B42848; S33903

R.Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.,  
J. Biol. Chem. 267, 15552-15558, 1992

A.Title: Chimeric I6 anti-tumor antibody. Genomic construction, expression, and c

A.Reference number: A42848; MUID:92348410; PMID:1639794

A.Accession: B42848

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-120 <FE1>

A.Cross-references: GB:M90690; NID:G195065; P1DN:A438146.1; P1D:G195066

A.Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P109961)

A.Accession: S33903

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-120 <FE2>

A.Cross-references: EMBL:M90691

C.Superfamily: immunoglobulin V region; immunoglobulin homology

F.15-98/Domain: immunoglobulin homology <ITM>

Query Match 84.1%; Score 543.5; DB 2; Length 120;

Best Local Similarity 84.3%; Pred. No. 1.9e-40;

Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSQPELKKRGETVKIICKASGYITFYGNMWWKQAPGKGLKMMGINTYTGEPY 60

Db 1 QILVQSGPELKKRGETVKIICKASGYITFYGNMWWKQAPGKGLKMMGINTYTGEPY 60

QY 61 ADDFKGRFAFLETSASTAYVQINLKKEEDATFYFCA-LTQNSPKGFAYMGQGLTVNS 118

Db 61 ADDFKGRFAFLETSASTAYVQINLKKEEDATFYFCA-LTQNSPKGFAYMGQGLTVNS 118

QY 119 A 119

Db 120 S 120

RESULT 2

S33905 Ig heavy chain precursor V region - synthetic

C.Species: synthetic

C.Date: 13-Jan-1995 #sequence revision 30-Apr-1998 #text\_change 20-Oct-2000

C.Accession: S33905

R.Liu, A.Y.; Robinson, R.R.; Helicstrom, K.S.; Murray Jr., E.D.; Chang, C.P.; Hall

Proc. Natl. Acad. Sci. U.S.A. 84, 3438-3443, 1987

A.Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells

A.Reference number: S33905; MUID:87204152; PMID:3106970

A.Accession: S33905

A;Molecule type: mRNA  
A;Residues: 1-146 <LIU>  
A;Cross-references: EMBL:MI6072; NID:g195270; PIDN:AAA8229.1; PID:g195271

Query Match 84.1%; Score 543.5; DB 4; Length 146;  
Best Local Similarity 84.3%; Pred. No. 2.3e-40;  
Matches 100; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 20 QIQLVQSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 79  
QY 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 118  
DB 80 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 138

QY 119 A 119  
DB 139 S 139

## RESULT 3

A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C;Accession: A53285  
R;Swada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991  
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.  
A;Reference number: A53285; MID:92017897; PMID:1922102  
A;Accession: A53285  
A;Status: preliminary  
A;Molecule type: DNA; protein  
A;Residues: 1-119 <SAM>  
A;Cross-references: GB:D12736; NID:9220595; PIDN:BA02228.1; PID:9220596  
C;Note: sequence extracted from NCBI backbone (NCBI:63271, NCBI:63289)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 535; DB 2; Length 119;  
Best Local Similarity 83.2%; Pred. No. 1e-39; 13; Indels 0; Gaps 0;  
Matches 99; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 EVKLVSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 1 QIQLVQSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
QY 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119  
DB 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119

## RESULT 4

S19967

Ig heavy chain V region (M-T406) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19967  
R;Weissenborn, W.; Riehmüller, G.; Weiss, E.M.; Rieber, B.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19967  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-118 <WEI>  
A;Cross-references: EMBL:X65090  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 533; DB 2; Length 118;  
Best Local Similarity 84.7%; Pred. No. 1.5e-39;  
Matches 100; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 4 LVSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADD 63  
DB 1 LVQSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADD 60  
QY 64 FKGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119  
DB 61 FKGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 118

## RESULT 5

S32190

Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S32190  
R;Izui, S.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S32185  
A;Accession: S32190  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-117 <IZU>  
A;Cross-references: EMBL:X70098; NID:9288258; PIDN:CAA49702.1; PID:9288259  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 529; DB 2; Length 117;  
Best Local Similarity 81.5%; Pred. No. 3.3e-39;  
Matches 97; Conservative 11; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVKLVSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 1 QIQLVQSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
QY 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119  
DB 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 117

## RESULT 6

S37204

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000  
C;Accession: S37204  
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
submitted to the EMBL Data Library, August 1993  
A;Description: Production and cloning of TMV-specific monoclonal antibodies.  
A;Reference number: S37200  
A;Accession: S37204  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-118 <FIS>  
A;Cross-references: EMBL:X74589; NID:9402599; PIDN:CAA52666.1; PID:g1333981  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 525.5; DB 2; Length 118;  
Best Local Similarity 83.2%; Pred. No. 6.7e-39;  
Matches 99; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 EVKLVSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 1 QIQLVQSGBELKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
QY 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119  
DB 61 ADPFGRFAPSLSTASATYAIQINNLKNEEDATYFCALYGNSPKGFAYWGQTLVTVA 119

Db 61 ADPFKGRFAPSLFETSAAYLQINNLKNEEDTATYFCALYGNYS-AMFYYGQGLTVTSA 118

## RESULT 7

S26325

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000

C/Accession: S26325

R/Stark, S.B.; Caton, A.J.

U. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 &lt;STA&gt;

A/Cross-references: EMBL:X59210; NID:G52080; PID:G1334043

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/5-88/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 81.0%; Score 523.5; DB 2; Length 109;

Matches 100; Conservative 0; Mismatches 4; Indels 9; Gaps 2;

QY 11 LKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPYADDFKGRFAF 70

Db 1 LKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPYADDFKGRFAF 60

QY 71 SLETSASTAYLQINNLKNEEDTATYFCALYGNSP-----KGFAYWGQGLTVTS 118

Db 61 SLETSASTAYLQINNLKNEEDTATYFCALYGNSP-----RPFAYWDGFAWGGQTLTVTS 109

## RESULT 8

S35759

BHD9D10 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S35759

R/Froyen, G.F.V.

Submitted to the EMBL Data Library, May 1993

A/Reference number: S35759

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-136 &lt;FRO&gt;

A/Cross-references: EMBL:X72796; NID:G312496; PID:CAAS1316.1; PID:G312497

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/34-117/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 80.8%; Score 522; DB 2; Length 136;

Matches 98; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 60

Db 20 QIQLVQSGPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 79

QY 61 ADPFKGRFAPSLFETSAAYLQINNLKNEEDTATYFCALYGNSPKGF---AYWGQGLTVTV 117

Db 80 VDDFKGRFVFSLETSASAYLQINNLKNEEDTATYFCALYGNSPKGF---RQGFYAMDYWGQGLTVTV 134

QY 118 SA 119

Db 135 SS 136

## RESULT 9

B36259

Ig heavy chain V region T324 - mouse

C/Species: Mus musculus (house mouse)

## Query Match

Best Local Similarity 80.8%; Score 522; DB 2; Length 136;

Matches 98; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 60

Db 20 QIQLVQSGPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 79

QY 61 ADPFKGRFAPSLFETSAAYLQINNLKNEEDTATYFCALYGNSPKGF---AYWGQGLTVTV 117

Db 80 VDDFKGRFVFSLETSASAYLQINNLKNEEDTATYFCALYGNSPKGF---RQGFYAMDYWGQGLTVTV 134

## RESULT 10

S32187

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C/Accession: S32187

R/Izui, S.

Submitted to the EMBL Data Library, February 1993

A/Reference number: S32185

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-117 &lt;IZU&gt;

A/Cross-references: EMBL:X70091; NID:G288251; PID:CAAA6696.1; PID:G288252

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 79.1%; Score 511; DB 2; Length 117;

Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 60

Db 1 QIQLVQSGPELKKPGETVTKISCKASGYIFPNYGMNWKQAPGKGLKMMGMINITYGEPY 60

QY 61 ADPFKGRFAPSLFETSAAYLQINNLKNEEDTATYFCALYGNSPKGFAYWGQGLTVTVA 119

Db 61 ADPFKGRFAPSLFETSAAYLQINNLKNEEDTATYFCALYGNSPKGFAYWGQGLTVTVA 117

## RESULT 11

S19968

Ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C/Accession: S19968

R/Walshorn, W.; Rietmuller, G.; Weise, B.M.; Rieber, E.P.

Submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of C4 mAb.

A/Reference number: S19963

A/Accession: S19968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 &lt;WEI&gt;

A:Cross-references: EMBL:X65089  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 508.5; DB 2; Length 115;  
Best Local Similarity 80.5%; Pred. No. 2e-37;  
Matches 95; Conservative 6; Mismatches 10; Indels 7; Gaps 2;

QY 6 ESGPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADDFK 65  
DB 1 QSGPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADDFK 60

QY 66 GRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPK----GFAYNGSGTLVTVSA 119  
DB 61 GRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPK----RGFPYRFSDVWGQSTLTIVSS 115

## RESULT 12

PH1404  
Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000  
C:Accession: PH1404; PH1406  
R:Shitahara, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta  
J. Exp. Med. 176, 1209-1214, 1992  
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in  
la virus.  
A:Reference number: PH1403; MUID:93018837; PMID:1402663  
A:Accession: PH1404  
A:Molecule type: DNA  
A:Residues: 1-124 <SH2>  
A:Accession: PH1406  
A:Molecule type: DNA  
A:Residues: 115-121 <SH2>  
C:Genetics:  
A:Insertions: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 508; DB 2; Length 124;  
Best Local Similarity 85.3%; Pred. No. 2.3e-37;  
Matches 93; Conservative 7; Mismatches 3; Indels 6; Gaps 1;

QY 1 EVKLVSSEPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 21 QIQLVSGPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 80

QY 61 ADDPKGRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPKGFAYW 109  
DB 81 ADDPKGRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPKGFAYW 123

## RESULT 13

PH1965  
Ig heavy chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S19965  
R:Weissenhorn, W.; Rietmuller, G.; Weiss, B.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S19963  
A:Accession: S19965  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE1>  
A:Note: sequence extracted from NCI back bone (NCBIP:120597)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 504.5; DB 2; Length 115;  
Best Local Similarity 84.3%; Pred. No. 4.4e-37;  
Matches 97; Conservative 5; Mismatches 10; Indels 3; Gaps 2;

QY 8 GPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADDFK 67  
DB 1 GPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPYADDFK 60

QY 68 FAFSLTSASTAVLQINNKNEDTATYFCALYGNSPK----PGFAYNGSGTLVTVSA 119  
DB 61 FAFSLTSASTAVLQINNKNEDTATYFCALYGNSPK----LDVYGQGSVTV 115

## RESULT 14

PH1225  
Ig heavy chain precursor V region (M-T151) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
C:Accession: PH1225  
R:Weissenhorn, W.; Scheuer, W.; Kalza, B.; Schwitzke, M.; Reiter, C.; Flieger, E.  
Gene 121, 271-278, 1992  
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4  
A:Reference number: PH1224; MUID:93077041; PMID:1446824  
A:Accession: PH1225  
A:Molecule type: mRNA  
A:Residues: 1-139 <MB1>  
A:Cross-references: GB:S50263; NID:9260763; PIDN:AA824319.1; PID:9260764  
A:Note: this mouse sequence was hybridized and fused with a human constant region  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-139/Product: Ig heavy chain V region #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 504.5; DB 2; Length 139;  
Best Local Similarity 77.2%; Pred. No. 5.3e-37;  
Matches 95; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

QY 1 EVKLVSSEPELKKPGETVTKISCKASGYFTNYGMNWKQAPGKGLKMMGMINITYGEPY 60  
DB 20 QIQLVSGPELKKPGETVTKISCKASGYFTIDYSIHVWKQAPGKGLKMMGMINITYGEPY 79

QY 61 ADDPKGRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPKGFAYW 116  
DB 80 ADDPKGRFAFSLTSASTAVLQINNKNEDTATYFCALYGNSPKGFAYW 136

QY 117 VSA 119  
DB 137 VSS 139

## RESULT 15

H45722  
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 109) - m

C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: H45722  
R:Simpon, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites  
A:Reference number: H45722; MUID:93100833; PMID:7677958  
A:Accession: H45722  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-119 <SIM>  
A:Note: sequence extracted from NCI back bone (NCBIP:120597)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 504; DB 2; Length 119;  
Best Local Similarity 78.0%; Pred. No. 5e-37;  
Matches 96; Conservative 9; Mismatches 10; Indels 8; Gaps 3;

```

Qy 1 EVKLVSGBELKKPGEIVYKISCKASGYIFITNYGMWYKQAPGKGLKMGW-INTYTGEP 59
Db 1 QIOLVQSGTELMKPEIVKISCKASGYITFTYGVWYKQAPGKGLKMGWINTYTGEP 60
Qy 60 YADDFKGRFASFLETSASTAYLQIINNLIKNEBDTATYFCALYGNSPKGFPA--YMGQSTLVT 116
Db 61 YVDDFKGRFASFLETSANTAYLQIINNLIKNDMATYFCA---RAQSPGYFDYWGQGTLLT 116
Qy 117 VSA 119
Db 117 VSS 119

```

Search completed: November 7, 2003, 07:36:18  
 Job time : 15.512 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:19 ; Search time 3.57944 Seconds  
(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-82\_COPY\_1\_119

Perfect score: 646  
Sequence: 1 EVKLVSQPELKKPGETVKI.....GNSPKGFAYWGQTLVTVSA 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348	53.9	140	1 HV02 MOUSE	P01746 mus musculus
2	344	53.3	120	1 HV03 MOUSE	P01747 mus musculus
3	331.5	51.3	122	1 HV36 HUMAN	P01768 homo sapien
4	330.5	51.2	118	1 HV51 MOUSE	P06330 mus musculus
5	330	51.1	115	1 HV32 MOUSE	P01801 mus musculus
6	325.5	50.4	139	1 HV07 MOUSE	P01751 mus musculus
7	325	50.3	117	1 HV12 MOUSE	P01756 mus musculus
8	325	50.3	117	1 HV13 MOUSE	P01757 mus musculus
9	324	50.2	113	1 HV33 MOUSE	P01799 mus musculus
10	323	50.0	115	1 HV33 MOUSE	P01802 mus musculus
11	321	49.7	121	1 HV01 MOUSE	P01745 mus musculus
12	321	49.7	136	1 HV15 MOUSE	P01759 mus musculus
13	321	49.7	138	1 HV48 MOUSE	P03980 mus musculus
14	320.5	49.6	136	1 HV16 MOUSE	P01783 mus musculus
15	319	49.4	113	1 HV27 MOUSE	P01796 mus musculus
16	318.5	49.3	114	1 HV01 CANEA	P01784 canis fami
17	318	49.2	121	1 HV31 HUMAN	P01771 homo sapien
18	316.5	49.0	119	1 HV37 MOUSE	P01807 mus musculus
19	316.5	49.0	113	1 HV11 MOUSE	P01755 mus musculus
20	316	48.9	137	1 HV31 MOUSE	P01800 mus musculus
21	316	48.9	142	1 HV01 RAT	P01805 rattus norv
22	315.5	48.8	116	1 HV31 HUMAN	P01781 homo sapien
23	314	48.6	117	1 HV18 HUMAN	P01743 homo sapien
24	313.5	48.5	119	1 HV40 MOUSE	P01810 mus musculus
25	313	48.5	113	1 HV28 MOUSE	P01797 mus musculus
26	311	48.1	117	1 HV19 HUMAN	P23083 homo sapien
27	310	48.0	113	1 HV19 MOUSE	P01798 mus musculus
28	309.5	47.9	120	1 HV30 HUMAN	P01782 homo sapien
29	309.5	47.9	147	1 HV1C HUMAN	P01744 homo sapien
30	309	47.8	117	1 HV02 CANEA	P01785 canis fami
31	309	47.8	119	1 HV31 HUMAN	P01770 homo sapien
32	307	47.5	117	1 HV52 MOUSE	P06327 mus musculus
33	305	47.2	117	1 HV17 MOUSE	P01786 mus musculus

## ALIGNMENTS

### RESULT 1

HV02\_MOUSE  
ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
RT immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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EMBL: J00493, AAA38128.1; --  
PIR: A94264; HVMSG7.  
HSSP: P01810; 2FBJ.  
InterPro: IPR007110; Ig-like.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003596; Ig\_v.  
Pfam: PF00047; Ig\_1.  
SMART: SM00406; IGV; 1.  
PROSITE: PS00835; IG\_LIKE; 1.  
IMMUNOGLOBULIN V region; Hybridoma; Signal.  
SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.  
FT DOMAIN 20 139 IG-LIKE.  
FT NON TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 53.9%; Score 348; DB 1; Length 140;  
Best Local Similarity 54.1%; Pred. No. 1.3e-28;  
Matches 66; Conservative 24; Mismatches 28; Indels 4; Gaps 2;

QY 1 EVKLVSQPELKKPGETVKISKASGVFTNYGMNVKQAPGKLGKMGWINTYTGPEY 60

Db 20 EVQLQQSGAEIVRAGSVKSCASGVFTTSYGINVWKQPGQGLEWIGYINFGYINY 79

QY 61 ADDFKGRFAFSLSTASTAYLVQINLNKEDATYFCA---LYGNSPKGFAYWGQGLTVTV 117

```
DB 80 NEKFKGKTLTLDKSSSTAYMQLRSLTSDSAVYFCARSHYGGG-YDFDYGQGGPLFV 138
QY 118 SA 119
DB 139 SS 140

RESULT 2
HV3G MOUSE STANDARD; PRT; 120 AA.
AC P01747:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production; the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Bur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; PF04E4A167B654AF CRC64;

Query Match 53.3%; Score 344; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 2.9e-28;
Matches 65; Conservative 24; Mismatches 28; Indels 4; Gaps 2;

QY 2 VLVESGPELKKPGETVKISKASGYIFTNGMNVKQAPGKGLKMWGINTYTGPTVA 61
DB 1 VQLQSGAEVLVAGSSVSKASGYFTSYGLNWKVQKQGGQLEWIGYINPCNGYTKN 60
QY 62 DDFKGFAPFSLTSASTAYLIQNNKEDATVFCA---LYGNSPKGFAYWGQGLTVTS 118
DB 61 EFKFGKTLTLDKSSSTAYMQLRSLTSDSAVYFCARSHYGGG-YDFDYGQGGTLTVS 119
QY 119 A 119
DB 120 S 120

RESULT 3
HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01758:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUAM.
DR HSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 51.3%; Score 331.5; DB 1; Length 122;
Best Local Similarity 50.4%; Pred. No. 5.5e-27;
Matches 62; Conservative 26; Mismatches 30; Indels 5; Gaps 2;

QY 1 EVLVESGPELKKPGETVKISKASGYIFTNGMNVKQAPGKGLKMWGINTYTGPTVA 60
DB 1 QVELVESGGVGVZGSRSLSCAASGFTFSYAMHWVRQPPGKGLWVAIVSYBGBBKY 60
QY 61 ADDEKGFAPFSLTSASTAYLIQNNKEDATVFCA---LYGNSPKGFAYWGQGLTVT 116
DB 61 ABSVKGRTTISDRBSKFTLYLQMSLRABTAVTYCARDRLPYLGBY-RAFNYWGQGLTVT 119
QY 117 VSA 119
DB 120 VSS 122

RESULT 4
HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205-12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
```

```

SEQUENCE      139 AA;    154119 NW;   1B57DD4FD0C9F465 CRC64;

Query Match          50.4%; Score 325.5; DB 1; Length 139;
Best Local Similarity 50.0%; Pred. No. 2.6e-26;
Matches 61; Conservative 28; Mismatches 28; Indels 5; Gaps 2;

1 EVKLVESPELKKPGETVKISKASGYIPTNMGWVVKQAPKGLKWGWINTYTYGEPT 60
  : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
20 QVOIQOQAELVKPQASVKLSCKASGYFTTSYMHHWVKRQPRGSLIEWIGRIDPN 79
  : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

61 ADDPKGFAPSLETSASTAYTLQINLNKNEDTATYFCA---LYGNSPKGFAYWGQT 117
  : : | : : : : : : : : : : : | : | : | : | : | : | : | : | : |
80 NEKFPSKATLVDPSSSTAYMQLSLEDTSADSVYCARYDYIGSS--YFDYMQGGTT 137
  : : | : : : : : : : : : : : | : | : | : | : | : | : | : | : |

118 SA 119
| :
138 SS 139
DB

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RESULT 7
HV12 MOUSE STANDARD; PRT; 117 AA.
ID HV12 MOUSE
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=63075344; Pubmed=6816276;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MEMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IgV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8AC84BE447E41 CRC64;

Query Match 50.3%; Score 325; DB 1; Length 117;
Best Local Similarity 52.0%; Pred. No. 2.4e-26;
Matches 64; Conservative 21; Mismatches 28; Indels 10; Gaps 2;

QY 1 EYKLVESGPELKKPGETVTKISCKASGYITFTNTGMNWKQAPGKGLKMMGINTTYGEPY 60
DB 1 EYQLQSGPELVKPGASVVKMSCKASGYITFTDYMKVKQSHGKSLWIGDINPNNGTSTY 60
QY 61 ADDEKGRFAPSLSTASTAYVLOINNLKNEEDATYFCA----LYGNSPKGFAYWGQTLVT 116
DB 61 NQKFKGKATLTVDKSSSTAYVQWLNLSLSEDSAVYYCARDYDWT-----FDVWGAGTIVT 114
QY 117 VSA 119
DB 115 VSS 117

RESULT 8
HV13 MOUSE STANDARD; PRT; 117 AA.
ID HV13 MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=80078170; Pubmed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;

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RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MEMS75.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IgV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 50.3%; Score 325; DB 1; Length 117;
Best Local Similarity 52.0%; Pred. No. 2.4e-26;
Matches 64; Conservative 21; Mismatches 28; Indels 10; Gaps 2;

QY 1 EYKLVESGPELKKPGETVTKISCKASGYITFTNTGMNWKQAPGKGLKMMGINTTYGEPY 60
DB 1 EYQLQSGPELVKPGASVVKMSCKASGYITFTDYMKVKQSHGKSLWIGDINPNNGTSTY 60
QY 61 ADDEKGRFAPSLSTASTAYVLOINNLKNEEDATYFCA----LYGNSPKGFAYWGQTLVT 116
DB 61 NQKFKGKATLTVDKSSSTAYVQWLNLSLSEDSAVYYCARDYDWT-----FDVWGAGTIVT 114
QY 117 VSA 119
DB 115 VSS 117

RESULT 9
HV30 MOUSE STANDARD; PRT; 113 AA.
ID HV30 MOUSE
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=77134726; Pubmed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RT protein.";
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IgV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113

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SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 50.2%; Score 324; DB 1; Length 113;

Best Local Similarity 53.8%; Pred. No. 2.9e-26;

Matches 64; Conservative 19; Mismatches 28; Indels 8; Gaps 2;

QY 1 EVKLVEGPELKKRGVETVKISCKASGYIFFTNYGMNWKQAPGKGLKMMGWT--NTYTGE 58  
DB 1 EVKLVEGSGGLVPGSGMKLSCVAGFTSNVMMWVROSPKGLGVVAEIRLKSHTVAT 60  
DB 59 TYADDFKGRFAPSLETSASTAYVQLNNLKNEEDTATYFCALYGNSPKGPAYMGQGLTVTV 117  
61 HYAESVKGRTTISRDSKSVYLQNNLNLAEDTATYCCS-----TGFAYMGQGLTVTV 113

RESULT 10

HV33 MOUSE STANDARD; PRT; 115 AA.

AC P01802;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-111 region W3082.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RX MEDLINE=8209361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L.;  
RT "The complete V domain amino acid sequences of two myeloma immunoglobulin proteins";  
RT binding proteins";  
RT J. Immunol. 128:302-307(1982).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS INULIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR: D92811; AVMS82.  
DR HSSP: P01810; 2PB1.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS0835; IG LIKE; 1.  
DR Immunoglobulin V region.  
KW DOMAIN  
FT 1 114 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NON\_TER 115  
SQ SEQUENCE 115 AA; 12887 MW; 984517648C121C5A CRC64;

Query Match 50.0%; Score 323; DB 1; Length 115;

Best Local Similarity 52.9%; Pred. No. 3.8e-26;

Matches 64; Conservative 19; Mismatches 30; Indels 8; Gaps 2;

QY 1 EVKLVEGPELKKRGVETVKISCKASGYIFFTNYGMNWKQAPGKGLKMMGWT--NTYTGE 58  
DB 1 EVKLVEGSGGLVPGSGMKLSCVAGFTSNVMMWVROSPKGLGVVAEIRLKSHTVAT 60  
QY 59 TYADDFKGRFAPSLETSASTAYVQLNNLKNEEDTATYFCALYGNSPKGPAYMGQGLTVTV 118  
DB 61 HYAESVKGRTTISRDSKSVYLQNNLNLAEDTATYCCS-----TGFAYMGQGLTVTV 114  
QY 119 A 119  
DB 115 A 115

RESULT 11

HV01 MOUSE

ID HV01 MOUSE STANDARD; PRT; 121 AA.

AC P01745;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region MPC 11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RX MEDLINE=81053741; PubMed=6253904;  
RA Zakut R., Cohen J., Givol D.;  
RT "Cloning and sequence of the cDNA corresponding to the variable  
RT region of immunoglobulin heavy chain MPC11.";  
RT Nucleic Acids Res. 8:3591-3601(1980).  
RN [2]  
RP REVISIONS.

RA Zakut R., Cohen J., Givol D.;  
RL Nucleic Acids Res. 8:4839-4840(1980).  
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
CC FROM A MYELOMA THAT SECRETES IG3B.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR: A93708; GYMS11.  
DR HSSP: P01810; 2PB1.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS0835; IG LIKE; 1.  
DR Immunoglobulin V region.  
KW DOMAIN  
FT 1 112 IG-LIKE.  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3BEC56D09B CRC64;

Query Match 49.7%; Score 321; DB 1; Length 121;

Best Local Similarity 51.2%; Pred. No. 6.4e-26;

Matches 62; Conservative 23; Mismatches 34; Indels 2; Gaps 1;

QY 1 EVKLVEGPELKKRGVETVKISCKASGYIFFTNYGMNWKQAPGKGLKMMGWTNTYTGE 60  
DB 1 EAQLOQSGAEIVRGVETVKISCKASGYIFFTNYGMNWKQAPGKGLKMMGWTNTYTGE 60  
QY 61 ADDFKGRFAPSLETSASTAYVQLNNLKNEEDTATYFCALYGNSPKGPAYMGQGLTVTV 118  
DB 61 NDNLKGRATLTADSSSTAYVQLSSLTSEDSATYHCAAGVYNNSPFDSMGQGLTVTV 120  
QY 119 A 119  
DB 121 S 121

RESULT 12

HV15 MOUSE

ID HV15 MOUSE STANDARD; PRT; 136 AA.

AC P01759;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region BCL1 precursor.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8222262; PubMed=6806821;

RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,

RA Blatner F.R.;

RT "Simultaneous expression of immunoglobulin mu and delta heavy chains

RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared

RT Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).  
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 39.243 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-82\_Copy\_1\_119  
Perfect score: 646  
Sequence: 1 EVKLVSSEGLKRGERTVKT.....GNSPKGFAYMGQSTLYTVSA 119

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23: \*  
1: sp archaea: \*  
2: sp bacteria: \*  
3: sp fungi: \*  
4: sp human: \*  
5: sp invertebrate: \*  
6: sp mammal: \*  
7: sp mhc: \*  
8: sp organelle: \*  
9: sp phase: \*  
10: sp plant: \*  
11: sp rodent: \*  
12: sp virus: \*  
13: sp vertebrate: \*  
14: sp unclassified: \*  
15: sp viirus: \*  
16: sp bacteriap: \*  
17: sp archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545.5	84.4	241	11 Q921A6	Q921A6 mus musculus
2	495	76.6	484	11 Q921A6	Q921A6 mus musculus
3	486.5	75.3	218	11 Q921A6	Q921A6 mus musculus
4	461	71.4	102	11 Q921A6	Q921A6 mus musculus
5	395	61.1	120	11 Q920E8	Q920E8 mus musculus
6	377	58.4	119	4 Q921A6	Q921A6 mus musculus
7	376.5	58.3	124	4 Q921A6	Q921A6 mus musculus
8	364	56.3	125	4 Q921A6	Q921A6 mus musculus
9	362	56.0	473	11 Q921A6	Q921A6 mus musculus
10	356.5	55.2	159	4 Q920E8	Q920E8 mus musculus
11	355	55.0	123	11 Q921A6	Q921A6 mus musculus
12	354	54.8	497	4 Q921A6	Q921A6 mus musculus
13	353	54.6	119	11 Q920E7	Q920E7 mus musculus
14	347.5	53.8	488	11 Q921A6	Q921A6 mus musculus
15	347	53.7	480	11 Q921A6	Q921A6 mus musculus
16	344	53.3	147	11 Q921A6	Q921A6 mus musculus

17	343	53.1	119	5 Q921A6	Q921A6 mus musculus
18	342.5	53.0	481	11 Q921A6	Q921A6 mus musculus
19	340	52.6	481	11 Q921A6	Q921A6 mus musculus
20	340	52.6	597	4 Q921A6	Q921A6 mus musculus
21	338.5	52.4	139	11 Q921A6	Q921A6 mus musculus
22	338	52.3	117	11 Q921A6	Q921A6 mus musculus
23	338	52.3	168	11 Q921A6	Q921A6 mus musculus
24	335	51.9	113	4 Q921A6	Q921A6 mus musculus
25	335	51.9	117	11 Q921A6	Q921A6 mus musculus
26	334.5	51.8	109	11 Q921A6	Q921A6 mus musculus
27	332.5	51.5	118	4 Q921A6	Q921A6 mus musculus
28	332	51.4	146	11 Q921A6	Q921A6 mus musculus
29	331.5	51.3	463	11 Q921A6	Q921A6 mus musculus
30	331	51.2	614	4 Q921A6	Q921A6 mus musculus
31	330.5	51.2	469	11 Q921A6	Q921A6 mus musculus
32	330	51.1	116	4 Q921A6	Q921A6 mus musculus
33	330	51.1	144	11 Q921A6	Q921A6 mus musculus
34	329.5	51.0	145	11 Q921A6	Q921A6 mus musculus
35	327.5	50.7	143	11 Q921A6	Q921A6 mus musculus
36	327	50.6	150	4 Q921A6	Q921A6 mus musculus
37	326	50.5	142	11 Q921A6	Q921A6 mus musculus
38	325.5	50.4	145	11 Q921A6	Q921A6 mus musculus
39	325.5	50.4	573	4 Q921A6	Q921A6 mus musculus
40	324	50.2	146	11 Q921A6	Q921A6 mus musculus
41	323	50.0	489	11 Q921A6	Q921A6 mus musculus
42	322.5	49.9	613	4 Q921A6	Q921A6 mus musculus
43	320.5	49.6	116	4 Q921A6	Q921A6 mus musculus
44	319	49.4	142	11 Q921A6	Q921A6 mus musculus
45	318.5	49.3	110	11 Q921A6	Q921A6 mus musculus

## ALIGNMENTS

### RESULT 1

Q921A6 PRELIMINARY: PRT; 241 AA.  
AC Q921A6; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Mus musculus (Mouse).  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Scurgnathi; Muridae; Murinae; Mus.  
RN NCBI\_TaxID=10090;  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scFv)."  
RL Mol. Cells 7:816-818 (1997).  
DR EMBL; U88067; AAB48044.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_MHC.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; Ig\_2.  
DR PROSITE; PS50835; Ig\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 241  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 84.4%; Score 545.5; DB 11; Length 241;  
Best Local Similarity 86.6%; Pred. No. 1.5e-46;

Matches 103; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 EVKLVSSEGLKRGERTVKTSCASGYIFPNYGNWYKAPGKGLKMGWINTYGEPT 60  
DB 1 QVTLQSGPELKKRGERTVKTSCASGYIFPNYGNWYKAPGKGLKMGWINTYGEPT 60

QY 61 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSA 119  
 Db 61 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSS 118

## RESULT 2

Q991A6 PRELIMINARY; PRT; 484 AA.  
 ID 0991A6  
 AC 0991A6  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 52.6 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX STRAUBERG R.;  
 RP SEQUENCE FROM N.A.  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003495; AA003495.1; -  
 DR HSSP; P01810; 2FBJ. -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 484 AA; 52567 MW; 8EAEAF9BCE582817 CRC64;

Query Match 76.6%; Score 495; DB 11; Length 484;  
 Best Local Similarity 76.9%; Pred. No. 3.8e-41;  
 Matches 93; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVKLVSSEGLKPKGRTYKISCRASGYITFYGNVWYKQAPGKGLKMGWINTYGEPT 60  
 Db 20 QIVLQSGPELKKRGEIVKISCRASGYITFYDSHWYKQAPGKGLKMGWINTYGEPT 79  
 QY 61 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSS 118  
 Db 80 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSS 139  
 QY 119 A 119  
 Db 140 S 140

## RESULT 3

Q925S1 PRELIMINARY; PRT; 218 AA.  
 ID 0925S1  
 AC 0925S1  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE MRP5 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX STRAIN=BA1B/C;  
 RP SEQUENCE FROM N.A.  
 RL the repair of intestinal epithelium after irradiation in mice.;  
 RT World J. Gastroenterol. 6:709-717(2000).  
 RN [2]

QY 16 ETVKISCRASGYITFYGNVWYKQAPGKGLKMGWINTYGEPTADDPKGRFAPFSLST 75  
 Db 1 ETVKISCRASGYITFYDSHWYKQAPGKGLKMGWINTYGEPTADDPKGRFAPFSLST 60  
 QY 76 ASTAVLQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSA 119

## SEQUENCE FROM N.A.

RC STRAIN=BA1B/C;  
 RA Chi D., Zeng G., Yan X., Li X., Su C.;  
 RT "Cloning of mouse genes related to repairing of intestinal epithelium  
 of the irradiated mice by treatment with the intestinal RNA of mice of  
 the same strain."  
 RT Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
 DR EMBL; AF240168; AA043733.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 218  
 SQ SEQUENCE 218 AA; 23013 MW; 527E4E8F7982817 CRC64;

Query Match 75.3%; Score 486.5; DB 11; Length 218;  
 Best Local Similarity 75.6%; Pred. No. 1e-40;  
 Matches 90; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVKLVSSEGLKPKGRTYKISCRASGYITFYGNVWYKQAPGKGLKMGWINTYGEPT 60  
 Db 3 QIVLQSGPELKKRGEIVKISCRASGYITFYDSHWYKQAPGKGLKMGWINTYGEPT 79  
 QY 61 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSA 119  
 Db 63 ADDPKGRFAPFSLSTASATYALQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSS 120

## RESULT 4

Q9JL79 PRELIMINARY; PRT; 102 AA.  
 ID 09JL79  
 AC 09JL79  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anti-myosin immunoglobulin heavy chain variable region  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX STRAIN=N.CA;  
 RP SEQUENCE FROM N.A.  
 RL MEDLINE=20448942; PubMed=10992488;  
 RA Maikael S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-cell-dependent antibody response to the dominant epitope of  
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 with cardiac myosin."  
 RT Infect. Immun. 68:5803-5808(2000).  
 DR EMBL; AF206027; AA069325.1; -  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 102  
 SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 71.4%; Score 461; DB 11; Length 102;  
 Best Local Similarity 85.6%; Pred. No. 1.5e-38;  
 Matches 89; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 16 ETVKISCRASGYITFYGNVWYKQAPGKGLKMGWINTYGEPTADDPKGRFAPFSLST 75  
 Db 1 ETVKISCRASGYITFYDSHWYKQAPGKGLKMGWINTYGEPTADDPKGRFAPFSLST 60  
 QY 76 ASTAVLQINNLKNEEDTATYFCALYGNPKGPAVYGGQITLVVSA 119



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AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.V., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: A035019; AAD56255.1; -.
DR HSSP: P01810; 2PBJ.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C23248BAC CRC64;

Query Match 56.3%; Score 364; DB 4; Length 125;
Best Local Similarity 52.8%; Pred. No. 9.1e-29;
Matches 66; Conservative 24; Mismatches 29; Indels 6; Gaps 1;

QY 1 EVLVESGPGLKPKGVTYKISCRASGYFTFYGNWVWQAPGKGLKMGWNTYTGEPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQVSSGAEVKKPKGASVYKSCASGYFTFYGNWVWQAPGQGLEWNGINPNSGTTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCALYGNSEK-----GRAVGGTL 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQRVGRVTWTRDTTSTAYMELSLRSDTAVYCARSGGRIAAADAPDIMGQGTW 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 115 VTVSA 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VTVSS 125

RESULT 9
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1810060009R1k protein.
GN IGH-1 OR 1810060009R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21085660; PubMed=11217951;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochava H.,
RA Kuentz P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guerinich S., Hill D., Hofmann M., Hume D.A., Kantya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli U., Mombereis P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL: AK007918; BAB25349.1; -.
DR HSSP: P01842; 7PAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 4.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51639 MW; 9DE57A514475FBB CRC64;

Query Match 56.0%; Score 362; DB 11; Length 473;
Best Local Similarity 57.1%; Pred. No. 7.1e-28;
Matches 68; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVLVESGPGLKPKGVTYKISCRASGYFTFYGNWVWQAPGKGLKMGWNTYTGEPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKKPKGASVYKSCASGYFTFYGNWVWQAPGQGLEWNGINPNSGTTY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCALYGNSEK-----GRAVGGTL 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFKGKATLADKSSSTAYVQLSLTSDSAVYFCARSGVDYDMFAWGGTLTVTSA 138
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO;
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY039025; AAK2649.1; -.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_Like; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D295378881FAF02 CRC64;

Query Match 55.2%; Score 356.5; DB 4; Length 159;
Best Local Similarity 52.3%; Pred. No. 6.8e-28;
Matches 68; Conservative 22; Mismatches 29; Indels 11; Gaps 2;

QY 1 EVLVESGPGLKPKGVTYKISCRASGYFTFYGNWVWQAPGKGLKMGWNTYTGEPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKKPKGASVYKSCASGYFTFYGNWVWQAPGQGLEWNGINPNSGTTY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCALYGNSEK-----GRAVGGTL 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 80 S0KFGRLTMTPTDSTSTVYMDLSLRSDDTAVYFCAREMETTGGAGVSKGRTYYGMDVA 139

QY 110 GGGTTLVTVA 119  
|||  
140 GGGTTLVTSS 149

## RESULT 11

Q8VTJ1 PRELIMINARY; PRT; 123 AA.

AC Q8VTJ1;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-DNA heavy chain (fragment).  
GN J558.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HeJ-1pr/1pr;  
RX MEDLINE=96409289; PubMed=8814271;  
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;  
RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
anti-DNA from C3H-1pr mice and lupus mice with nephritis."  
RL Eur. J. Immunol. 26:2225-2233(1996).  
DR EMBL; U59154; AAB02916.1; -  
DR InterPro; IPR007110; IG\_Like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG\_Like; 1.  
FT NON\_TER 1  
FT NON\_TER 123  
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match 55.0%; Score 355; DB 11; Length 123;  
Best Local Similarity 56.1%; Pred. No. 7e-28;  
Matches 69; Conservative 20; Mismatches 30; Indels 4; Gaps 2;

QY 1 EVKLVSSEPELKKRGFTVTKISCKASGYTFNYGNMVKQAPGKGLKMGWINTYTGEPY 60  
|||  
1 EIQLOQSGTGLVPGSVKISCKASGYTFNYGNMVKQAPGKGLKMGWINTYTGEPY 60

Db 61 ADDPKGRFAPSLSTASSTAYLIQINLNKEDTATYFCA--LYGNSPKG-FAYWGGTTLVT 116  
|||  
61 S0KFKKATLTVDKSSRTATYMQNLSLSDSAVYICARPDYTYTIDEGCFAYWGGTTLVT 120

QY 117 VSA 119  
|||  
121 VSA 123

## RESULT 12

Q8WY24 PRELIMINARY; PRT; 497 AA.

AC Q8WY24;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE SMC6 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;  
RT "Identification and characterization of SMC6, a Ig-like gene which is  
down-regulated in colorectal cancer."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -  
DR InterPro; IPR007110; IG\_Like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_4.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG\_Like; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 54.8%; Score 354; DB 4; Length 497;  
Best Local Similarity 54.0%; Pred. No. 4.7e-27;  
Matches 67; Conservative 21; Mismatches 28; Indels 8; Gaps 3;

QY 3 KLVESGPELKKRGFTVTKISCKASGYTFNYGNMVKQAPGKGLKMGWINTYTGEPY 62  
|||  
22 Q0EGAEVTKFGASVAVKSCASGYTFAYLDNMVRAPOGGLFWGMNPGTGNTFEQ 81

Db 63 DEKGRFAPSLSTASSTAYLIQINLNKEDTATYFCA--LYGNSPKG-FAYWGGTTLVT 115  
|||  
62 KFGRLTSTRTSINTATMTLSLSDSAVYICARPDYTYTIDEGCFAYWGGTTLVT 140

QY 116 TVSA 119  
|||  
141 TVSS 144

## RESULT 13

Q920E7 PRELIMINARY; PRT; 119 AA.

AC Q920E7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Pterin-mimicking anti-idiotope heavy chain variable region  
(fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horvath O., Cotton R.G.H.;  
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed  
in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307937; AAL09421.1; -  
DR InterPro; IPR007110; IG\_Like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PS50835; IG\_Like; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13025 MW; FEE904044381CAVC CRC64;

Query Match 54.6%; Score 353; DB 11; Length 119;  
Best Local Similarity 54.6%; Pred. No. 1.1e-27;  
Matches 65; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVKLVSSEPELKKRGFTVTKISCKASGYTFNYGNMVKQAPGKGLKMGWINTYTGEPY 60  
|||  
1 EVKLVSSEPELKKRGFTVTKISCKASGYTFNYGNMVKQAPGKGLKMGWINTYTGEPY 60

Db 61 ADDPKGRFAPSLSTASSTAYLIQINLNKEDTATYFCA--LYGNSPKG-FAYWGGTTLVT 119  
|||  
61 PDSVGRFTLSRDNAKNTLYLQMSLSKSEDTATYICARHGDYDVGAFAYWGGTTLVT 119

## RESULT 14

Q91WR1

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ID Q91MR1 PRELIMINARY; PRT; 488 AA.
AC Q91MR1;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN IGH-V4558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -.
DR MGI; MGI:96486; Igh-V4558.
DR InterPro; IPR007110; Iq_1like.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Iq_LIKE; 4.
DR PROSITE; PS50290; Iq_MHC; 2.
KM Hypothetical protein.
SQ
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 53.8%; Score 347.5; DB 11; Length 488;
Best Local Similarity 53.6%; Pred. No. 2.1e-26;
Matches 67; Conservative 23; Mismatches 28; Indels 7; Gaps 2;

QY 1 EVKLVSQPELKKPGFTVKISCKASGYITFTYGMNMYKQAPGKGLKMGWINTYTGEPY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQSGPELVKPGKAVLKISCKASGYITFTDYVMNVKQSHGKSLKIDINPYNGGTSY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKGRFAPSLTSTAYLQINNLKNEDTATYFCA-----LYGNSPKGFAYWGQGT 114
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGKATLTVDKSSIAVMQNLNLTSDSAVYICARGPVYYSYSDRG-DYWGQGT 138
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 115 VTVSA 119
   ||||
Db 139 VTVSA 143

RESULT 15
Q8KOZ4 PRELIMINARY; PRT; 480 AA.
ID Q8KOZ4;
AC Q8KOZ4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to expressed sequence A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; AAH29188.1; -.
DR InterPro; IPR003599; Iq.
DR InterPro; IPR007110; Iq_1like.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 4.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Iq_LIKE; 4.

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DR PROSITE; PS00290; Iq_MHC; 2.
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 53.7%; Score 347; DB 11; Length 480;
Best Local Similarity 52.9%; Pred. No. 2.3e-26;
Matches 63; Conservative 26; Mismatches 28; Indels 2; Gaps 1;

QY 1 EVKLVSQPELKKPGFTVKISCKASGYITFTYGMNMYKQAPGKGLKMGWINTYTGEPY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQSGPELVKPGKAVLKISCKASGYITFTSDYVMNVKQSHGKSLKIDINPYNGGTSY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADDPKGRFAPSLTSTAYLQINNLKNEDTATYFCA-----LYGNSPKGFAYWGQGT 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGKATLTVDKSSIAVMQNLNLTSDSAVYICARGPVYYSYSDRG-DYWGQGT 136
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: November 7, 2003, 07:34:32
Job time : 42.343 secs

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XX 13-SEP-2000; 2000MO-EP08936.  
 PF 14-SEP-1999; 99AT-0001576.  
 XX (BAXT) BAXTER AG.  
 PA  
 XX Schefflinger F, Kerschbaumer R, Falkner F, Dorner F;  
 PI MPI: 2001-290358/30.  
 XX N-PSDB: AAF30723.  
 DR  
 XX New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 XX Claim 8; Fig 14; 138pp; English.  
 PS  
 CC The present sequence is that of a single chain Fv (scFv) derivative  
 CC of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain  
 CC variable regions of 193/AD3 joined by an artificial, flexible linker  
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
 CC 193/AD3 VH and VL regions and cloning in vector pDAP2. 193/AD3 is  
 CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIIa)  
 CC antibodies of the invention. Anti-FIX/FIIa and their derivatives,  
 CC including scFv and CDR3 fragments, have Factor VIII (FVIII) cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIII inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis.  
 CC  
 SQ Sequence 242 AA;  
 Query Match 100.0%; Score 646; DB 22; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-46;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVKLVSQPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGEPY 60  
 DB 1 EVKLVSQPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGEPY 60  
 QY 61 ADDFKGRFAPFSLSTASSTAYLQINNLKNEEDTATYFCALYGNPKGFAYWGQGLTVTVA 119  
 DB 61 ADDFKGRFAPFSLSTASSTAYLQINNLKNEEDTATYFCALYGNPKGFAYWGQGLTVTVA 119  
 RESULT 2  
 AA029158  
 ID AA029158 standard; Protein; 137 AA.  
 AC  
 XX AA029158;  
 AC  
 XX 27-JAN-2003 (first entry)  
 DT  
 XX  
 DE Chimeric 31.1 antibody heavy chain variable region.  
 KW 31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;  
 KW heavy chain variable region.  
 XX  
 OS Unidentified.  
 XX  
 FN MO200274251-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 15-MAR-2002; 2002MO-US09193.  
 XX  
 PR 15-MAR-2001; 2001US-276284P.  
 XX

PA (TBI-) INT BIOMIMUNE SYSTEMS INC.  
 XX  
 XX Arien M, Tsang KY;  
 XX  
 DR MPI: 2002-759857/82.  
 DR N-PSDB: AAD46728.  
 XX  
 PT New nucleic acid encoding light and heavy chain variable regions of the  
 PT antibody 31.1, useful for expressing chimerized 31.1 antibodies for  
 PT treating pancreatic cancer or for diagnosing pancreatic carcinoma  
 XX  
 XX Claim 5; Fig 4; 40pp; English.  
 PS  
 CC The present invention relates to novel nucleic acid sequences encoding  
 CC light and heavy chain variable regions of the antibody 31.1. Sequences  
 CC of the invention are useful in expressing chimerized 31.1 antibodies,  
 CC which can be used for treating pancreatic cancer or for diagnosing  
 CC pancreatic carcinoma. They are also used in antibody therapy. The present  
 CC sequence is chimeric 31.1 antibody heavy chain variable region.  
 CC  
 SQ Sequence 137 AA;  
 Query Match 86.6%; Score 559.5; DB 23; Length 137;  
 Best Local Similarity 86.8%; Pred. No. 3e-39;  
 Matches 105; Conservative 6; Mismatches 5; Indels 5; Gaps 2;  
 QY 1 EVKLVSQPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGEPY 60  
 DB 20 QIQLVQSGPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGEPY 79  
 QY 61 ADDFKGRFAPFSLSTASSTAYLQINNLKNEEDTATYFCALYGNPKGFAYWGQGLTVTVA 119  
 DB 80 ADDFKGRFAPFSLSTASSTAYLQINNLKNEEDTATYFCALYGNPKGFAYWGQGLTVTVA 136  
 QY 119 A 119  
 DB 137 S 137  
 RESULT 3  
 AA022278  
 ID AA022278 standard; Protein; 250 AA.  
 AC  
 XX AA022278;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 29-OCT-1996 (first entry)  
 XX  
 DE 741F8 anti-c-erbB-2 two single chain Fv construct.  
 KW 741F8; anti-c-erbB-2; monoclonal antibody; single chain Fv; scFv;  
 KW construct; polypeptide linker; C-terminal amino acid sequence;  
 KW in vivo imaging; drug targeting experiment; homodimer;  
 KW increased; binding avidity; tissue retention time.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US5534254-A.  
 XX  
 PD 09-JUL-1996.  
 XX  
 PF 07-OCT-1993; 93US-0133804.  
 XX  
 PR 07-OCT-1993; 93US-0133804.  
 PR 06-FEB-1992; 92US-0831967.  
 XX  
 Key Location/Qualifiers  
 Peptide 122..135  
 Peptide /label= linker  
 Peptide 246..250  
 /note="claimed C-terminal tail to facilitate  
 crosslinking of two scFv polypeptides"

Query	Subject	Query Match	Score	DB	Length	250,
Db	1 EVKLVSGPELKKPPEYVVISCKASGYLFTVYGMVAVQAPGKGLKMMGINTVYGEPT	85.4%;	552;	DB 17;	Length 250,	
Qy	3 EQLVQSGPELKKPPEYVVISCKASGYLFTVYGMVAVQAPGKGLKMMGINTVYGEPT	85.4%;	552;	DB 17;	Length 250,	
Qy	61 ADDEFGRAFSLESTASTAYVLIQINLKNEDRTYCA---LYGNSPGRAYWGGLT	85.4%;	552;	DB 17;	Length 250,	
Qy	63 AEEFGRAFSLESTASTAYVLIQINLKNEDRTYCA---LYGNSPGRAYWGGLT	85.4%;	552;	DB 17;	Length 250,	
Qy	117 VSA 119	85.4%;	552;	DB 17;	Length 250,	
Qy	119 VSA 121	85.4%;	552;	DB 17;	Length 250,	
Db	119 VSA 121	85.4%;	552;	DB 17;	Length 250,	
RESULT 4						
AAW29261						
ID	AAW29261 standard; Protein; 250 AA.					
XX	AAW29261;					
XX	25-MAR-2003 (updated)					
XX	07-JAN-1998 (first entry)					
XX	Anti-c-erbB-2 single chain antibody 741F8.					
XX	Adenovirus; B1A; transactivator; transcription activator; stimulate;					
XX	expression vector; single-chain binding protein; VAI; enhance; PCR;					
XX	translation; production; immortal; eukaryotic cell; scfv; primer;					
XX	single-chain antibody fragment; imaging; tumour; breast cancer;					
XX	ovarian cancer; c-erbB-2 antigen; digoxin intoxication.					
XX	Synthetic.					
XX	US5658763-A.					
XX	19-AUG-1997.					

Pf		05-JUN-1995;	95US-0463675.
PX			
PR		25-OCT-1993;	93US-0143498.
XX		05-JUN-1995;	95US-0463675.
PA	(CREA-) CREATIVE BIOMOLECULES INC.		
PI	Dorai H, Oppermann H;		
DR	WPI; 1997-424235/39.		
N-PESD:	AAT91837.		
Pt	Producing single chain binding protein in immortalised eukaryotic		
Ft	cells - which comprise protein coding sequences, a transcription		
Pr	activator and translation promotion sequences, provides high		
Xx	expression at low copy number		
Example 2;	Column 29-32; 24dp; English.		
Cc	This sequence is a single chain anti-C-erbB-2 antibody (scFv)		
Cc	derived from hybridoma 74IF8. The protein product includes a C-terminal		
Cc	tail Gly4-Cys in some constructs. Single-chain antibodies can be		
Cc	produced using a novel method which comprises culturing an immortalised		
Cc	eukaryotic cell having transfected DNA sequences (encoding the protein		
Cc	of interest), integrated into its genome. In particular expression		
Cc	effector vectors containing a non-native reporter DNA (encoding the scFv)		
Cc	and viral sequences to promote transcription and translation (e.g. the		
Cc	adenovirus EIA and VAI genes as shown in AAT91831 and AAT91834		
Cc	respectively) are used. The scfv that is produced, when properly folded,		
Cc	has a structure with mono- or bi-functional binding activity. The method		
Cc	is especially used to produce single-chain antibody fragments (scFv),		
Cc	e.g. for imaging tumours or delivering therapeutic agents to them,"		
Cc	particularly breast and ovarian cancers that express the c-erbB-2'		
Cc	antigen. Other scfv are used in model studies and for treating digoxin		
CC	intoxication.		
CC	(Updated on 25-MAR-2003 to correct PF field.)		
SQ	Sequence    250 AA;		
Query Match	85.4%; Score 552; DB 18; Length 250;		
Best Local Similarity	85.4%; Pred. NO. 2.3e-35;		
Matches 105; Conservative	5; Mismatches    5; Indels    8; Gaps    2;		
Oy	1 EVKLVESGPELKKPGETVTKISCRASGYITFTNYGMNWKQA PGKGLKNMGMINITYGEPTY 60  ::  ::		
Db	3 ELGVQSOPELKKRGERVTIKSCRASGYTFTNYGMNWKQA PGKGLKNMGMININTYGEPTI 62  ::  ::		
Oy	61 ADDEKGFAFSLETSASTAYILQINLNKNEDTATYFCQ----LVGNSEPGPAYWCQTLLVT 116  ::  ::		
Db	63 AEERGGFFAFSLSTSASTAVYLQINNLKNEDTATYFGCGRGFTTYG---GFANMVGQLTVLT 118  ::  ::		
Oy	117 VSA 119 		
DB	119 VSA 121		
RESULT 5			
AAW22400	AAW22400 standard; Protein; 250 AA.		
XX	AAW22400;		
AC			
XX	25-MAR-2003 (updated)		
DT	09-OCT-1997 (first entry)		
Single chain antibody 74IF8 protein sequence.			
KV	Production; single-chain; binding protein; antibody; eukaryote; virus;		
KV	transcription activator; promoter; expression; adenovirus; EIA; PCR;		
KV	polymerase chain reaction; amplification; primer; herpes simplex virus;		
KV	thyridine kinase; vector; enhancer; transfection; heterologous.		
DS	Synthetic.		

XX US631158-A.  
 XX 20-MAY-1997.  
 XX  
 XX 05-JUN-1995; 95US-0461184.  
 XX  
 XX 25-OCT-1993; 93US-0143498.  
 XX 05-JUN-1995; 95US-0461184.  
 XX  
 XX (CREA-) CREATIVE BIOMOLECULES INC.  
 XX  
 XX Dorai H, Oppermann H;  
 XX WPI; 1997-288577/26.  
 XX N-PSDB; AAT78879.  
 XX  
 XX Production of cell line for producing single-chain binding protein -  
 PT using construct containing DNA encoding viral transcription  
 PT activator protein  
 XX  
 XX Example 2; Column 29-32; 24pp; English.  
 XX  
 CC The invention relates to methods of increasing production of a  
 CC single-chain binding protein, especially a single chain antibody,  
 CC by generating eukaryotic cell lines containing DNA encoding either  
 CC a viral transcription activator protein that acts on and stimulates  
 CC a viral promoter controlling the expression of DNA encoding the  
 CC single-chain binding protein, such as the adenovirus Ad2 E1a protein  
 CC encoded by the sequence AAT78873, or an RNA sequence able to promote  
 CC translation of the RNA transcript from the heterologous gene, such as  
 CC the adenoviral VA1 gene (AAT78876).  
 CC The sequence presented here is the amino acid sequence of the  
 CC anti-c-erbB2 single chain antibody 741. The coding sequence was  
 CC constructed by amplifying the variable heavy and light chain genes  
 CC which were then cloned into a pUC vector. For secretion from mammalian  
 CC cells, the sequence is preceded by the signal peptide sequence from  
 CC the monoclonal antibody 5209 (AAT78880) or from Pac1 (AAT78881).  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 250 AA;  
 Query Match 85.4%; Score 552; DB 18; Length 250;  
 Best Local Similarity 85.4%; Pred. No. 2.3e-38;  
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;  
 QY 1 EVKLVSGLPKKPGETVTKISCKASGYIFTNVGMWVKAQPGKGLKMMGWINTYTGEPY 60  
 DB 3 EIQLVQSGPELKKPGETVTKISCKASGYFTNVMWVKAQPGKGLKMMGWINTYTGEPY 62  
 QY 61 ADDEKGRPAFSLSTASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQTLVT 116  
 DB 63 AEEFKGRPAFSLSTASTAYLQINNLKNEDTATYFCGRQFTTYG---GFANWGQTLVT 118  
 QY 117 VSA 119  
 DB 119 VSA 121  
 DB  
 RESULT 6  
 AAM53168  
 ID AAM53168 standard; Protein; 250 AA.  
 XX  
 AC AAM53168;  
 XX  
 DT 16-JUL-1998 (first entry)  
 XX  
 DE 741F8 anti-c-erbB-2 sfv' dimeric construct protein sequence.  
 XX  
 KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer;  
 XX c-erbB-2; tumour; diagnosis.  
 XX  
 OS Synthetic.

OS Mus sp.  
 XX Key  
 XX Peptide  
 XX Peptide  
 XX Peptide  
 XX Peptide  
 XX US5753204-A.  
 XX 19-MAY-1998.  
 XX  
 XX 05-JUN-1995; 95US-0461838.  
 XX  
 XX 07-OCT-1993; 93US-0133804.  
 XX 06-FEB-1992; 92US-0831967.  
 XX 05-JUN-1995; 95US-0461838.  
 XX  
 XX (CHIR) CHIRON CORP.  
 XX (CREA-) CREATIVE BIOMOLECULES INC.  
 XX  
 XX Houston JL, Huston JS, Oppermann H, Ring DB;  
 XX WPI; 1998-31318/27.  
 XX N-PSDB; AAV21796.  
 XX  
 XX Imaging of antigens in vivo - using dimers of single-chain antibody  
 XX Fv fragments  
 XX  
 XX Example 1; Columns 25-28; 30pp; English.  
 XX  
 CC This represents the protein sequence of a 741F8 sfv' (single chain Fv)  
 CC C-terminal Gly4-Cys construct. This was constructed by connecting the Vh  
 CC and Vh genes with a DNA sequence encoding a 14 residue polypeptide  
 CC linker. 741F8 is a monoclonal antibody useful in targeting c-erbB-2  
 CC antigen. This dimeric construct can be used in the methods of invention  
 CC of imaging a preselected antigen expressed in a mammal. The methods are  
 CC used in magnetic resonance imaging of c-erbB-2 or related antigens in  
 CC cancer diagnosis. The biosynthetic constructs have enhanced properties  
 CC as in vivo targeting agents in comparison with intact monoclonal  
 CC antibodies or their Fab fragments. The dimeric constructs permit the  
 CC in vivo targeting of an epitope on an antigen with greater apparent  
 CC avidity, including greater tumour specificity, tumour localisation and  
 CC tumour retention properties than that of the Fab fragment having the same  
 CC CDRs as the construct.  
 XX  
 SQ Sequence 250 AA;  
 Query Match 85.4%; Score 552; DB 19; Length 250;  
 Best Local Similarity 85.4%; Pred. No. 2.3e-38;  
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;  
 QY 1 EVKLVSGLPKKPGETVTKISCKASGYIFTNVGMWVKAQPGKGLKMMGWINTYTGEPY 60  
 DB 3 EIQLVQSGPELKKPGETVTKISCKASGYFTNVMWVKAQPGKGLKMMGWINTYTGEPY 62  
 QY 61 ADDEKGRPAFSLSTASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQTLVT 116  
 DB 63 AEEFKGRPAFSLSTASTAYLQINNLKNEDTATYFCGRQFTTYG---GFANWGQTLVT 118  
 QY 117 VSA 119  
 DB 119 VSA 121  
 DB  
 RESULT 7  
 AAM47012  
 ID AAM47012 standard; Protein; 250 AA.  
 XX  
 AC AAM47012;  
 XX  
 DT 13-JUL-1998 (first entry)  
 XX

OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	Peptide
FT	122..135
XX	/note= "linker."
XX	
XX	US5837846-A.
XX	
PD	17-NOV-1998.
XX	
PX	05-JUN-1995;
XX	95US-0461386.
PR	07-OCT-1993;
PR	93US-0133804.
PR	06-FEB-1992;
PR	92US-0831967.
XX	05-JUN-1995;
XX	95US-0461386.
PA	(CHIR ) CHIRON CORP.
PA	(CREA-) CREATIVE BIOMOLECULES INC.
PI	Houston LI., Hueton JS., Oppermann H., Ring DB;
DR	WPI; 1999-023541/02.
DR	N-PESDB; AAV63397.
XX	
PT	Nucleic acid encoding single-chain Fv fragment specific for antigens
PT	- and having C-terminal tail for crosslinking to form dimer with
PT	improved pharmacokinetic properties, used to deliver drugs and
PT	imaging agents, especially to tumours
PS	Example 1, Columns 27-30; 29pp; English.
CC	The present sequence represents an anti-C-erbB-2 sFv'. C-erbB-2 is an
CC	antigen that is overexpressed on the surface of tumor cells. An
CC	antibody designated 741f78 binds c-erbB-2. Variable heavy and light
CC	sequences of antibody 741f78 are connected, together with a linker, to
CC	produce the present single chain Fv gene. Anti-c-erbB-2 sFv' exemplifies
CC	the invention. Dimers of the single chain Fv are used for targeted
CC	delivery of drugs or imaging agents (e.g. cytotoxins, prodrugs or
CC	99m-technetium) to antigen-expressing cells, particularly for treatment
CC	or diagnosis of tumors (especially of ovary or breast).
SC	Sequence      250 AA;
	Query Match                  85.4%; Score 552; DB 20; Length 250;
	Best Local Similarity        85.4%; Pred No. 52.3e-38;
Matches	105; Conservative     5; Mismatches     5; Indels     8; Gaps     2;
OY	1 EVKLIVSGEPILKKRGETVKISCSASGYIFITNGMMVVKQAPKGGLKMGMINTYTGBPTY 60 ::: :: :
DG	3 EIQVVGSGPELKRGRGTVKIISCASGYTFPTNQGMMVVKQAPKGGLKMGMINTNTNGEPTY 62 : :: :: :
OY	61 ADPPKGFARSLTSASTAYVLGINNKEDATNYCA-----LYGNSPKGFAYWGGLTYT 116 ::: :: :
DG	63 ABEPKGRFAFSLETSSASTAYVLGINNKEDATNYFCGGNQFITYG---GFANWGGLTYT 118    :: :
OY	117 VSA 119
DG	119 VSA 121
Db	
RESULT 9	
AAR09428	
ID	AAR09428 standard; Protein; 139 AA.
XX	
AA	AAR09428;
AC	
DF	25-MAR-2003 (updated)
DT	04-MAR-1993 (first entry)
XX	
DB	Kmi0 Heavy Chain V Region (mouse).
XX	
FM	Monoclonal antibody; chimera; light; heavy; chain; constant; variable; antitumor; diagnosis; cancer; tumor

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XX OS Mus musculus.
XX PN WO9002569-A.
XX XX
XX PD 22-MAR-1990.
XX XX
XX PF 06-SEP-1989; 89WO-US03852.
XX XX
XX PR 06-SEP-1988; 88US-0240624.
XX PR 08-SEP-1988; 88US-0241744.
XX PR 13-SEP-1988; 88US-0243739.
XX PR 04-OCT-1988; 88US-0253002.
XX PR 19-JUN-1989; 89US-0367641.
XX PR 21-JUL-1989; 89US-0382768.
XX PA (ITGE-) INT GENETIC ENG INC.
XX PA (INGE-) INGENE INT GENETIC.
XX PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX DR WPI; 1990-115825/15.
XX DR N-PSDB; AAQ08610.
XX PT Chimeric mouse-human antibodies - prepd. using genes coding for
XX PT constant human region murine variable region, esp. to 3 tumour
XX PT antigen
XX PS Claim 13; Page 123 + Fig 36; 173pp; English.
XX XX
XX CC The sequence is used in the produ. of a chimeric antibody mol.
XX CC comprising two light chains and two heavy chains, each having a
XX CC constant region (human) and a variable region (murine) having a
XX CC specificity to an antigen bound by murine monoclonal antibody
XX CC (Mab) KM10. The chimeric antibodies can be used for any purpose for
XX CC which the original murine Mabs can be used, with the advantage that
XX CC they are more compatible with the human body. They are esp. used for
XX CC the diagnosis and treatment of cancer.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 139 AA;

Query Match 84.9%; Score 548.5; DB 11; Length 139;
Best Local Similarity 84.9%; Pred. No. 2.5e-38;
Matches 101; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 EVKLVSQPELKKPGETVKISKASGYFTNNGMNVKQAPGKGLKMMGMINTYTGSEPT 60
DB 20 QIOLVOSGPBLMKPGETVKISKASGYFTNNGMNVKQAPGKGLKMMGMINTYTGSEPT 79
QY 61 ADDPKRFAFSLSTASAVYLQINNLKNEEDTATYFCALYGNSPKGPAYWGQGLVTVSA 119
DB 80 ADDPKRFAFSLSTASAVYLQINNLKNEEDTATYFCARWGS-YGMDYWGQGSVTWSS 137

RESULT 10
AAM06217
ID AAM06217 standard; Protein; 139 AA.
XX AC AAM06217;
XX AC
XX DT 25-MAR-2003 (updated)
XX DT 13-FEB-1997 (first entry)
XX DE Mab KM10 heavy chain variable region.
XX XX
XX KW Chimeric antibody; monoclonal antibody; MAb; antibody engineering;
XX KW tumour; antigen; colon carcinoma; stomach carcinoma;
XX KW pancreas carcinoma; oesophagus carcinoma; cancer; diagnosis;
XX KW therapy; heavy chain.
XX OS Mus sp.
XX PN

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PN US576184-A.
XX XX
XX PD 19-NOV-1996.
XX XX
XX PF 27-DEC-1994; 94US-0364001.
XX XX
XX PR 06-MAY-1991; 91US-0659401.
XX PR 06-SEP-1988; 88US-0240624.
XX PR 08-SEP-1988; 88US-0241744.
XX PR 13-SEP-1988; 88US-0243739.
XX PR 04-OCT-1988; 88US-0253002.
XX PR 19-JUN-1989; 89US-0367641.
XX PR 21-JUL-1989; 89US-0382768.
XX PR 27-DEC-1994; 94US-0364001.
XX PA (XOMA ) XOMA CORP.
XX PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX DR WPI; 1997-011249/01.
XX DR N-PSDB; AAT43442.
XX PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
XX PT used for the treatment and diagnosis of human cancers
XX PS Example 3; Fig 36; 102pp; English.
XX XX
XX CC The heavy chain variable region (AAM06217) of mouse monoclonal
XX CC antibody KM10 is the product of a cDNA clone (AAT43442) isolated
XX CC from a KM10 hybridoma cDNA library. Mab KM10 (IgG1) binds to an
XX CC antigen that is expressed on the surface of human colon, stomach,
XX CC pancreas and oesophagus carcinomas, but not on most normal adult
XX CC tissues. The heavy chain and light chain variable regions (see
XX CC also AAM06218) of KM10 can be linked to human constant regions and
XX CC expressed in transformed host cells. Novel mouse-human chimeric
XX CC antibodies (see also AAM06209-16) can be produced that have
XX CC specificity to human tumour antigens for use in the treatment and
XX CC diagnosis of human cancer.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 139 AA;

Query Match 84.9%; Score 548.5; DB 18; Length 139;
Best Local Similarity 84.9%; Pred. No. 2.5e-38;
Matches 101; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 EVKLVSQPELKKPGETVKISKASGYFTNNGMNVKQAPGKGLKMMGMINTYTGSEPT 60
DB 20 QIOLVOSGPBLMKPGETVKISKASGYFTNNGMNVKQAPGKGLKMMGMINTYTGSEPT 79
QY 61 ADDPKRFAFSLSTASAVYLQINNLKNEEDTATYFCALYGNSPKGPAYWGQGLVTVSA 119
DB 80 ADDPKRFAFSLSTASAVYLQINNLKNEEDTATYFCARWGS-YGMDYWGQGSVTWSS 137

RESULT 11
AAM85064
ID AAM85064 standard; Protein; 139 AA.
XX AC AAM85064;
XX AC
XX DT 20-MAR-2003 (updated)
XX DT 16-APR-1999 (first entry)
XX DE Mouse KM10 heavy chain variable region.
XX XX
XX KW Heavy chain variable region; murine antibody KM10; antibody ING-1;
XX KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
XX KW treatment; human cancer.
XX OS Mus sp.
XX PN US5843685-A.

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XX 01-DEC-1998.
XX 06-JUN-1995; 95US-0466034.
XX 06-SEP-1989; 89WO-US03852.
XX 06-MAY-1991; 91US-0659401.
XX 27-DEC-1994; 94US-0364001.
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX WPI; 1999-044574/04.
XX N-PSDB; AAV71160.
XX
XX Chimeric antibody specific for human tumour antigen - useful as
XX immunosensy, imaging or antitumour agent
XX
XX Example 3; Fig 36; 92pp; English.
XX
XX The present sequence represents the heavy chain variable region of
XX murine antibody XM10. The sequence was used to create chimeric
XX mouse-human immunoglobulins which recognise the human tumour
XX antigen bound by antibody ING-1 (produced by hybridoma cell line
XX ATCC HB 9812). The chimeric antibodies also have an antigen-binding
XX site that competitively inhibits the binding of antibody ING-1, and
XX mediate complement-dependent cytotoxicity of target cells or
XX antibody-dependent cellular cytotoxicity to target cells. The
XX chimeric antibodies can be used for therapeutic purposes in the
XX treatment of human cancer.
XX (Updated on 20-MAR-2003 to correct PR field.)
XX
XX Sequence 139 AA;
XX
XX Query Match 84.9%; Score 548.5; DB 20; Length 139;
XX Best Local Similarity 84.9%; Pred. No. 2.5e-38;
XX Matches 101; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
XX
XX 1 EVKLVSQGPGLKPGFTVTKISCAAGYITNTNGMMVWVKAQPKGKLMGMINITYGEPY 60
XX ::::|||||
XX 20 QIQLVQSGPELMPKPGSTVTKISCAAGYITNTNGMMVWVKAQPKGKLMGMINITYGEPY 79
XX
XX 61 ADPFKGRFAPSLSTASTAYLQINLNKEDTATYPCALYGNPKGFAYWGQGLTVTVSA 119
XX |||||
XX 80 ADPFKGRFAPSLSTASTAYLQINLNKEDTATYPCALYGNPKGFAYWGQGLTVTVSS 137
XX
XX
XX RESULT 12
XX ABUS8898
XX ID ABUS8898 standard; Protein; 139 AA.
XX
XX AC ABUS8898;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE Mouse antibody heavy chain variable region #5.
XX
XX KW Mouse; human tumour antigen; anti-human tumour antigen-antibody;
XX ING-1 antibody; cell line HB9812; immunoassay; imaging;
XX tumour diagnosis; tumour therapy; cytostatic;
XX heavy chain variable region.
XX
XX OS Mus sp.
XX
XX US6461824-B1.
XX

```

```

XX 08-OCT-2002.
XX 06-JUN-1995; 95US-0467142.
XX 06-SEP-1989; 89US-0659401.
XX 06-SEP-1989; 89WO-US03852.
XX 27-DEC-1994; 94US-0364001.
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX
XX (XOMA ) XOMA TECHNOLOGY LTD.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX WPI; 2003-196707/19.
XX N-PSDB; ABR79245.
XX
XX Antibody for detecting antigen in animal or killing cells carrying
XX antigen comprises human constant region and variable region having
XX specificity for human tumor antigen bound by ING-1 antibody
XX
XX Example 3; Fig 36; 101pp; English.
XX
XX The invention describes an antibody comprising a human constant region
XX and a variable region having specificity for the human tumour antigen
XX bound by the ING-1 antibody, where the ING-1 is produced by cell line
XX HB9812 as deposited with ATCC, and the antibody has the same affinity as
XX the ING-1 for the human tumour antigen. The antibody is useful in an
XX immunoassay method for detecting an antigen in a sample by contacting a
XX label-detectable antigen in the sample with the antibody, detecting the
XX label and relating the detected label to the presence of the antigen; for
XX use in an imaging method for revealing the presence of a label-detectable
XX antigen in an animal by contacting the antibody with a part of the animal
XX suspected of containing the antigen, detecting the label and relating the
XX detected label to the presence of the antigen; and for killing cells
XX carrying an antigen by contacting the cells with the antibody and
XX allowing the killing to occur. The antibodies are useful in tumour
XX diagnosis and therapy. The chimeric antibodies bind to the surface of
XX human tumour cells but do not bind detectably to normal cells, e.g.,
XX fibroblasts, endothelial cells or epithelial cells in the major organs.
XX The high biological activity of the chimeric antibodies against human
XX tumour cell lines combined with minimal reactivity with normal tissues
XX imply that these antibodies may mediate selective destruction of
XX malignant tissue. The presence of human rather than murine antigenic
XX determinants on the chimeric antibodies increases their resistance to
XX rapid clearance from the body relative to the original murine mAbs. This
XX resistance to clearance enhances the potential utility of these chimeric
XX antibodies, as well as their derivatives, in tumour diagnosis and
XX therapy. This is the amino acid sequence of a mouse antibody heavy chain
XX variable region used in the creation of an anti-human tumour
XX antigen-antibody.
XX
XX Sequence 139 AA;
XX
XX Query Match 84.9%; Score 548.5; DB 24; Length 139;
XX Best Local Similarity 84.9%; Pred. No. 2.5e-38;
XX Matches 101; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
XX
XX 1 EVKLVSQGPGLKPGFTVTKISCAAGYITNTNGMMVWVKAQPKGKLMGMINITYGEPY 60
XX ::::|||||
XX 20 QIQLVQSGPELMPKPGSTVTKISCAAGYITNTNGMMVWVKAQPKGKLMGMINITYGEPY 79
XX
XX 61 ADPFKGRFAPSLSTASTAYLQINLNKEDTATYPCALYGNPKGFAYWGQGLTVTVSA 119
XX |||||
XX 80 ADPFKGRFAPSLSTASTAYLQINLNKEDTATYPCALYGNPKGFAYWGQGLTVTVSS 137
XX
XX
XX RESULT 13
XX AAF64232
XX

```

ID	AA064232 standard; Protein; 140 AA.
AC	AA064232;
DT	25-MAR-2003 (updated)
XX	17-JUL-1995 (first entry)
XX	
DE	MAB L243 VH region.
XX	
XX	Humanized antibody; antibody engineering; MHC class I;
XX	major histocompatibility region; HLA; monoclonal antibody; MAb;
XX	L243; immunological disease; transplantation; light chain;
XX	heavy chain; variable region; complementarity determining region;
XX	CDR.
OS	Mus sp.
XX	
PN	W09429451-A2.
XX	
PD	22-DEC-1994.
XX	
PF	15-JUN-1994; 94MO-GB01291.
XX	
PR	16-JUN-1993; 93GB-0012415.
XX	
PR	27-JAN-1994; 94GB-0001597.
XX	
PR	09-FEB-1994; 94GB-0002499.
XX	
XX	29-MAR-1994; 94GB-0006222.
PA	(CLUT ) CELLTECH LTD.
PI	Achwal DS, Bodmer MW, Entage JS, Morgan SA;
XX	
DR	WPI; 1995-036480/05.
XX	
DR	N-PSDB; AA080360.
XX	
PT	New humanised anti-HLA DR antibodies - used for diagnosis and
XX	treatment of immunological diseases and transplantation related
PT	conditions
XX	
PS	Disclosure; Fig. 2; 68pp; English.
XX	
CC	L243 is a mouse MAb raised against human MHC class II. The
XX	nucleotide and amino acid sequences of L243 VL and VH regions are
CC	given in AA080359/R64231 and AA080360/R64232, respectively.
CC	CDR-grafted humanized antibodies based on these sequences have
CC	been constructed.
CC	(updated on 25-MAR-2003 to correct PN field.)
XX	
XX	
SQ	Sequence 140 AA:
	Query Match 84.5%; Score 546; DB 16; Length 140;
	Best Local Similarity 83.5%; Pred. No. 4, 1e-38;
	Matches 101; Conservative 8; Mismatches 10; Indels 2; Gaps 1
QY	1 EVKLIVSEPELKKPEETVTKISCKASGYFTNNGMMWVQCAPKSGIKMGIMNTYGEPT 60
DB	20 QIQLVSGELKKPEETVTKISCKASGYFTNNGMMWVQCAPKSGIKMGIMNTYREPT 79
QY	61 ADDEGKRAFSLETSASTAYLIQINNKKEDTATYCA--LYGNSPKGFAYWQGTILVTS 118
DB	80 ADDEGKRAFSLETSASTAYLIQINNKKEDTAKYFCARDITAVFTGPDYWGQGTILVTS 139
QY	119 A 119
DB	140 S 140
RESULT 14	
ID	AA064257
AC	AA064257; standard; Protein; 140 AA.
XX	
XX	

DT	25-MAR-2003	(updated)
DT	31-JUL-1995	(first entry)
XX		
DE	MHC-II MAb I243 heavy chain.	
XX		
KM	I243; heavy chain; VH; monoclonal antibody; MAb; MHC-II;	
KM	major histocompatibility complex class II; immunosuppressive;	
KM	variable region; Fc receptor 1; FcRI; antibody engineering;	
KM	cancer; immunotherapy.	
XX		
OS	Mus sp.	
XX		
PN	MO9429351-A2.	
XX		
PD	22-DEC-1994.	
XX		
PF	15-JUN-1994; 94WO-GB01290.	
XX		
PR	16-JUN-1993; 93GB-0012415.	
PR	27-JAN-1994; 94GB-0001597.	
PR	09-FEB-1994; 94GB-0002499.	
PR	29-MAR-1994; 94GB-0006244.	
PR	29-MAR-1994; 94GB-0006222.	
XX		
PA	(CELLT ) CELLTECH LTD.	
XX		
PI	Athwal DS, Bodmer MW, Entage JS, Morgan SA;	
XX		
DR	WPI, 1995-036409/05.	
XX		
DR	N-PSDB; AAQ80426.	
XX		
PT	New antibodies with altered ability to fix complement - having	
XX	one or more amino acid residues in the N-terminal region of the	
PT	constant chain heavy domain altered	
XX		
PS	Disclosure; Fig. 3; 91pp; English.	
XX		
CC	cDNA for mouse anti-human MHC-II MAb I243 (ATCC HB 55) heavy chain	
CC	variable region was cloned by PCR. Clone PE1702 was obtained that	
CC	contained a VH insert having the sequence given in AAQ80426; the	
CC	deduced amino acid sequence is given in AA864257. Altered	
CC	antibodies have been prepared that retain immunosuppressive	
CC	properties but show reduced binding to FcRI.	
CC	(updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 140 AA;	
	Query Match 84.5%; Score 546; DB 16; Length 140;	
	Best Local Similarity 83.5%; Pred. No. 4, 1e-38;	
	Matches 101; Conservative 8; Mismatches 10; Indels 2; Gaps 1;	
QY	1 EVKLVSPELKKGEYTKISKASGYIFTNYGNWYQAQKGLKMWGINITYTGEPTY 60	
	:::     :     :     :     :     :     :     :     :	
DB	20 QIQLVQSPFLKKGEYTKISKASGYIFTNYGNWYQAQKGLKMWGINITYTRETYY 79	
	:     :     :     :     :     :     :     :	
QY	61 ADDRKGKPAFLSTASATAYQIINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLYTVS 118	
	:     :     :     :     :     :     :     :	
DB	80 ADDEGKPAFLSTASATAYQIINNLKNEDTAKYFCARDITAYVPTGFDYWGQGTLYTVS 139	
	:     :     :     :     :     :     :     :	
QY	119 A 119	
	:     :     :     :     :     :     :     :	
DB	140 S 140	
	:     :     :     :     :     :     :     :	
	RESULT 15	
	AA837717	
ID	AA837717 standard; Protein, 138 AA.	
XX		
AC	AA837717;	
XX		
DT	25-MAR-2003 (updated)	
DT	30-SEP-1993 (first entry)	
XX		

DE Mouse 4C10 anti-idiotypic Ab heavy chain V region.

XX  
KM MA1A; monoclonal antibody; hybridoma; organ transplant rejection;  
KW immuno-modulator; cancer; treatment; diagnosis; melanoma;  
KW anti-cancer immunity; enhancement; suppression.

XX  
OS Mus musculus.

XX  
PN M09310221-A1.

XX  
PD 27-MAY-1993.

XX  
PF 12-NOV-1992; 92WC-US10166.

XX  
PR 13-NOV-1991; 91US-0791934.

XX  
PA (REGC ) UNTV CALIFORNIA.

XX  
PI Hastings A, Irie RF, Morrison SL;

XX  
DR WPI; 1993-182538/22.

XX  
PT Chimeric murine-human anti-idiotypic monoclonal antibodies -  
PT useful as immuno-modulators for treating and diagnosing cancers,  
PT and for suppressing organ transplant rejection and auto-immune  
PT diseases

XX  
PS Disclosure; Page 33; 46pp; English.

XX  
CC The sequence is that of the 4C10 anti-idiotypic Ab heavy chain V region  
CC which was used in the construction of a murine/human monoclonal  
CC anti-idiotypic antibody (MA1A). The MA1A elicits an anti-ganglioside  
CC response and produces antibodies which induce cytotoxic destruction  
CC of cancer cells bearing the gangliosides. It can be used for treating  
CC cancers parvic, melanomas. It can also be used as an immunomodulator to  
CC enhance anti-cancer immunity, suppress organ transplant rejection and  
CC suppress auto-immune disease. The MA1A can also be used in the diagnosis  
CC of cancers.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX  
SQ Sequence 138 AA;

Query Match 84.2%; Score 544; DB 14; Length 138;

Best Local Similarity 84.0%; Pred. No. 5.9e-38;

Matches 100; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

```
QY      1 EVKLVESSPELKKPGFTVTKISCKASGYITFTNGKQWVKQAPKSLKNGKMINVTYGEPT 60
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      20 QIOLVQSGPELKKPGFTVTKISCKASGYITFTNGKQWVKQAPKSLKNGKMINVTYGEPT 79
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 ADPFKGRFPAFSLTASSTAYVLOINNLKQNEDTATYFCALYQNSPKGFAYWGGCTLVTVSA 119
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      80 TEEFKGRFPAFSLTASSTAYVLOINNLKQNEDTATYFCALYQNSPKGFAYWGGCTLVTVSA 138
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: November 7, 2003, 07:26:59  
Job time : 52.3178 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 104.383 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992b-82\_COPY\_1\_119

Perfect score: 646  
Sequence: 1 EVKLVSGPELKKRGKGVTKI.....GNSPKGPAHWGGTLTVSA 119

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCRUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	85.4	250	10	US-09-867-853-2
2	543.5	84.1	118	12	US-10-422-049-19
3	536	83.0	160	12	US-10-222-026A-35
4	532.5	82.4	118	12	US-10-268-883-9
5	532.5	82.4	137	12	US-10-268-883-8
6	530	82.0	243	10	US-09-887-853-6
7	529.5	82.0	116	10	US-09-971-543-8
8	529.5	82.0	253	10	US-09-971-543-2
9	528.5	81.8	118	12	US-10-127-890-124
10	526.5	81.5	116	12	US-10-138-727A-2
11	526.5	81.5	116	12	US-10-138-727A-26
12	526	81.4	119	12	US-10-268-883-3
13	526	81.4	119	15	US-10-269-010-1
14	526	81.4	138	12	US-10-268-883-2
15	525	81.3	138	11	US-09-977-283A-13

16	522.5	80.9	116	12	US-10-138-727A-25
17	522	80.8	123	9	US-09-056-160B-9
18	522	80.8	123	10	US-10-234-671-9
19	520.5	80.6	118	12	US-09-949-559-106
20	520.5	80.6	118	11	US-09-875-221A-106
21	520	80.5	128	11	US-09-977-283A-15
22	516.5	80.0	116	12	US-10-138-727A-18
23	516.5	80.0	116	12	US-10-310-719-30
24	516.5	80.0	579	12	US-10-138-727A-41
25	515	79.7	121	10	US-09-965-099-7
26	515	79.7	121	10	US-09-965-099-111
27	515	79.7	121	14	US-10-051-852-7
28	515	79.7	121	14	US-10-051-852-111
29	515	79.7	123	10	US-09-965-099-109
30	515	79.7	123	14	US-10-051-852-109
31	513	79.4	138	11	US-09-977-283A-11
32	512.5	79.3	116	12	US-10-138-727A-24
33	512	79.3	136	11	US-09-967-719C-2
34	510.5	79.0	118	12	US-10-422-049-15
35	509.5	78.9	116	12	US-10-138-727A-23
36	507	78.5	135	11	US-09-967-719C-8
37	506.5	78.4	116	12	US-10-138-727A-20
38	500.5	77.5	116	12	US-10-138-727A-21
39	500	77.4	119	11	US-09-977-283A-22
40	499.5	77.3	116	12	US-10-138-727A-80
41	499.5	77.3	116	12	US-10-310-719-33
42	499.5	77.3	579	12	US-10-310-719-32
43	494.5	76.5	122	11	US-09-982-464-3
44	493.5	76.4	116	12	US-10-138-727A-19
45	491	76.0	117	12	US-10-138-727A-35

#### ALIGNMENTS

RESULT 1  
US-09-867-853-2  
Sequence 2, Application US/09887853  
Patent No. US20020166375A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
Oppermann, Hermann  
Houston, L. L.  
Ring, David B.  
TITLE OF INVENTION: Biochemical Binding Proteins For Imaging  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/867,853  
FILING DATE: 21-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/133,804  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelley, Robin D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100

/ INFORMATION FOR SEQ ID NO: 2:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 250 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-887-853-2

Query Match 85.4%; Score 552; DB 10; Length 250;  
 Best Local Similarity 85.4%; Pred. No. 2.9e-41;  
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSSEPLKKGGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 60  
 DB 3 EIQLVQSGPELKKGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 62  
 QY 61 ADFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCALYGNSPKGFVWQGTLYVTS 116  
 DB 63 ADFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCGRQFTYVQ---GFANWGQGTLYV 118  
 QY 117 VSA 119  
 DB 119 VSA 121

# RESULT 2

US-10-422-049-19  
 / Sequence 19, Application US/10422049  
 / Publication No. US20030199679A1

/ GENERAL INFORMATION:  
 / APPLICANT: Adair, John Robert  
 / APPLICANT: Athwal, Diljeet Singh  
 / APPLICANT: Emtage, John Spencer  
 / APPLICANT: Bodmer, Mark William  
 / TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha  
 / FILE REFERENCE: CARP0063

/ CURRENT APPLICATION NUMBER: US/10/422,049  
 / CURRENT FILING DATE: 2003-04-22  
 / PRIOR APPLICATION NUMBER: US/09/267,281  
 / PRIOR FILING DATE: 1999-03-12  
 / PRIOR APPLICATION NUMBER: 08/456,418  
 / PRIOR FILING DATE: 1995-06-01  
 / PRIOR APPLICATION NUMBER: 08/373,882  
 / PRIOR FILING DATE: 1995-01-17  
 / PRIOR APPLICATION NUMBER: 07/920,378  
 / PRIOR FILING DATE: 1992-09-28  
 / NUMBER OF SEQ ID NOS: 20  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 19  
 / LENGTH: 118  
 / TYPE: PRT  
 / ORGANISM: Murine  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: Humanized  
 / OTHER INFORMATION: Antibody  
 US-10-422-049-19

Query Match 84.1%; Score 543.5; DB 12; Length 118;  
 Best Local Similarity 85.1%; Pred. No. 8e-41;  
 Matches 103; Conservative 5; Mismatches 6; Indels 7; Gaps 2;

QY 2 VKLVSEPELKKGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 61  
 DB 2 IQLVQSGPELKKGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 61  
 QY 62 DDFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCALYGNSPKGFVWQGTLYVTS 118  
 DB 62 DDFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCALYGNSPKGFVWQGTLYVTS 117  
 QY 119 A 119  
 DB 118 S 118

# RESULT 3

US-10-222-026A-35  
 / Sequence 35, Application US/10222026A  
 / Publication No. US20030186322A1

/ GENERAL INFORMATION:  
 / APPLICANT: Janda, Kim D.  
 / APPLICANT: Mitzsching, Peter  
 / APPLICANT: Lerner, Richard A.

/ TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC  
 / TITLE OF INVENTION: PROTEINS ON FILAMENTOUS PHAGE USING PVI1 AND PIX  
 / TITLE OF INVENTION: COMPOSITIONS, VECTORS AND COMBINATORIAL LIBRARIES

/ FILE REFERENCE: TSRI 693.0 D1  
 / CURRENT APPLICATION NUMBER: US/10/222,026A  
 / CURRENT FILING DATE: 2002-08-14  
 / PRIOR APPLICATION NUMBER: US/09/318,786  
 / PRIOR FILING DATE: 1999-05-25  
 / NUMBER OF SEQ ID NOS: 41  
 / SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 35  
 / LENGTH: 160  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthesized

US-10-222-026A-35

Query Match 83.0%; Score 536; DB 12; Length 160;  
 Best Local Similarity 85.7%; Pred. No. 4.9e-40;  
 Matches 102; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY 1 EVKLVSSEPLKKGGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 60  
 DB 3 EIQLVQSGPELKKGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 62  
 QY 61 ADFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCALYGNSPKGFVWQGTLYVTS 119  
 DB 63 ADFKGRFAPSLFETASATAYLQINNLKNEEDTATYFCALYGNSPKGFVWQGTLYVTS 119

# RESULT 4

US-10-268-883-9  
 / Sequence 9, Application US/10268883  
 / Publication No. US20030138862A1

/ GENERAL INFORMATION:  
 / APPLICANT: Iseo, J. Yun  
 / APPLICANT: Green, Jennifer Macphate

/ TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof  
 / FILE REFERENCE: 05882.0062.NPUS01  
 / CURRENT APPLICATION NUMBER: US/10/268,883  
 / CURRENT FILING DATE: 2003-03-26  
 / PRIOR APPLICATION NUMBER: USSN 60/329,178  
 / PRIOR FILING DATE: 2001-10-10  
 / PRIOR APPLICATION NUMBER: USSN 60/331,965  
 / PRIOR FILING DATE: 2001-11-21  
 / NUMBER OF SEQ ID NOS: 16  
 / SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 9  
 / LENGTH: 118  
 / TYPE: PRT  
 / ORGANISM: Mouse

US-10-268-883-9

Query Match 82.4%; Score 532.5; DB 12; Length 118;  
 Best Local Similarity 82.0%; Pred. No. 7.5e-40;  
 Matches 100; Conservative 6; Mismatches 9; Indels 7; Gaps 2;

QY 1 EVKLVSSEPLKKGGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 60  
 DB 1 IQLVQSGPELKKGEYTKISCKASGYFTNYGMNWKQAPGKGLKMGWINTYTGSEPTY 60

QY 61 ADFPKGFASLSTSTASTAYLQINLNKEDTATYFCA---LYGNSPKGFAYMGGLIVY 117  
Db 61 ADFPKGFASLSTSTASTAYLQINLNKEDMATYFCANGDYG---PFDYMGGLTIV 116  
QY 118 SA 119  
Db 117 SS 118

```

1      RESULT 5
2      US-10-268-883-8
3      ; Sequence 8, Application US/10268883
4      ; Publication No. US20030138662A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: TSO, J. Yun
7      ; APPLICANT: Green, Jennifer Macphate
8      ; TITLE OF INVENTION: Anti-H1A-DR Antibodies and the Methods of Using Thereof
9      ; FILE REFERENCE: 05882.1NP0501
10     ; CURRENT APPLICATION NUMBER: US/10/268,883
11     ; CURRENT FILING DATE: 2003-03-26
12     ; PRIOR APPLICATION NUMBER: USSN 60/329,178
13     ; PRIOR FILING DATE: 2001-10-10
14     ; PRIOR APPLICATION NUMBER: USSN 60/331,965
15     ; PRIOR FILING DATE: 2001-11-21
16     ; NUMBER OF SEQ. ID NOS.: 16
17     ; SOFTWARE: PatentIn version 3.1
18     ; SEQ. ID NO. 8
19     ; LENGTH: 137
20     ; TYPE: PRT
21     ; ORGANISM: Mouse
22     ; US-10-268-883-8

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Query Match	82.4%;	Score 532.5;	DB 12;	Length 137;
Best Local Similarity	82.0%;	Pred. No. 8.6e-40;		
Matches 100;	Conservative	6;	Mismatches 9;	Indels 7;
				Gaps 2

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Qy      EKVLVSGPELKKPGSTVVISCKASGYITNTNGNMVWQQAQSGKGLKMMGINTVAGPTV 60
      :::
Db      QILNQSGPELKKPGSTVVISCKASGYITNTNGNMVWQQAQSGKGLKMMGINTVNGEPTV 79
Qy      61 ADDEKRPFAFSLSTASVYLIQINLKKNDPTATFCA---LQGNSPKQFAVGGCTLVV 117
      :
Db      80 ADDEKRPFAFSLSTASVYLIQINLKKNDMATVFCANGDYVG---PFDYMGQGITLVV 135
Qy      118 SA 119
      :
Db      136 SS 137

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RESULT 6  
 US-09-887-853-6  
 Sequence 6, Application US/09887853  
 Patent No. US20020168375A1  
 GENERAL INFORMATION:  
 APPLICANT: Huston, James S.  
 Oppermann, Hermann  
 Houston, L. L.  
 Ring, David B.  
 TITLE OF INVENTION: Biosynthetic Binding Proteins For  
 Imaging  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Tasta, Hurwitz & Thibeault/Patent Department  
 STREET: Exchange Place, 53 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/887,853
3 FILING DATE: 21-Jun-2001
4 CLASSIFICATION: <Unknown>
5
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US/08/133,804
8 FILING DATE: <Unknown>
9
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Kelley, Robin D.
12 REGISTRATION NUMBER: 34,637
13 REFERENCE/DOCKET NUMBER: 2054/22
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 617-248-7477
16 TELEFAX: 617-248-7100
17
18 INFORMATION FOR SEQ ID NO: 6:
19
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 243 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 MOLECULE TYPE: protein
25 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
26
27 US-09-887-853-6

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Query Match	82.0%;	Score 530;	DB 10;	Length 243;
Best Local Similarity	82.4%;	Pred. No. 2.5e-39;		
Matches 98;	Conservative 10;	Mismatches 7;	Indels 4;	Gaps 1;

[illegible]

RESULT 7  
 US-09-971-543--8  
 Sequence 8, Application US/09971543  
 Patent No. US20020146846a1  
 GENERAL INFORMATION:  
 APPLICANT: PLOCKTHUN, ANDREAS  
 APPLICANT: HONEGGER, ANNEMARIE  
 APPLICANT: WILDUDA, JOEG  
 TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC  
 TITLE OF INVENTION: IMMUNOGLOBULIN OR IMMUNOGLOBULIN FRAGMENTS, AND  
 TITLE OF INVENTION: STABILIZED ANTI-EGF-2 scFv FRAGMENT  
 TITLE REFERENCE: PUCK-3 CON  
 CURRENT APPLICATION NUMBER: US/09/971,543  
 CURRENT FILING DATE: 2001-10-04  
 PRIOR APPLICATION NUMBER: PCT/EP00/03176  
 PRIOR FILING DATE: 2000-04-10  
 PRIOR APPLICATION NUMBER: EP 99 10 7030.1  
 PRIOR FILING DATE: 1999-04-09  
 NUMBER OF SEQ. ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 8  
 LENGTH: 116  
 TYPE: PRT  
 ORGANISM: Mus sp.  
 US-09-971-543--8

Query Match	82.0%;	Score 529.5;	DB 10;	Length 116;
Best Local Similarity	84.0%;	Pred. No. 1.3e-39;		
Matches 100;	Conservative	8;	Mismatches	8;
			Indels	3;
			Gaps	2;

[illegible]

```

RESULT 8
US-09-971-543-2
; Sequence 2, Application US/09971543
; Patent No. US20020146846A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHORN, ANDREAS
; APPLICANT: HONEGGER, ANNEMARIE
; APPLICANT: WILDADA, JORG
; TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC
; TITLE OF INVENTION: IMMUNOGLOBULINS OR IMMUNOGLOBULIN FRAGMENTS, AND
; TITLE OF INVENTION: STABILIZED ANTI-BSP-2 bcfv FRAGMENT
; FILE REFERENCE: PLUCK-3 CON
; CURRENT APPLICATION NUMBER: US/09/971,543
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PCT/EP00/03176
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: EP 99 10 7030.1
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-971-543-2

Query Match          82.0%; Score 529.5; DB:10; Length 253;
Best Local Similarity 84.0%; Pred. No. 2,9e-39;
Matches 100; Conservative 8; Mismatches 8; Indels 3; Gaps 2

QY      1 EVKLVEGSELKPKSEETVYKISCKASGYTFITNGMNVYKAPGGLKMGKINTYTGSEPT 60
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      138 QVQLQDSGSELKPKPEETVYKISCKASGYFTFYGMNVYKQAPGGLKMGKINTYTGSE 197
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 ADDPKRPFSLSETASTAYVQINNLKREDATPCALYGNSPKGFAYWGQGLTVVSA 119
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      198 ADDPKRPFSLSETASNAVQINNLKREDATITFCARF--AIKG-DYWGQGLTVVSS 253
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-127-890-124
; Sequence 124, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994

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      APPLICATION NUMBER: US 08/064,691
      FILING DATE: 12-MAY-1993
      APPLICATION NUMBER: US 07/988,430
      FILING DATE: 09-DEC-1992
      APPLICATION NUMBER: US 07/901,707
      FILING DATE: 19-JUN-1992
      APPLICATION NUMBER: US 07/787,567
      FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Monicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 368-1248
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 124:
US-10-127-890-124

Query Match          81.8%; Score 528.5; DB 12; Length 118;
Best Local Similarity 83.2%; Pred. No. 1.7e-39;
Matches 99; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Y Y   1 EVKIVSGPELKKRGEFTVKISCKASGYTFITNYGNMWYKQAPGKGGLRMWGWINTYTGEPTY 60
    ::::::::::::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  1 QIQIVSQSPFLKKRGFTVKISCKASGYTFITNYGNMWYKQAPGKGGLRMWGWINTYTGEPTY 60

        61 ADDPKGFAPSFLETSASTAVYLQINNLNEDPATYFCALYGNSPGFAFYWGQGLVTYSA 119
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  61 ADDPKGFAPSFLETSASTAVYLQINNLNEDPATYFCRTRRGID-WYFDWAGTIVTYS 118

RESULT 10
US-10-138-727A-2
Sequence 2, Application US/10138727A
Publication No. US20030157054A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
FILE REFERENCE: LEX-019
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: KS VH mouse
US-10-138-727A-2

Query Match          81.5%; Score 526.5; DB 12; Length 116;
Best Local Similarity 81.5%; Pred. No. 2.5e-39;
Matches 97; Conservative 11; Mismatches 8; Indels 3; Gaps 2;

Y Y   1 EVKIVSGPELKKRGEFTVKISCKASGYTFITNYGNMWYKQAPGKGGLRMWGWINTYTGEPTY 60
    ::::::::::::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  1 QIQIVSQSPFLKKRGFTVKISCKASGYTFITNYGNMWYKQAPGKGGLRMWGWINTYTGEPTY 60

        61 ADDPKGFAPSFLETSASTAVYLQINNLNEDPATYFCALYGNSPGFAFYWGQGLVTYSA 119
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```



RESULT 15

US-09-977-283A-13  
 ; Sequence 13, Application US/09977283A  
 ; Publication No. US20030031664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Guy L.  
 ; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
 ; FILE REFERENCE: 0609.4320003  
 ; CURRENT APPLICATION NUMBER: US/09/977,283A  
 ; CURRENT FILING DATE: 2001-10-16  
 ; PRIOR APPLICATION NUMBER: 08/934,000  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/026,356  
 ; PRIOR FILING DATE: 1996-09-20  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 13  
 ; LENGTH: 138  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (-18)..  
 ; OTHER INFORMATION: May be either Asp or Ala  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (-14)..  
 ; OTHER INFORMATION: May be either Asn or Thr  
 US-09-977-283A-13

Query Match

Best Local Similarity 81.3%; Score 525; DB 11; Length 138;  
 Matches 96; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 EVKLVSQPELKKPGETVKISKASGYIFITVGNWVWQAPGKGLKMWGINTYTGSEPTY 60  
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 20 QIQVQSGPELKKPGETVKISKASGYIFITVGNWVWQAPGKGLKMWGINTYTGSEPTY 79  
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 ADDEKGRFAPSLETSASTAYLQINNLLKNEDEATYFCALYGNSPKGFAYWGGLVTVSA 119  
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 80 AEFKGRFAPSLETSASTAYLQINNLLKNEDEATYFCALYGNWPGTYAMDYWGGLVTVSS 138  
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 7, 2003, 08:16:50  
 Job time : 104.383 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 17.4766 Seconds  
(without alignments)  
288,098 Million cell updates/sec

Title: US-09-661-992B-82\_COPY\_1\_119  
Perfect score: 646  
Sequence: 1 EVKLVSQPELKKRGEYTKL.....GNSPKGPAVMGQTLVTVSA 119

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgm2\_6/ptodata/1/iaa/PTUS\_COMB.pep: \*  
6: /cgm2\_6/ptodata/1/iaa/backfltest.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	552	85.4	250	1	US-08-133-804-2
2	552	85.4	250	1	US-08-461-184-8
3	552	85.4	250	1	US-08-463-675-8
4	552	85.4	250	1	US-08-464-589-8
5	552	85.4	250	1	US-08-461-838-2
6	552	85.4	250	2	US-08-461-386-2
7	552	85.4	622	2	US-08-356-786-16
8	546	84.5	140	3	US-08-569-147-76
9	543.5	84.1	252	3	US-08-279-772A-6
10	543.5	84.1	252	3	US-08-902-486-9
11	539.5	83.5	365	3	US-08-875-811-53
12	539.5	83.5	366	3	US-08-875-811-55
13	536	83.0	160	4	US-09-318-786-35
14	530	82.0	115	4	US-08-483-749A-24
15	530	82.0	243	1	US-08-133-804-6
16	530	82.0	243	1	US-08-461-838-6
17	530	82.0	243	2	US-08-461-386-6
18	530	82.0	243	2	US-08-356-786-4
19	530	82.0	534	2	US-08-356-786-10
20	528.5	81.8	118	1	US-08-425-336-124
21	528.5	81.8	118	1	US-08-488-113B-124
22	528.5	81.8	118	1	US-08-477-484B-124
23	528.5	81.8	118	1	US-08-107-669D-28
24	528.5	81.8	118	1	US-08-472-788A-28
25	528.5	81.8	118	2	US-08-477-531B-26
26	528.5	81.8	118	2	US-08-646-360-124
27	528.5	81.8	118	2	US-08-082-842A-28

28	528.5	81.8	118	3	US-08-839-765-124	Sequence 124, App
29	528.5	81.8	118	3	US-09-136-389-124	Sequence 124, App
30	528.5	81.8	118	4	US-09-610-838-124	Sequence 124, App
31	526	81.4	278	3	US-09-184-658-47	Sequence 47, Appl
32	525.5	81.3	118	1	US-08-107-669D-66	Sequence 66, Appl
33	525.5	81.3	118	1	US-08-472-788A-88	Sequence 88, Appl
34	525.5	81.3	118	2	US-08-477-531B-66	Sequence 66, Appl
35	525.5	81.3	118	2	US-08-082-842A-88	Sequence 88, Appl
36	525	81.3	138	2	US-08-933-983-13	Sequence 13, Appl
37	524	81.0	119	4	US-08-481-845-2	Sequence 2, Appl
38	523	81.0	136	3	US-09-184-658-32	Sequence 32, Appl
39	523	81.0	284	3	US-09-184-658-40	Sequence 40, Appl
40	521	80.7	118	4	US-09-406-532-21	Sequence 21, Appl
41	520	80.5	138	3	US-08-933-983-15	Sequence 15, Appl
42	515	79.7	121	3	US-08-783-853A-7	Sequence 7, Appl
43	515	79.7	121	3	US-08-783-853A-111	Sequence 111, App
44	515	79.7	121	4	US-09-344-050-7	Sequence 7, Appl
45	515	79.7	121	4	US-09-344-050-111	Sequence 111, App

## ALIGNMENTS

```
RESULT 1
US-08-133-804-2
Sequence 2, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huelton, James S.
APPLICANT: Opertmann, Hermann
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133, 804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: Protein
US-08-133-804-2
Query Match 85.4%; Score 552; DB 1; Length 250;
Best Local Similarity 85.4%; Pred. No. 2.2e+43;
Matches 105; Conservative 5; Mismatches 8; Gaps 2;
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1 EVKLVSQPELKKRGEYTKLSCASGYLFTYGNMVMQAQSGKXMGMINITYGSEPTY 60  
3 EKLVSQPELKKRGEYTKLSCASGYLFTYGNMVMQAQSGKXMGMINITYGSEPTY 62

QY 61 ADDFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 116  
DB 63 AEEFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 118  
QY 117 VSA 119  
DB 119 VSA 121

## RESULT 2

US-08-461-184-8  
Sequence 8, Application US/08461184  
Patent No. 5631158  
GENERAL INFORMATION:  
APPLICANT: DORAI, HAIMANTI  
APPLICANT: OPPERMAN, HERMANN  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN  
TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 07148  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,184  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/143,498  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP093  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/248-7000  
TELEFAX: 617/248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-184-8

Query Match 85.4%; Score 552; DB 1; Length 250;  
Best Local Similarity 85.4%; Pred. No. 2.2e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSSEPLKKGKGGTIVKISCAASGYITFTYGMNWKQAPGKGLKMGMINNTTGEPT 60  
DB 3 EIQLVSGPELKKKGKGGTIVKISCAASGYITFTYGMNWKQAPGKGLKMGMINNTTGEPT 62  
QY 61 ADDFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 116  
DB 63 AEEFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 118  
QY 117 VSA 119  
DB 119 VSA 121

RESULT 3  
US-08-463-675-8

Sequence 8, Application US/08463675  
Patent No. 5658763  
GENERAL INFORMATION:  
APPLICANT: DORAI, HAIMANTI  
APPLICANT: OPPERMAN, HERMANN  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN  
TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 07148  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,675  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/143,498  
FILING DATE: 25-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP093  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/248-7000  
TELEFAX: 617/248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-675-8

Query Match 85.4%; Score 552; DB 1; Length 250;  
Best Local Similarity 85.4%; Pred. No. 2.2e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSSEPLKKGKGGTIVKISCAASGYITFTYGMNWKQAPGKGLKMGMINNTTGEPT 60  
DB 3 EIQLVSGPELKKKGKGGTIVKISCAASGYITFTYGMNWKQAPGKGLKMGMINNTTGEPT 62  
QY 61 ADDFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 116  
DB 63 AEEFKRFAFSLSTASTAYLQINNKEDTATYFCA----LYGNSPKGFAYWGQGLT 118  
QY 117 VSA 119  
DB 119 VSA 121

RESULT 4  
US-08-464-589-8  
Sequence 8, Application US/08464589  
Patent No. 5733782  
GENERAL INFORMATION:  
APPLICANT: DORAI, HAIMANTI  
APPLICANT: OPPERMAN, HERMANN  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN  
TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON

STATE: MA  
COUNTRY: USA  
ZIP: 07148  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/464,589  
APPLICATION NUMBER: US/08/464,589  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,498  
FILING DATE: 25-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: CRP093  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/248-7000  
TELEFAX: 617/248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-589-8

Query Match 85.4%; Score 552; DB 1; Length 250;  
Best Local Similarity 85.4%; Pred. No. 2,2e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSGPELKKPEETVKISKASGYIFETNYGMWVQAQKGLKMMGWINTYGEPTV 60  
DB 3 EIQIVQSGPELKKPEETVKISKASGYIFETNYGMWVQAQKGLKMMGWINTYGEPTV 62  
QY 61 ADDFKGRFAFSLETSASTAYVLIQINNLIKNEEDTATYFCA---LYGNSPKGFAVWGQGLTVT 116  
DB 63 AEEFKGRFAFSLETSASTAYVLIQINNLIKNEEDTATYFCA---LYGNSPKGFAVWGQGLTVT 118  
QY 117 VSA 119  
DB 119 VSA 121

RESULT 5  
US-08-461-838-2  
Sequence 2, Application US/08461838  
Patent No. 5753204  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
SOFTWARE: Patentin Release #1.0, Version #1.25  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,838

FILING DATE: 424  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-838-2

Query Match 85.4%; Score 552; DB 1; Length 250;  
Best Local Similarity 85.4%; Pred. No. 2,2e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSGPELKKPEETVKISKASGYIFETNYGMWVQAQKGLKMMGWINTYGEPTV 60  
DB 3 EIQIVQSGPELKKPEETVKISKASGYIFETNYGMWVQAQKGLKMMGWINTYGEPTV 62  
QY 61 ADDFKGRFAFSLETSASTAYVLIQINNLIKNEEDTATYFCA---LYGNSPKGFAVWGQGLTVT 116  
DB 63 AEEFKGRFAFSLETSASTAYVLIQINNLIKNEEDTATYFCA---LYGNSPKGFAVWGQGLTVT 118  
QY 117 VSA 119  
DB 119 VSA 121

RESULT 6  
US-08-461-386-2  
Sequence 2, Application US/08461386  
Patent No. 5837846  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Proteins For  
SOFTWARE: Patentin Release #1.0, Version #1.25  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,386  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: 2054/22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7477  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-386-2

Query Match 85.4%; Score 552; DB 2; Length 250;  
Best Local Similarity 85.4%; Pred. No. 2,2e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 60  
|:::|  
DB 3 EIQLVQSGPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 62

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCA---LYGNSPKGFAYWGCTLT 116  
|:::|  
DB 63 ABEFKGRFAFSLSTASTAYLQINLNKEDTATYFCGRQFTYD---GFANWGCTLT 118

QY 117 VSA 119  
|||  
DB 119 VSA 121

## RESULT 7

US-08-356-786-16  
; Sequence 16, Application US/08356786  
; Patent No. 587305

## GENERAL INFORMATION:

APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
TITLE OF INVENTION: Marker  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 622 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-16

Query Match 85.4%; Score 552; DB 2; Length 622;  
Best Local Similarity 85.4%; Pred. No. 5.7e-43;  
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 60  
|:::|

DB 3 EIQLVQSGPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 62

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCA---LYGNSPKGFAYWGCTLT 116  
|:::|  
DB 63 ABEFKGRFAFSLSTASTAYLQINLNKEDTATYFCGRQFTYD---GFANWGCTLT 118

QY 117 VSA 119  
|||  
DB 119 VSA 121

## RESULT 8

US-08-569-147-76  
; Sequence 76, Application US/08569147  
; Patent No. 6180377

## GENERAL INFORMATION:

APPLICANT: HUMANISED ANTIBODIES  
TITLE OF INVENTION: 95  
NUMBER OF SEQUENCES: 95

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: No. 6180377's, LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,147  
FILING DATE: 25-March-1996

CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yacko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CRP-0047

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3439  
TELEFAX: (215) 568-3100

## INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-147-76

Query Match 84.5%; Score 546; DB 3; Length 140;  
Best Local Similarity 83.5%; Pred. No. 4.1e-43;  
Matches 101; Conservative 8; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVKLVSQPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 60  
|:::|  
DB 20 QIQLVQSGPELKKPGETVTKISCKASGYFTNYGNMVKQAPGKGLKMGWINTYGEPT 79

QY 61 ADDPKRFAFSLSTASTAYLQINLNKEDTATYFCA---LYGNSPKGFAYWGCTLT 118  
|:::|  
DB 80 ABEFKGRFAFSLSTASTAYLQINLNKEDTATYFCARDITAVPTGFDYWGCTLT 139

QY 119 A 119  
|||  
DB 140 S 140

## RESULT 9

US-08-279-772A-6  
; Sequence 6, Application US/08279772A  
; Patent No. 6080560

## GENERAL INFORMATION:

APPLICANT: Russell, David R  
TITLE OF INVENTION: Method for Producing Antibodies in Plant  
TITLE OF INVENTION: Cells  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles and Brady  
STREET: PO Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: United States of America  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9097-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEO ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-279-772A-6

Query Match 84.1%; Score 543.5; DB 3; Length 252;  
Best Local Similarity 84.3%; Pred. No. 1.3e-42;  
Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSGBELKKPEETVKISCKASGYLFTNYGNMVKQAFGKGLKMMGMINTYTGPTY 60  
DB 131 QIQVOSGBELKKPEETVKISCKASGYLFTNYGNMVKQAFGKGLKMMGMINTYTGPTY 190  
QY 61 ADDPKGRPAFSLFETASRYAIQINNLKNEDEATYFCA--LYGNPKGPAVYGGCTLTYS 118  
DB 191 ADDPKGRPAFSLFETASRYAIQINNLKNEDEATYFCAFEYSYNS-RVADYWGQCTTLTYS 249  
QY 119 A 119  
DB 250 S 250

RESULT 10  
US-08-902-486-9  
Sequence 9, Application US/08902486  
Patent No. 6140075  
GENERAL INFORMATION:  
APPLICANT: Russell, David R.  
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,486  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 670513.90261  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEO ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-486-9

Query Match 84.1%; Score 543.5; DB 3; Length 252;  
Best Local Similarity 84.3%; Pred. No. 1.3e-42;  
Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSGBELKKPEETVKISCKASGYLFTNYGNMVKQAFGKGLKMMGMINTYTGPTY 60  
DB 131 QIQVOSGBELKKPEETVKISCKASGYLFTNYGNMVKQAFGKGLKMMGMINTYTGPTY 190  
QY 61 ADDPKGRPAFSLFETASRYAIQINNLKNEDEATYFCA--LYGNPKGPAVYGGCTLTYS 118  
DB 191 ADDPKGRPAFSLFETASRYAIQINNLKNEDEATYFCAFEYSYNS-RVADYWGQCTTLTYS 249  
QY 119 A 119  
DB 250 S 250

RESULT 11  
US-08-875-811-53  
Sequence 53, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO FCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-53

Query Match 83.5%; Score 539.5; DB 3; Length 365;  
Best Local Similarity 86.6%; Pred. No. 4.5e-42;  
Matches 103; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSSEPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSEPT 60  
DB 119 QVKLQSGPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSESTY 178

QY 61 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119  
DB 179 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCARF--AIKG-DYWGQGLTVTVSS 234

## RESULT 12

US-08-875-811-55  
Sequence 55, Application US/08875811  
Patent No. 6045793

## GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Diane L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fairis, Susan K.

## REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-875-811-55

Query Match 83.5%; Score 539.5; DB 3; Length 365;  
Best Local Similarity 86.6%; Pred. No. 4.5e-42;  
Matches 103; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVKLVSSEPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSEPT 60  
DB 2 QVKLQSGPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSESTY 61

QY 61 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119  
DB 62 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCARF--AIKG-DYWGQGLTVTVSS 117

## RESULT 13

US-09-318-786-35  
Sequence 35, Application US/09318786  
Patent No. 6472147

## GENERAL INFORMATION:

APPLICANT: Janda, Kim D  
APPLICANT: Mirsching, Peter  
APPLICANT: Lerner, Richard A  
APPLICANT: Gao, Changshou  
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON  
TITLE OF INVENTION: FILAMENTOUS PHAGE USING PVI AND PIX, COMPOSITIONS,  
FILE REFERENCE: TSR03055  
CURRENT APPLICATION NUMBER: US/09/318,786  
CURRENT FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 35  
LENGTH: 160  
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: fusion

OTHER INFORMATION: polypeptide

US-09-318-786-35

Query Match 83.0%; Score 536; DB 4; Length 160;  
Best Local Similarity 85.7%; Pred. No. 3.9e-42;  
Matches 102; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY 1 EVKLVSSEPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSEPT 60  
DB 3 EVKLQSGPELKKPGFTVKISCKASGYIFFTNYGNNWVKQAPGKGLKMMGMINITYGSEPT 62

QY 61 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119  
DB 63 ADDPKGRFAFSLSTASSTAYLQIINNLKNEDTATYFCRFL--DPLG-DYWGQGLTVTVSS 119

## RESULT 14

US-08-483-749A-24  
Sequence 24, Application US/08483749A  
Patent No. 6054561

## GENERAL INFORMATION:

APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097

COMPUTER READABLE FORM: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

US-08-483-749A-24

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483,749A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SAVERIDE, PAUL B.  
 REGISTRATION NUMBER: 36,914  
 REFERENCE/DOCKET NUMBER: 0508,008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-2585  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-483-749A-24

Query Match 82.0%; Score 530; DB 3; Length 115;  
 Best Local Similarity 82.4%; Pred. No. 9,8e-42;  
 Matches 98; Conservative 10; Mismatches 7; Indels 4; Gaps 1;

QY 1 EVLVESGPELKKPGSTVTKISCKASGYFTNYGMNVKQAPGKGLKMGWINTYTGPTT 60  
 DB 1 EIQLVSGPELKKPGSTVTKISCKASGYFTNYGMNVKQAPGKGLKMGWINTYTGOSTY 60  
 QY 61 ADPFKRFAPFSLSTASTAYLQINLNKEDATYFCALYGNSEPKFAYWGQGLTVTVA 119  
 DB 61 ADPFKRFAPFSLSTASTAYLQINLNKEDSATYFCA---RRFGFAYWGQGLTVSVSA 115

RESULT 15  
 US-08-133-804-6  
 Sequence 6, Application US/08133804  
 Patent No. 5534254  
 GENERAL INFORMATION:  
 APPLICANT: Huston, James S.  
 APPLICANT: Oppermann, Hermann  
 APPLICANT: Houston, L. L.  
 APPLICANT: Ring, David B.  
 TITLE OF INVENTION: Biosynthetic Binding Proteins For  
 TITLE OF INVENTION: Imaging  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Tesca, Hurwitz & Thibault/Patent Department  
 STREET: Exchange Place, 53 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/133,804  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kelley, Robin D.  
 REGISTRATION NUMBER: 34,637  
 REFERENCE/DOCKET NUMBER: 2054/22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-248-7100  
 TELEFAX: 617-248-7477  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 243 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-133-804-6

Query Match 82.0%; Score 530; DB 1; Length 243;  
 Best Local Similarity 82.4%; Pred. No. 2.2e-41;  
 Matches 98; Conservative 10; Mismatches 7; Indels 4; Gaps 1;

QY 1 EVLVESGPELKKPGSTVTKISCKASGYFTNYGMNVKQAPGKGLKMGWINTYTGPTT 60  
 DB 1 EIQLVSGPELKKPGSTVTKISCKASGYFTNYGMNVKQAPGKGLKMGWINTYTGOSTY 60  
 QY 61 ADPFKRFAPFSLSTASTAYLQINLNKEDATYFCALYGNSEPKFAYWGQGLTVTVA 119  
 DB 61 ADPFKRFAPFSLSTASTAYLQINLNKEDSATYFCA---RRFGFAYWGQGLTVSVSA 115

Search completed: November 7, 2003, 07:30:07  
 Job time: 18.4766 secs

GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 13.9866 seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992B-82\_COPY\_135\_242  
Perfect score: 572  
Sequence: 1 DIQWTQSPKELIVSAGSDRV.....QDPYGSPTFGGCTKLEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510.5	89.2	225	2 S37484	Ig kappa chain - m
2	487	85.1	127	2 S04577	Ig kappa chain pre
3	479	83.7	107	2 S09864	Ig kappa chain V-J
4	473	82.7	115	2 B25924	Ig kappa chain pre
5	466	81.5	149	1 KVM521	Ig kappa chain pre
6	456	79.7	107	2 D53285	Ig kappa chain V a
7	455	79.5	119	2 PC0265	Ig kappa chain V x
8	450	78.7	107	2 S32192	Ig kappa chain V x
9	445	77.8	107	2 S32191	Ig kappa chain V x
10	434	75.9	115	2 A25924	Ig kappa chain pre
11	432.5	75.6	108	2 PLU083	Ig kappa chain V x
12	423	74.0	152	2 S30751	Ig kappa chain pre
13	419	73.3	108	2 PL0204	Ig kappa chain pre
14	419	73.3	117	2 S42466	Ig kappa chain V x
15	412	72.0	107	2 A28195	Ig kappa chain V x
16	409	71.5	214	2 S68212	Ig kappa chain (Ma
17	407	71.2	131	2 PL0207	Ig kappa chain (Ma
18	404	70.6	107	2 S09967	Ig kappa chain V-J
19	404	70.6	128	2 A47159	Ig kappa chain V-J
20	403	70.5	111	2 D37266	Ig kappa chain V x
21	402	70.3	220	2 A31790	Ig kappa chain V x
22	399	69.8	136	1 KVM521	Ig kappa chain pre
23	398.5	69.7	133	2 PS0023	Ig kappa chain pre
24	398	69.6	107	2 S33132	Ig kappa chain pre
25	398	69.6	108	2 B49047	Ig kappa chain V x
26	396	69.2	107	2 B28195	Ig kappa chain V x
27	394.5	69.0	108	2 B44371	Ig kappa chain V x
28	394	68.9	113	2 PL0264	Ig kappa chain V x
29	394	68.9	135	2 S38807	Ig light chain V-J

30	393	68.7	98	2 PH1073	Ig light chain V x
31	393	68.7	111	2 B37266	Ig kappa chain V x
32	392	68.5	100	2 H38601	Ig kappa chain V x
33	392	68.5	114	1 K4HUN	Ig kappa chain V-I
34	392	68.5	114	2 S44119	Ig kappa chain V-J
35	392	68.5	240	2 S06084	Ig kappa chain pre
36	391.5	68.4	112	2 S43103	Ig kappa chain V-J
37	391.5	68.4	133	1 K4HUI	Ig kappa chain pre
38	391	68.4	113	2 JC2270	Ig kappa chain pre
39	391	68.4	129	2 S40317	Ig kappa chain - h
40	391	68.4	134	2 PC1214	Ig kappa chain pre
41	390	68.2	127	2 S40367	Ig kappa chain V-J
42	389.5	68.1	107	2 S36275	Ig lambda chain V
43	389.5	68.1	113	2 PR0407	Ig light chain V x
44	389.5	68.1	118	2 PR0356	Ig kappa chain V x
45	389	68.0	112	2 B30538	Ig kappa chain V x

#### ALIGNMENTS

##### RESULT 1

S37484  
Ig kappa chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_rev150n 06-Jan-1995 #text\_change 11-Jan-2000  
C/Accession: S37484  
R/Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A/Reference number: S37483  
A/Accession: S37484  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-225 <DUC>  
A/Cross-references: EMBL:X70424; NID:G406254; PIDN:CAA49869.1; PID:G406255  
C/Keywords: heterotetramer; immunoglobulin V region; immunoglobulin homology

##### Query Match

Best Local Similarity 89.2%; Score 510.5; DB 2; Length 225;  
Best Local Similarity 92.5%; Pred. No. 5.9e-39;  
Matches 99; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY	2	IOMTSPKELIVSAGSDRVITTCRKSOSVSDVAVYQKPGSPFLMYVSNRYGVPR 61
DB	14	IOMTSPKELIVSAGSDRVITTCRKSOSVSDVAVYQKPGSPFLMYVSNRYGVPR 73
QY	62	FTGSGVGTDFFTTSTVQAEPLAVYPCQDDYSGSPPTGGCTKLEIKR 108
DB	74	FTGSGVGTDFFTTSTVQAEPLAVYPCQDDYSGSPPTGGCTKLEIKR 119

##### RESULT 2

S04577  
Ig kappa chain precursor V region (MRI-RF28L) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Jun-1992 #sequence\_rev150n 30-Jun-1992 #text\_change 21-Jan-2000  
C/Accession: S04577  
R/Kofler, R.; Duchosal, M.A.; Dixon, F.J.  
submitted to the EMBL Data Library, March 1989  
A/Description: Complexity, polymorphism and connectivity of murine V(kappa) gene  
A/Reference number: S04577  
A/Accession: S04577  
A/Molecule type: mRNA  
A/Residues: 1-127 <KOF>  
A/Cross-references: EMBL:X14622; NID:G52400; PIDN:CAA32775.1; PID:G52401  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/21-127/Product: Ig kappa chain V region (fragment) #status predicted <MNT>  
F/36-110/Domain: immunoglobulin homology <IMH>

Query Match 85.1%; Score 487; DB 2; Length 127;  
Best Local Similarity 87.7%; Pred. No. 4.3e-37;

Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 IQMTQSPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDPDR 61  
 DB 22 IVMOTQPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDPDR 81

QY 62 FTGSGYGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 107  
 DB 82 FTGSGSGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 127

## RESULT 3

S09964  
 Ig kappa chain V-J region (105-2H) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
 C/Accession: S09964  
 R/Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Tsui, S.  
 Eur. J. Immunol. 20, 771-777, 1990  
 A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
 A/Reference number: S09955; MUID:90269328; PMID:2347362  
 A/Accession: S09964  
 A/Molecule type: mRNA  
 A/Residues: 1-107 <Ref>  
 A/Cross-references: EMBL:X51852; NID:955393; PIND:CAA36145.1; PID:9930229  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 479; DB 2; Length 107;  
 Best Local Similarity 84.1%; Pred. No. 1.9e-36;  
 Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 60  
 DB 1 EIVLTQPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 60  
 QY 61 FTGSGYGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 107  
 DB 61 FTGSGSGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 107

## RESULT 4

B25924  
 Ig kappa chain precursor V region (Ser-b) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 21-Jan-2000  
 C/Accession: B25924  
 R/Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986  
 A/Title: Structural differences in a single gene encoding the V-kappa-Ser group of light  
 A/Reference number: A94141; MUID:87067464; PMID:3097643  
 A/Accession: B25924  
 A/Molecule type: DNA  
 A/Residues: 1-115 <BOY>  
 A/Cross-references: GB:M14360; NID:9197464; PIND:AAA39034.1; PID:9197465  
 A/Experimental source: strain BALB/c  
 C/Genetics: 17/1  
 A/Intons: 17/1  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/1-20/Domain: signal sequence #status predicted <SIG>  
 F/21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>  
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 473; DB 2; Length 115;  
 Best Local Similarity 94.7%; Pred. No. 7.2e-36;  
 Matches 89; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IQMTQSPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDPDR 61  
 DB 22 IVMOTQPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDPDR 81

QY 62 FTGSGYGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 107  
 DB 82 FTGSGSGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 115

## RESULT 5

KVMS11  
 Ig kappa chain precursor V region (MPC11) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 21-Jan-2000  
 C/Accession: A90823; A90753; A90298; A01916  
 R/Kelly, D.E.; Coleclough, C.; Perry, R.P.  
 Cell 29, 681-689, 1982  
 A/Title: Functional significance and evolutionary development of the 5'-terminal  
 A/Reference number: A90823; MUID:83001944; PMID:6288267  
 A/Accession: A90823

A/Molecule type: DNA  
 A/Residues: 1-71 <KEL>  
 A/Note: the sequence was determined from the differentiated gene  
 R/Rabbits, T.H.; Hamlyn, P.H.; Matchessens, G.; Roe, B.A.  
 Can. J. Biochem. 58, 176-187, 1980  
 A/Title: The variability, arrangement, and rearrangement of immunoglobulin genes  
 A/Reference number: A90753; MUID:80176554; PMID:6245773  
 A/Accession: A90753  
 A/Molecule type: mRNA  
 A/Residues: 41-149 <RAB>  
 R/Smith, G.P.  
 Biochem. J. 171, 337-347, 1978

A/Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma  
 A/Reference number: A90298; MUID:78186617; PMID:418775  
 A/Contents: myeloma protein MPC11  
 A/Accession: A90298

A/Molecule type: protein  
 A/Residues: 30-149 <SMT>  
 A/Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were  
 C/Comment: The mature chain has 12 additional residues at its amino end, due to a  
 42 corresponds to the amino-terminal residue of typical kappa chains.  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical 119  
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: duplication; heterotetramer; immunoglobulin  
 F/1-29/Domain: signal sequence #status predicted <SIG>  
 F/30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>  
 F/57-131/Domain: immunoglobulin homology <IMM>  
 F/64-129/Disulfide bonds: #status predicted

Query Match 81.5%; Score 466; DB 1; Length 149;  
 Best Local Similarity 82.4%; Pred. No. 4e-35;  
 Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPKFLVSAAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 60  
 DB 42 DIQMTQSHKFNSTGVDRVITCKASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 101  
 QY 61 FTGSGYGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 108  
 DB 102 FTGSGSGTDFFTTISTVQAEIDLAVYFCQDDYGSPTFGGTYKLEIK 149

## RESULT 6

D53285  
 Ig kappa chain V and J regions, monoclonal antibody SCET.M6.1 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
 C/Accession: D53285  
 R/Sawada, J.; Mizusawa, S.; Tero, T.; Naito, M.; Kurosawa, Y.  
 Mol. Immunol. 28, 1063-1072, 1991  
 A/Title: Molecular characterization of monoclonal anti-steroid antibodies: primary  
 and their pH-reactivity profiles.  
 A/Reference number: A53285; MUID:92017897; PMID:1922102  
 A/Accession: D53285  
 A/Status: preliminary  
 A/Molecule type: DNA; protein

A:Residues: 1-107 <SAM>  
 A:Cross-references: GB:D12737; NID:g220597; PIDN:BA02229.1; PID:g220598  
 A:Note: sequence extracted from NCBI backbone (NCBIN:63304, NCBI:P:63309)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 456; DB 2; Length 107;  
 Best Local Similarity 82.1%; Pred. No. 2.3e-34;  
 Matches 87; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
 QY 2 IOMTOSPKFLVNSAGDRVTITCKASOSVSNVAVYQOKPGQSPKLLMYASNRRTGYVD 61  
 DB 2 IVMTQSHKFMSTVSGDRVSITCKASQSDVSTVAVYQOKPGQSPKLLMYASNRRTGYVD 61  
 QY 62 FTGSGYGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107  
 DB 62 FTGSGYGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107

## RESULT 7

P00265  
 Ig kappa chain V region (MC1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
 C:Accession: P00265  
 R:Johman, K.L.; Carrillo, M.A.; Kennedy, R.C.  
 Gene 105, 283-284, 1991  
 A:Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal  
 A:Reference number: P00265; MUID:92039046; PMID:1937027  
 A:Accession: P00265  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <LOH>  
 A:Cross-references: GB:M59985  
 C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:28-102/Domain: immunoglobulin homology <IMM>  
 F:36-46/Region: complementarity-determining 1  
 F:62-68/Region: complementarity-determining 2  
 F:101-109/Region: complementarity-determining 3

Query Match 79.5%; Score 455; DB 2; Length 119;  
 Best Local Similarity 81.3%; Pred. No. 3.1e-34;  
 Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 DIQMTOSPKELVNSAGDRVTITCKASOSVSNVAVYQOKPGQSPKLLMYASNRRTGYVD 60  
 DB 13 DIVMTQSHKFMSTVSGDRVSITCKASQSDVSTVAVYQOKPGQSPKLLMYASNRRTGYVD 72  
 QY 61 RFTSGYGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107  
 DB 73 RFTSGSGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 119

## RESULT 8

S32192  
 Ig kappa chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S32192  
 R:Zhu, S.  
 Submitted to the EMBL Data Library, February 1993  
 A:Reference number: S32185  
 A:Accession: S32192  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <IZU>  
 A:Cross-references: EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PID:g288263  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 450; DB 2; Length 107;  
 Best Local Similarity 81.3%; Pred. No. 7.8e-34;  
 Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 DIQMTOSPKELVNSAGDRVTITCKASOSVSNVAVYQOKPGQSPKLLMYASNRRTGYVD 60  
 DB 1 DIVMTQSHKFMSTVSGDRVSITCKASQSDVSTVAVYQOKPGQSPKLLMYASNRRTGYVD 60

QY 61 RFTSGYGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107  
 DB 61 RFTSGSGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107

## RESULT 9

S32191  
 Ig kappa chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S32191  
 R:Zhu, S.  
 Submitted to the EMBL Data Library, February 1993  
 A:Reference number: S32185  
 A:Accession: S32191  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <IZU>  
 A:Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 445; DB 2; Length 107;  
 Best Local Similarity 80.4%; Pred. No. 2.2e-33;  
 Matches 86; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 DIQMTOSPKELVNSAGDRVTITCKASOSVSNVAVYQOKPGQSPKLLMYASNRRTGYVD 60  
 DB 1 DIVMTQSHKFMSTVSGDRVSITCKASQSDVSTVAVYQOKPGQSPKLLMYASNRRTGYVD 60  
 QY 61 RFTSGYGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107  
 DB 61 RFTSGSGTDTFTTISTVQAEADLAVYFCQODYGSPPPTGGGKLEIK 107

## RESULT 10

A25924  
 Ig kappa chain precursor V region (Ser-a) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 21-Jan-2000  
 C:Accession: A25924  
 R:Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986  
 A:Title: Structural differences in a single gene encoding the V-kappa-Ser group  
 A:Reference number: A94141; MUID:87067464; PMID:3057643  
 A:Accession: A25924  
 A:Molecule type: DNA  
 A:Residues: 1-115 <BOY>  
 A:Cross-references: GB:M14361; NID:g197466; PIDN:AAA3035.1; PID:g197467  
 A:Experimental source: strain C.C58  
 C:Genetics:  
 A:Introns: 17/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-115/Product: Ig kappa chain V region Ser-a #status predicted <MAT>  
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 434; DB 2; Length 115;  
 Best Local Similarity 87.2%; Pred. No. 2.3e-32;  
 Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 2 IOMTOSPKFLVNSAGDRVTITCKASOSVSNVAVYQOKPGQSPKLLMYASNRRTGYVD 61  
 DB 2 IVMTQSHKFMSTVSGDRVSITCKASQSDVSTVAVYQOKPGQSPKLLMYASNRRTGYVD 61

Db 22 IVMQTQPKFLVPSAGDRTVITCKASQSVGNVAVYQKQPGQSPKLLIYYASNRRTGVDP 81  
QY 62 FTSGSGYGTDFFTTISTVQAEADLAVYFCQDYGSP 95  
|||||  
Db 82 FTSGSGGTDFFTTISVQAEADLAVYFCQDHYSSP 115

## RESULT 11

PL0083  
Ig kappa chain V region (E3) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C/Accession: PL0083  
R/Smith, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A/Title: Structural characterization of antidiotypic antibodies: evidence that Ab2s are  
A/Reference number: PL0080; MUID:89094248; PMID:2452056  
A/Accession: PL0083  
A/Molecule type: mRNA  
A/Residues: 1-108 <ME>  
A/Experimental source: strain BALB/c  
A/Note: the sequence shown here is from the V kappa region of an antidiotypic monoclonal  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IM>

Query Match 75.6%; Score 432.5; DB 2; Length 108;  
Best Local Similarity 78.7%; Pred. No. 3e-32;  
Matches 85; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIQWTSKPKFLVPSAGDRTVITCKASQSVNDVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
|||||  
Db 1 DIWMTQSHRFMTSVGRVSTICKASQSVSTAVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
QY 61 FTSGSGYGT-DEFTTISTVQAEADLAVYFCQDYGSPPTFGGTRLEIK 107  
|||||  
Db 61 FTSGSGGTDFFTTISTVQAEADLAVYFCQDHYSTPTFGGTRLEIK 108

## RESULT 12

S30751  
Ig kappa chain precursor V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000  
C/Accession: S30751  
R/Giant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.  
Nucleic Acids Res. 15, 5496, 1987  
A/Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.  
A/Reference number: S30751; MUID:87260030; PMID:3601683  
A/Accession: S30751  
A/Molecule type: mRNA  
A/Residues: 1-152 <GR>  
A/Cross-references: EMBL:X05877; NID:952195; PIDN:CAA29301.1; PID:952196  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;45-119/Domain: immunoglobulin homology <IM>  
F;118-152/Domain: C region (C-kappa) (fragment) #status predicted <CR>

Query Match 74.0%; Score 423; DB 2; Length 152;  
Best Local Similarity 72.2%; Pred. No. 3e-31;  
Matches 78; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQWTSKPKFLVPSAGDRTVITCKASQSVNDVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
|||||  
Db 30 DIWMTQSHRFMTSVGRVSTICKASQSDVTAVSVYQKQPGQSPKLLIYYASNRRTGVDP 89  
QY 61 FTSGSGYGTDFFTTISTVQAEADLAVYFCQDYGSPPTFGGTRLEIK 108  
|||||  
Db 90 FTSGSGGTDFFTTISTVQAEADLAVYFCQDHYSTPTFGGTRLEIK 137

## RESULT 13

PL0204

anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: PL0204  
R/Smith, R.G.; Voss Jr., E.W.  
Mol. Immunol. 27, 463-470, 1990  
A/Title: Variable region primary structures of monoclonal anti-DNA autoantibodies  
A/Reference number: PL0198; MUID:90309768; PMID:2114528  
A/Accession: PL0204  
A/Molecule type: mRNA  
A/Residues: 1-108 <SMI>  
A/Cross-references: GB:X53644; NID:950198; PIDN:CAA37695.1; PID:9530144  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IM>  
F;24-34/Region: complementarity-determining 1  
F;50-56/Region: complementarity-determining 2  
F;89-97/Region: complementarity-determining 3  
F;96-108/Region: VH region

Query Match 73.3%; Score 419; DB 2; Length 108;  
Best Local Similarity 75.0%; Pred. No. 4.9e-31;  
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIQWTSKPKFLVPSAGDRTVITCKASQSVNDVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
|||||  
Db 1 DIWMTQSHRFMTSVGRVSTICKASQSVSTAVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
QY 61 FTSGSGYGTDFFTTISTVQAEADLAVYFCQDYGSPPTFGGTRLEIK 108  
|||||  
Db 61 FTSGSGGTDFFTTISTVQAEADLAVYFCQDHYSTPTFGGTRLEIK 108

## RESULT 14

S42466  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S42466  
R/Shiyanov, P.A.; Bessalov, I.A.; Terletskaia, H.N.; Deyev, S.M.  
submitted to the EMBL Data Library, March 1994  
A/Reference number: S42466  
A/Accession: S42466  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-117 <SHI>  
A/Cross-references: EMBL:X78108; NID:9460824; PIDN:CAA54998.1; PID:9460825  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;26-100/Domain: immunoglobulin homology <IM>

Query Match 73.3%; Score 419; DB 2; Length 117;  
Best Local Similarity 76.6%; Pred. No. 5.3e-31;  
Matches 82; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQWTSKPKFLVPSAGDRTVITCKASQSVNDVAVYQKQPGQSPKLLIYYASNRRTGVDP 60  
|||||  
Db 11 DIWMTQSHRFMTSVGRVSTICKASQSDVTAVSVYQKQPGQSPKLLIYYASNRRTGVDP 70  
QY 61 FTSGSGYGTDFFTTISTVQAEADLAVYFCQDYGSPPTFGGTRLEIK 107  
|||||  
Db 71 FTSGSGGTDFFTTISTVQAEADLAVYFCQDHYSTPTFGGTRLEIK 117

## RESULT 15

A28195  
Ig kappa chain V region (anti-haloperidol antibody A) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 21-Jan-2000  
C/Accession: A28195  
R/Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A/Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amin  
A/Reference number: A28195; MUID:88153717; PMID:3267217

A:Accession: A28195  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SHE>  
 A/Cross-references: GB:M19766; NID:g197039; PID:AAA38891.1; PID:g197040  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 412; DB 2; Length 107;  
 Best Local Similarity 73.8%; Pred. No. 2, 1e-30;  
 Matches 79; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 DIQMTQSPKFLVSAQDRVTITCKASQSVSNDVANYQQKPGQSPKRLMYASNRYTGVPD 60  
 Db 1 DILMTQSQKFMSTSVQDRVSTCKASQVGNVAVHQQKPGQSPKRLITYSASRYSGVPD 60  
 QY 61 RFTGSGGTDFETFTISTVQAEPLAVYPCQODVGSPTREGGKLEIK 107  
 Db 61 RFTGSGGTDFETFTITVQSEDLAEYPCQQINSYPYRFGGKLEIK 107

Search completed: November 7, 2003, 07:36:19  
 Job time : 15.086 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 7.78638 seconds  
(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-82\_COPY\_135\_242  
Perfect score: 572  
Sequence: 1 DQMTQSPKFLVYSGDRVT.....QQPYGSPFTGGGTALKEIR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	81.5	149	1	KV5A_MOUSE
2	399	69.8	136	1	KV5B_MOUSE
3	391.5	68.4	133	1	KV4B_HUMAN
4	391	68.4	114	1	KV4A_HUMAN
5	387	67.7	134	1	KV4C_HUMAN
6	386	67.5	108	1	KV1M_HUMAN
7	378	66.1	108	1	KV1Y_HUMAN
8	376	65.7	108	1	KV1H_HUMAN
9	372	65.7	108	1	KV1N_HUMAN
10	372	65.0	114	1	KV1A_MOUSE
11	370.5	64.8	109	1	KV3D_HUMAN
12	370	64.7	129	1	KV1W_HUMAN
13	368	64.3	108	1	KV3A_HUMAN
14	367.5	64.2	129	1	KV3H_HUMAN
15	367	64.2	108	1	KV1P_HUMAN
16	366	64.0	108	1	KV1S_HUMAN
17	365	63.8	108	1	KV1K_HUMAN
18	365	63.5	108	1	KV5M_MOUSE
19	363.5	63.5	109	1	KV3B_HUMAN
20	363	63.5	108	1	KV1G_HUMAN
21	362.5	63.4	129	1	KV3L_HUMAN
22	361	63.1	108	1	KV1B_HUMAN
23	361	63.1	108	1	KV1O_HUMAN
24	360	62.9	108	1	KV1C_HUMAN
25	359	62.8	108	1	KV1V_HUMAN
26	358.5	62.7	109	1	KV3F_HUMAN
27	358	62.6	108	1	KV5P_MOUSE
28	357.5	62.5	129	1	KV3M_HUMAN
29	356.5	62.5	113	1	KV2G_MOUSE
30	356	62.2	108	1	KV5K_MOUSE
31	354	61.9	108	1	KV1F_HUMAN
32	354	61.9	108	1	KV1R_HUMAN
33	354	61.9	108	1	KV5O_MOUSE

34	353	61.7	108	1	KV5L_MOUSE
35	351	61.4	108	1	KV5N_MOUSE
36	350	61.2	108	1	KV1E_HUMAN
37	350	61.2	108	1	KV5S_MOUSE
38	350	61.2	129	1	KV1X_HUMAN
39	348.5	60.9	109	1	KV3E_HUMAN
40	348	60.8	108	1	KV1L_HUMAN
41	346.5	60.6	107	1	KV1D_HUMAN
42	345	60.3	108	1	KV5J_MOUSE
43	345	60.3	109	1	KV4D_HUMAN
44	345	60.3	128	1	KV3K_HUMAN
45	344	60.1	121	1	KV4O_HUMAN
					P01645 mus musculus
					P01647 mus musculus
					P01597 homo sapien
					P01652 mus musculus
					P04432 homo sapien
					P01623 homo sapien
					P01604 homo sapien
					P01596 homo sapien
					P01643 mus musculus
					P83593 homo sapien
					P06311 homo sapien
					P06312 homo sapien

## ALIGNMENTS

RESULT 1  
KV5A\_MOUSE STANDARD; PRT; 149 AA.  
ID KV5A\_MOUSE  
AC P01633;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 15 kappa chain V-V region MRC11 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE OF 1-71 FROM N.A.  
RX MEDLINE=83001944; PubMed=628826;  
RA Kelley D.E., Coleclough C., Perry R.P.;  
RT "functional significance and evolutionary development of the  
RT 5'-terminal regions of immunoglobulin variable-region genes";  
RL Cell 29:681-689(1982).  
[2]  
RP SEQUENCE OF 41-149 FROM N.A.  
RX MEDLINE=80176554; PubMed=6245773;  
RA Reddibits T.H., Hamlyn P.H., Mathysens G., Roe B.A.;  
RT "The variability, arrangement, and rearrangement of immunoglobulin  
RT genes";  
RL Can. J. Biochem. 58:176-187(1980).  
[3]  
RP SEQUENCE OF 30-149.  
RX MEDLINE=78186617; PubMed=418775;  
RA Smith G.P.;  
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
RT myeloma MPC 11";  
RL Biochem. J. 171:337-347(1978).  
[4]  
RP AMINO END, DUE TO A TRANDSM DUPLICATION OF 36 NUCLEOTIDES AFTER THE  
CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL  
RESIDUE OF TYPICAL KAPPA CHAINS.  
-----  
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-----  
DR EMBL: J00561; AAA38776.1; --  
DR PIR: A90823; KWSM11.  
DR HSSP: P80362; IWTUL.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Signal; Repeat.

FT SIGNAL 1 29  
 FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MECL1.  
 FT DOMAIN 42 64 FRAMEWORK-1.  
 FT DOMAIN 42 64 FRAMEWORK-1.  
 FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 76 90 FRAMEWORK-2.  
 FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 98 129 FRAMEWORK-3.  
 FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 139 148 FRAMEWORK-4.  
 FT REPEAT 26 35  
 FT REPEAT 38 47  
 FT NON\_TER 149 149  
 SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC36 CRC64;

Query Match 81.5%; Score 466; DB 1; Length 149;  
 Best Local Similarity 82.4%; Pred. No. 1,1e-42;  
 Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTSPKFLVLSAGDRVITTCASQSVSDVAVYQKQSPKLLMYASNRYTGVDP 60  
 DB 42 DIWMTQSHKFMSTYSGDRYSITCKASQDVSTVAVYQKQSPKLLMYASNRYTGVDP 101  
 QY 61 RFTGSGYGFDTFTTSTVOAEDLAVYFCQDYGSPPTGGGKLEIKR 108  
 DB 102 RFTGSGSGTDFTTTSSVQAEEDLAVYFCQDYSTPTGGGKLEIKR 149

## RESULT 2

KVAB\_MOUSE STANDARD; PRT; 136 AA.

AC P01634;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG kappa chain V-V region MOPC 21 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82059477; PubMed=6170937;  
 RA Hamlyn P.H., Galt M.J., Milestein C.;  
 RT "Complete sequence of an immunoglobulin mRNA using specific priming  
 and the dideoxynucleotide method of RNA sequencing.";  
 RL Nucleic Acids Res. 9:4485-4494(1981).  
 RN [2]  
 RP SEQUENCE OF 30-136.  
 RX MEDLINE=73053310; PubMed=4638343;  
 RA Svasti J., Milestein C.;  
 RT "The complete amino acid sequence of a mouse kappa light chain.";  
 RL Biochem. J. 128:427-444(1972).

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CC EMBL; V00810; CA24192.1; ALT\_TERM.  
 DR EMBL; A93736; KYMS21.  
 DR PDB; 1IGC; 03-JUN-95.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.

FT DOMAIN 30 52 FRAMEWORK-1.  
 FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 64 78 FRAMEWORK-2.  
 FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 127 136 FRAMEWORK-4.  
 FT NON\_TER 136 136  
 SQ SEQUENCE 136 AA; 14902 MW; 8CDD8511396D1C2 CRC64;

Query Match 69.8%; Score 399; DB 1; Length 136;  
 Best Local Similarity 72.9%; Pred. No. 1,4e-35;  
 Matches 78; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIOMTSPKFLVLSAGDRVITTCASQSVSDVAVYQKQSPKLLMYASNRYTGVDP 60  
 DB 30 NIVMTQSPKFMSTYSGDRYSITCKASQDVSTVAVYQKQSPKLLMYASNRYTGVDP 89  
 QY 61 RFTGSGYGFDTFTTSTVOAEDLAVYFCQDYGSPPTGGGKLEIKR 107  
 DB 90 RFTGSGSATDFTTTSSVQAEEDLAVYFCQDYSTPTGGGKLEIKR 136

## RESULT 3

KVAB\_HUMAN STANDARD; PRT; 133 AA.

AC P06313;  
 DT 01-JAN-1988 (Rel. 05, Created)  
 DT 01-JAN-1988 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-IV region JI precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041853; PubMed=2397712;  
 RA Klobbeck H.G., Bornkamm G.W., Moczkat R., Pohlman H.D.,  
 RA Zechau H.G.;  
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a  
 single germline gene.";  
 RL Nucleic Acids Res. 13:6515-6529(1985).

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CC EMBL; Z00022; CAAT7317.1;  
 DR EMBL; A01904; KAHUJ1.  
 DR HSP; P80362; IWT.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:000823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 61 75 FRAMEWORK-2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 123 132 FRAMEWORK-4.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON TER 133 133  
 SQ SEQUENCE 133 AA; 14632 MW; 5FB395306744AP4 CRC64;

Query Match  
 Best Local Similarity 68.4%; Score 391.5; DB 1; Length 133;  
 Matches 78; Conservative 13; Mismatches 16; Indels 7; Gaps 2;

QY 1 DIQMTSPKFLVLSAGDRVTITCKASQSV-----SNDVAMVQOKPGQSPKLLMYASNR 54  
 DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKXYLAHYQOKPGQSPKLLIYMASTR 80

QY 55 YTGVPDRFTSGSGYGTDTFTITSTVQAEEDLAVFYCCQDYSPPTGGSTKLEIKR 108  
 DB 81 ESGVDPDRFSGSGGTDTFTITSLQAEADVAVVYCOQYDTITPTGGSTKVEIKR 133

## RESULT 4

KV4A\_HUMAN STANDARD; PRT; 114 AA.  
 AC P01623;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-IV region Len.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBI\_Taxid=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=76004342; PubMed=50995;  
 RA Schneider M., Hilschmann N.;

RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RN [2]

RP REVISION TO 9.

RA Salomon A.;  
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.  
 CC -1 MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1 MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.

DR PDB: 1EEQ; 01-FEB-01.

DR PDB: 1EEU; 03-FEB-01.

DR PDB: 1EFQ; 09-FEB-01.

DR PDB: 1EK3; 06-MAR-01.

DR PDB: 1LVE; 21-JAN-98.

DR PDB: 3LVE; 18-MAY-99.

DR PDB: 5LVE; 28-MAR-01.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG\_V.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 41 55 FRAMEWORK-2.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 63 94 FRAMEWORK-3.

FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 102 113 FRAMEWORK-4.

FT NON TER 23 94 BY SIMILARITY.

SQ SEQUENCE 114 AA; 12640 MW; 0647FID17F236485 CRC64;  
 Query Match 68.4%; Score 391; DB 1; Length 114;  
 Best Local Similarity 67.5%; Pred. No. 8e-35;

Matches 77; Conservative 13; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIQMTSPKFLVLSAGDRVTITCKASQSV-----SNDVAMVQOKPGQSPKLLMYASNR 54  
 DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKXYLAHYQOKPGQSPKLLIYMASTR 60

QY 55 YTGVPDRFTSGSGYGTDTFTITSTVQAEEDLAVFYCCQDYSPPTGGSTKLEIKR 108  
 DB 61 ESGVDPDRFSGSGGTDTFTITSLQAEADVAVVYCOQYDTITPTGGSTKVEIKR 114

## RESULT 5

KV4C\_HUMAN STANDARD; PRT; 134 AA.  
 ID P06314;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-IV region B17 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBI\_Taxid=9606;  
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041854; PubMed=2997713;

RA Marsh P., Mills F., Gould H.;

RT "Detection of a unique human V kappa IV germline gene by a cloned  
 RT cDNA probe.";

RL Nucleic Acids Res. 13:6531-6544(1985).  
 RN [2]

RP REVISION TO 76.

RA Marsh P.;

RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: X02990; CA26733.1; -

DR HSP: P80362; 1WT.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG\_V.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT CHAIN 1 20 IG KAPPA CHAIN V-IV REGION B17.

FT DOMAIN 21 134 FRAMEWORK-1.

FT DOMAIN 22 43 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 44 60 FRAMEWORK-2.

FT DOMAIN 61 75 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 76 82 FRAMEWORK-3.

FT DOMAIN 83 114 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 115 121 FRAMEWORK-4.

FT DISULFID 122 133 FRAMEWORK-4.

FT NON TER 43 114 BY SIMILARITY.

SQ SEQUENCE 134 AA; 14966 MW; 6413A22FED0738832 CRC64;

Query Match 67.7%; Score 387; DB 1; Length 134;  
 Best Local Similarity 66.7%; Pred. No. 2.6e-34;  
 Matches 76; Conservative 13; Mismatches 19; Indels 6; Gaps 1;

QY 1 DIQMTSPKFLVLSAGDRVTITCKASQSV-----SNDVAMVQOKPGQSPKLLMYASNR 54

QY	DB	SEQUENCE	SCORE	DB 1	LENGTH	DB 2	SCORE	DB 3	LENGTH	DB 4	SCORE	DB 5	LENGTH	DB 6	SCORE	DB 7	LENGTH	DB 8	SCORE	DB 9	LENGTH	DB 10	SCORE	DB 11	LENGTH	DB 12	SCORE	DB 13	LENGTH	DB 14	SCORE	DB 15	LENGTH	DB 16	SCORE	DB 17	LENGTH	DB 18	SCORE	DB 19	LENGTH	DB 20	SCORE	DB 21	LENGTH	DB 22	SCORE	DB 23	LENGTH	DB 24	SCORE	DB 25	LENGTH	DB 26	SCORE	DB 27	LENGTH	DB 28	SCORE	DB 29	LENGTH	DB 30	SCORE	DB 31	LENGTH	DB 32	SCORE	DB 33	LENGTH	DB 34	SCORE	DB 35	LENGTH	DB 36	SCORE	DB 37	LENGTH	DB 38	SCORE	DB 39	LENGTH	DB 40	SCORE	DB 41	LENGTH	DB 42	SCORE	DB 43	LENGTH	DB 44	SCORE	DB 45	LENGTH	DB 46	SCORE	DB 47	LENGTH	DB 48	SCORE	DB 49	LENGTH	DB 50	SCORE	DB 51	LENGTH	DB 52	SCORE	DB 53	LENGTH	DB 54	SCORE	DB 55	LENGTH	DB 56	SCORE	DB 57	LENGTH	DB 58	SCORE	DB 59	LENGTH	DB 60	SCORE	DB 61	LENGTH	DB 62	SCORE	DB 63	LENGTH	DB 64	SCORE	DB 65	LENGTH	DB 66	SCORE	DB 67	LENGTH	DB 68	SCORE	DB 69	LENGTH	DB 70	SCORE	DB 71	LENGTH	DB 72	SCORE	DB 73	LENGTH	DB 74	SCORE	DB 75	LENGTH	DB 76	SCORE	DB 77	LENGTH	DB 78	SCORE	DB 79	LENGTH	DB 80	SCORE	DB 81	LENGTH	DB 82	SCORE	DB 83	LENGTH	DB 84	SCORE	DB 85	LENGTH	DB 86	SCORE	DB 87	LENGTH	DB 88	SCORE	DB 89	LENGTH	DB 90	SCORE	DB 91	LENGTH	DB 92	SCORE	DB 93	LENGTH	DB 94	SCORE	DB 95	LENGTH	DB 96	SCORE	DB 97	LENGTH	DB 98	SCORE	DB 99	LENGTH	DB 100	SCORE	DB 101	LENGTH	DB 102	SCORE	DB 103	LENGTH	DB 104	SCORE	DB 105	LENGTH	DB 106	SCORE	DB 107	LENGTH	DB 108	SCORE	DB 109	LENGTH	DB 110	SCORE	DB 111	LENGTH	DB 112	SCORE	DB 113	LENGTH	DB 114	SCORE	DB 115	LENGTH	DB 116	SCORE	DB 117	LENGTH	DB 118	SCORE	DB 119	LENGTH	DB 120	SCORE	DB 121	LENGTH	DB 122	SCORE	DB 123	LENGTH	DB 124	SCORE	DB 125	LENGTH	DB 126	SCORE	DB 127	LENGTH	DB 128	SCORE	DB 129	LENGTH	DB 130	SCORE	DB 131	LENGTH	DB 132	SCORE	DB 133	LENGTH	DB 134	SCORE	DB 135	LENGTH	DB 136	SCORE	DB 137	LENGTH	DB 138	SCORE	DB 139	LENGTH	DB 140	SCORE	DB 141	LENGTH	DB 142	SCORE	DB 143	LENGTH	DB 144	SCORE	DB 145	LENGTH	DB 146	SCORE	DB 147	LENGTH	DB 148	SCORE	DB 149	LENGTH	DB 150	SCORE	DB 151	LENGTH	DB 152	SCORE	DB 153	LENGTH	DB 154	SCORE	DB 155	LENGTH	DB 156	SCORE	DB 157	LENGTH	DB 158	SCORE	DB 159	LENGTH	DB 160	SCORE	DB 161	LENGTH	DB 162	SCORE	DB 163	LENGTH	DB 164	SCORE	DB 165	LENGTH	DB 166	SCORE	DB 167	LENGTH	DB 168	SCORE	DB 169	LENGTH	DB 170	SCORE	DB 171	LENGTH	DB 172	SCORE	DB 173	LENGTH	DB 174	SCORE	DB 175	LENGTH	DB 176	SCORE	DB 177	LENGTH	DB 178	SCORE	DB 179	LENGTH	DB 180	SCORE	DB 181	LENGTH	DB 182	SCORE	DB 183	LENGTH	DB 184	SCORE	DB 185	LENGTH	DB 186	SCORE	DB 187	LENGTH	DB 188	SCORE	DB 189	LENGTH	DB 190	SCORE	DB 191	LENGTH	DB 192	SCORE	DB 193	LENGTH	DB 194	SCORE	DB 195	LENGTH	DB 196	SCORE	DB 197	LENGTH	DB 198	SCORE	DB 199	LENGTH	DB 200	SCORE	DB 201	LENGTH	DB 202	SCORE	DB 203	LENGTH	DB 204	SCORE	DB 205	LENGTH	DB 206	SCORE	DB 207	LENGTH	DB 208	SCORE	DB 209	LENGTH	DB 210	SCORE	DB 211	LENGTH	DB 212	SCORE	DB 213	LENGTH	DB 214	SCORE	DB 215	LENGTH	DB 216	SCORE	DB 217	LENGTH	DB 218	SCORE	DB 219	LENGTH	DB 220	SCORE	DB 221	LENGTH	DB 222	SCORE	DB 223	LENGTH	DB 224	SCORE	DB 225	LENGTH	DB 226	SCORE	DB 227	LENGTH	DB 228	SCORE	DB 229	LENGTH	DB 230	SCORE	DB 231	LENGTH	DB
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QY		1	DIDMTGSKPFLVNSAGRVYTITTCRASQSVDNVAMVYQQKPPQSGPRLTLMVYASNRYYTGVPD	60
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Db      1 DQNTTQSPSSASAVGRVITITCRASDDITNNYNNMQAPQAPKYLITGASLTLETGPS 60
Qy      61 RFTSGGYGTDFTFTSTVQAEDLAVYFECQQDYGSPPTFGGGTLEIKR 108
Db      61 RFGSSGGGTDTFTTISLQPEDIAATYCCQGYDLPFTFGGGTVDIKR 108

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RESULT 8	KV1H_HUMAN		
ID	KV1H_HUMAN	STANDARD;	PRT; 108 AA.
AC	P01600		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	Ig kappa chain V-I region Hau.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=71032830; PubMed=4097974;		
RA	Varanabe S., Hilschmann N.;		
RT	"The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within		
RT	subgroups."		
RL	Hoppe-Seyler's Z. physiol. Chem. 351:1291-1295 (1970).		
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER		
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.		
DR	PIR; A01868; K1H0HU.		
DR	HSSP; P80362; 1MTL.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding activity; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	SMART; PF00047; Ig; 1.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PSS0835; IG LIKE; 1.		
KW	Immunoglobulin V region; Bence-Jones protein.		
FT	DOMAIN	1	23
FT	DOMAIN	24	34
FT	DOMAIN	35	49
FT	DOMAIN	50	56
FT	DOMAIN	57	88
FT	DOMAIN	89	97
FT	DOMAIN	98	107
FT	DISULFID	23	88
FT	NON TER	108	108
SQ	SEQUENCE	108 AA; 11671 MW; 08D3A616D8D0618 CRC64;	
		FRAMEWORK-1.	
		COMPLEMENTARITY-DETERMINING-1.	
		FRAMEWORK-2.	
		COMPLEMENTARITY-DETERMINING-2.	
		FRAMEWORK-3.	
		COMPLEMENTARITY-DETERMINING-3.	
		FRAMEWORK-4.	
		BY SIMILARITY.	

	Query Match	65.7%	Score 376;	DB 1;	Length 108;	
	Best Local Similarity	63.9%	Pred. No. 3e-33;			
	Matches	69;	Conservative	21;	Mismatches	18;
					Indels	0;
					Gaps	0
QY	1	DIDMTGSKFLVLSAGDVRVTTCRASGSVSNDVAMYOOKPFGSPFLMAYTNSKRYTGPD	60			
Db	1	DIQMTGSPSSLSASVGDRVTTCRRSOSISLSTLYOQKPGLAPVLIIYAASSLPFSGVPS	60			
QY	61	RFTGSGYGDTFTTISTVOAEDLAIVFCODYGSHPTTGCGTKLEIKR	108			
Db	61	RFSGSGGCTDFTLTIRISSIQPEDFAHYVCQNNVIPTTSFGQGTRVEIKR	108			
<b>RESULT 9</b>						
KVIN_HUMAN	ID	KVIN_HUMAN	STANDARD;	FRT;	108 AA.	
AC	P01606;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					

DE	Ig kappa chain V-I region OU.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxId:9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=70201507; PubMed=5447531;
RA	Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT	"Macroglobulin structure: Variable sequence of light and heavy
RT	chains.";
RL	Science 169:56-59 (1970).
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC	MACROGLOBULIN.
DR	PIR; A01872; K1HD0U.
DR	HSPF; P01607; IREI.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; IG-1ike.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
RW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 34
FT	DOMAIN 35 49
FT	DOMAIN 50 56
FT	DOMAIN 57 88
FT	DOMAIN 89 97
FT	DOMAIN 98 107
FT	DISULFID 23 88
FT	NON TER 108 108
SEQ	SEQUENCE 108 AA; 11777 MW; 8283D4A2A105827E CRC64;

RESULT 10			
KVLA_MOUSE			
ID	KVLA_MOUSE	STANDARD:	PRT: 114 AA.
AC	P01632		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	IG kappa chain V-I region S107A.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI	Taxid=10090;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=81241357; PubMed=6788890.		
RA	Kean S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;		
RT	"Nucleic acid and protein sequences of phosphocholine-binding light		
RL	chains";		
J.	Exp. Med. 153:1366-1370(1981).		
CC	-----		
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Query Match 64.7%; Score 370; DB 1; Length 129;  
 Best Local Similarity 66.4%; Pred. No. 1.6e-32;  
 Matches 71; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIOMTOSPKFLVTSAGDRVTITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 60  
 DB 23 DIOMTOSPSLSASVSDRVTITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 82  
 QY 61 RFTGSGYGTDFTTTISTVQAEIDLAVYFCQDYGSPPTFGGTYLLEIK 107  
 DB 83 RFGSGSGTDFLTITSLQPEDSATYCCQSYSTLITFGGTYLLEIK 129

## RESULT 13

KVLA\_HUMAN STANDARD; PRT; 108 AA.  
 ID 1  
 AC P01593;  
 DT 21-JUL-1986 (Rel. 01, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE Ig kappa chain V-1 region AG.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=69234734; PubMed=4893682;  
 RX Titani K., Shinoda T., Putnam F.W.,  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
 RT complete sequence and the location of the disulfide bridges.",  
 RU J. Biol. Chem. 244:3550-3560(1969)  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR HSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Bence-Jones protein.  
 KW DOMAIN 1 23  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 64.3%; Score 368; DB 1; Length 108;  
 Best Local Similarity 65.7%; Pred. No. 2.1e-32;  
 Matches 71; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 1 DIOMTOSPKFLVTSAGDRVTITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 60  
 DB 1 DIOMTOSPSLSASVSDRVTITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 60  
 QY 61 RFTGSGYGTDFTTTISTVQAEIDLAVYFCQDYGSPPTFGGTYLLEIK 108  
 DB 61 RFGSGSGTDFLTITSLQPEDSATYCCQSYSTLITFGGTYLLEIK 108

RESULT 14  
 KV3H\_HUMAN STANDARD; PRT; 129 AA.  
 ID 1

P04207;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-NOV-1990 (Rel. 16, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE Ig kappa chain V-III region CUL precursor (Rheumatoid factor).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86177570; PubMed=3083417;  
 RA Jirik P.R., Sarge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,  
 RA Goldfien R., Carson D.A.,  
 RT "Cloning and sequence determination of a human rheumatoid factor  
 RT light-chain gene.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).  
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 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 DR EMBL; M12740; AAA58992.1; -.  
 DR HSP; P80362; IWTU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR003596; Ig-like.  
 DR InterPro; IPR007110; Ig\_V.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 KW SIGNAL 1 20  
 FT CHAIN 1 20  
 FT DOMAIN 21 129  
 FT DOMAIN 21 43  
 FT DOMAIN 44 54  
 FT DOMAIN 55 69  
 FT DOMAIN 70 76  
 FT DOMAIN 77 108  
 FT DOMAIN 109 118  
 FT DOMAIN 119 129  
 FT DISULFID 43 108  
 FT NON TER 129  
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411B60CC14 CRC64;

Query Match 64.2%; Score 367.5; DB 1; Length 129;  
 Best Local Similarity 65.1%; Pred. No. 2.9e-32;  
 Matches 71; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

QY 1 DIOMTOSPKFLVTSAGDRVTITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 60  
 DB 21 EIVMTQSPRTLSVSGERATITCKASQSVSNVAVYQKPGSPKLMYYASNRVTGVPD 80  
 QY 61 RFTGSGYGTDFTTTISTVQAEIDLAVYFCQDYGSPPTFGGTYLLEIK 108  
 DB 81 RFGSGSGTDFLTITSLQPEDSATYCCQSYSTLITFGGTYLLEIK 129

RESULT 15  
 KV1P\_HUMAN STANDARD; PRT; 108 AA.  
 ID 1  
 AC P01608;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE Ig kappa chain V-1 region Roy.  
 OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=68362076; PubMed=5595110;  
 RA Hilschmann N.;  
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
 RT Cum.)";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).  
 RN [2]  
 RP REVISIONS TO 39 AND 41.  
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
 RA Steinmetz-Kayne M., Suter L., Matanabe S.;  
 RL (in) Franek F., Shugar D. (eds.);  
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,  
 RL New York (1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A91638; KIHURY.  
 DR HSSP; P80362; IWT.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006953; F:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003065; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11782 MM; PSACEDESA313DF3A CRC64;  
 Query Match 64.2%; Score 367; DB 1; Length 108;  
 Best Local Similarity 64.8%; Pred. No. 2,7e-32;  
 Matches 70; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 DIQMTGSPKFLVAGDPRVITTCASQSVSNDAVMAVYQKPGQSPKFLMAYYASNRVTGVPD 60  
 DB 1 DIQMTGSPSSLSASVGRVITTCQASQDISIFLNMVYQKPKAKPLIYDASIKLEAGVPS 60  
 QY 61 RFTGSGVGTDFFTFTISTVQAEADLAIVFCQDYGSPPTFGGKLEIKR 108  
 DB 61 RFTGSGGTDFFTFTISSIQEDIAIYVCOQFDNLPLTFGGGKIVDFKR 108

Search completed: November 7, 2003, 07:28:07  
 Job time : 7.78638 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 35.6155 Seconds  
(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992B-82\_COPY\_135\_242

Sequence: 1 DIQMOSPKVLVNSAGDRVT.....QDDYSGPPIRGSGTKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTRMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	507	88.6	99 11 Q9JL74	Q9JL74 mus musculus
2	399	69.8	108 11 Q8VJ70	Q8VJ70 mus musculus
3	382.5	66.9	107 4 Q96S89	Q96S89 homo sapien
4	377	65.9	108 4 Q9UL79	Q9UL79 homo sapien
5	376	65.7	108 4 Q9UL70	Q9UL70 homo sapien
6	376	65.7	108 4 Q9UL77	Q9UL77 homo sapien
7	370.5	64.8	107 4 Q9UL81	Q9UL81 homo sapien
8	370.5	64.8	109 4 Q9UL78	Q9UL78 homo sapien
9	366.5	64.1	109 4 Q9UL85	Q9UL85 homo sapien
10	366.5	64.1	107 11 Q8VC16	Q8VC16 mus musculus
11	360	62.9	107 11 Q9ER29	Q9ER29 mus musculus
12	359	62.8	108 4 Q9UL83	Q9UL83 homo sapien
13	358	62.6	234 4 Q8NEK1	Q8NEK1 mus musculus
14	349	61.0	234 11 Q9JWF8	Q9JWF8 mus musculus
15	346.5	60.6	238 11 Q9NM37	Q9NM37 mus musculus
16	342.5	59.9	239 11 Q8VC55	Q8VC55 mus musculus

17	338	59.1	233 11 Q9JWS9	Q9JWS9 mus musculus
18	335	58.6	111 11 Q920S9	Q920S9 mus musculus
19	333	58.2	109 11 Q8R062	Q8R062 mus musculus
20	332.5	58.1	239 4 Q9UL86	Q9UL86 homo sapien
21	331.5	58.0	239 4 Q8NEK0	Q8NEK0 homo sapien
22	331	57.9	214 11 Q9R1A5	Q9R1A5 mus musculus
23	330.5	57.8	114 11 Q8K1F1	Q8K1F1 mus musculus
24	329	57.5	116 4 Q96P66	Q96P66 homo sapien
25	327	57.2	109 11 Q920E6	Q920E6 mus musculus
26	325.5	56.9	112 11 Q8K1F3	Q8K1F3 mus musculus
27	323.5	56.6	104 11 Q9JL82	Q9JL82 mus musculus
28	323	56.5	107 11 Q9JL84	Q9JL84 mus musculus
29	320	55.9	298 11 Q9QYF0	Q9QYF0 mus musculus
30	318.5	55.7	112 11 Q8K1F2	Q8K1F2 mus musculus
31	314.5	55.0	239 4 Q8TCD0	Q8TCD0 homo sapien
32	312	54.5	234 11 Q8VCPO	Q8VCPO mus musculus
33	309.5	54.1	235 11 Q9JL12	Q9JL12 mus musculus
34	305	53.3	103 11 Q9JL80	Q9JL80 mus musculus
35	304	53.1	114 4 Q9JL80	Q9JL80 homo sapien
36	303.5	53.1	134 11 Q8VDD0	Q8VDD0 mus musculus
37	301.5	52.7	106 5 Q9U410	Q9U410 schistosoma
38	301.5	52.7	112 11 Q8K1F0	Q8K1F0 mus musculus
39	300	52.4	101 11 Q9JL78	Q9JL78 mus musculus
40	299.5	52.4	239 11 Q8K0F8	Q8K0F8 mus musculus
41	298	52.1	234 11 Q8R028	Q8R028 mus musculus
42	290.5	50.8	241 11 Q921A6	Q921A6 mus musculus
43	290	50.7	127 11 Q925S9	Q925S9 mus musculus
44	276	48.3	97 11 Q9JL76	Q9JL76 mus musculus
45	268	46.9	109 6 Q9N0W5	Q9N0W5 oryctolagus

## ALIGNMENTS

RESULT 1  
Q9JL74 PRELIMINARY; PRT; 99 AA.

AC Q9JL74;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-mycosin immunoglobulin light chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BAIB/C;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin".  
RT Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206032; AAF69330.1; --  
DR HSSP; P80362; IWT.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Icy\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT PROSITE; 1  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 99 AA; 10939 MW; 3825D0E784533224 CRC64;

Query Match 88.6%; Score 507; DB 11; Length 99;  
Best Local Similarity 97.0%; Pred. No. 4,8e-48;  
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 KFLVNSAGDRVTITCKASQSVSNDAVWYQKPGQSKLMYASNRKYGVPDRFTGSGYG 68

Db 1 KELLVSGDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDEFTSGYVG 60  
 QY 69 TDFTTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 107  
 Db 61 TDTFTTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 99

## RESULT 2

OSVJ10 PRELIMINARY; PRT; 108 AA.

AC OSVJ10 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-DNA light chain (Fragment).

GN VK19.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HeJ-1pr;  
 RX MEDLINE=96409289; PubMed=8614271;  
 RA Wlloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.,  
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
 RT anti-DNA from C3H-1pr mice and lupus mice with nephritis."  
 RL Eur. J. Immunol. 26:2225-2233(1996).  
 DR EMBL; U59155; AAB02917.1; -;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 69.8%; Score 399; DB 11; Length 108;  
 Best Local Similarity 72.2%; Pred. No. 3.8e-36;  
 Matches 78; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDP 60  
 Db 1 DIVMTQSPFLSTGVDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDPH 60  
 QY 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 108  
 Db 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 108

## RESULT 3

OSVSA9 PRELIMINARY; PRT; 107 AA.

AC OSVSA9 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain  
 DE variable region (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA "Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.,  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylgalactosamine/anti-mysin  
 RT antibody V region genes."

RL J. Immunol. 161:2020-2031(1998).

DR EMBL; U96396; AAB68785.1; -;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 66.9%; Score 382.5; DB 4; Length 107;  
 Best Local Similarity 68.5%; Pred. No. 2.4e-34;  
 Matches 74; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDP 60  
 Db 1 DIQMTQSPSLASVDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDP 60  
 QY 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 108  
 Db 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 107

## RESULT 4

OSVUL79 PRELIMINARY; PRT; 108 AA.

AC OSVUL79 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9827139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035035; AAD56271.1; -;  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 65.9%; Score 377; DB 4; Length 108;  
 Best Local Similarity 64.8%; Pred. No. 9.8e-34;  
 Matches 70; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDP 60  
 Db 1 DIVMTQSPSLASVDRVTITCKASQSVSNDAVWYQKPGQSPKLLITVYASNRVTGVDP 60  
 QY 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 108  
 Db 61 RFTSGSGYGFDTFTISTVQAEIDLAVYFCQODYGSPPFTFGGKLEIKR 108

## RESULT 5

OSVUL70

```

ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1996).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDCBA1FCCA37 CRC64;
SQ

```

```

Query Match 65.7%; Score 376; DB 4; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.3e-33;
Matches 72; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

```

```

QY 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
DB 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
QY 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108
DB 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108

```

## RESULT 6

```

ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1996).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ

```

```

FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
Query Match 65.7%; Score 376; DB 4; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.3e-33;
Matches 71; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

```

```

QY 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
DB 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
QY 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108
DB 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108

```

## RESULT 7

```

ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1996).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 107 AA; 11501 MW; 070549FDB0754748 CRC64;
SQ

```

```

Query Match 64.8%; Score 370.5; DB 4; Length 107;
Best Local Similarity 66.7%; Pred. No. 5e-33;
Matches 72; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

```

```

QY 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
DB 1 DIQWTSKPEFLVAGDRTVITCKASQSVNDVAVYQKQKPGSPKLMYYASNRRTGVDP 60
QY 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108
DB 61 RFTSGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGGKTLEIKR 108

```

## RESULT 8

```

ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
SQ

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 64.8%; Score 370.5; DB 4; Length 109;
Best Local Similarity 65.1%; Pred. No. 5.1e-33;
Matches 71; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSV--VAMYQKPGQSPKLLMYASNRYTGPV 59
DB 1 EIVMTQSPATLSVPSGRATLSCMASQSSISNLAHWLQKRGQAPELLIYGASSTRATGIP 60
QY 60 DRFTGSGYGTDFFTFTISTVQAEADLAIVFCQDYGSPPTFGGKLEIKR 108
DB 61 DRFGSGSGTDFLTITSRLEPDCAYVYQYQSGSPLTFGGKVEIKR 109

RESULT 9
Q9UL85 PRELIMINARY; PRT; 109 AA.
ID Q9UL85;
AC Q9UL85;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 64.1%; Score 366.5; DB 4; Length 109;
Best Local Similarity 64.2%; Pred. No. 1.4e-32;
Matches 70; Conservative 19; Mismatches 19; Indels 1; Gaps 1;

```

```

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSVNDVAMYQKPGQSPKLLMYASNRYTGPV 60
DB 1 EIVMTQSPATLSVPSGRATLSCMASQSSISNLAHWLQKRGQAPELLIYGASSTRATGIP 60
QY 61 RFTGSGYGTDFFTFTISTVQAEADLAIVFCQDYGSPPTFGGKLEIKR 108
DB 61 RFGSGSGTDFLTITSRLEPDCAYVYQYQSGSPLTFGGKVEIKR 109

RESULT 10
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16;
AC Q8VC16;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DDE5414AD CRC64;

Query Match 64.1%; Score 366.5; DB 11; Length 238;
Best Local Similarity 64.6%; Pred. No. 3.7e-32;
Matches 73; Conservative 14; Mismatches 21; Indels 5; Gaps 2;

QY 1 DIQMTQSPKFLVSGDRVTITCKASQSV--VAMYQKPGQSPKLLMYASNRY 55
DB 20 DVMTQTPLSLPVSLGDASISCSQSVHNSNTYKHWLQKRGSPKLLIKVSNRF 79
QY 56 TGVDPRTGSGYGTDFFTFTISTVQAEADLAIVFCQDYGSPPTFGGKLEIKR 108
DB 80 SGVDPRTGSGSGTDFLTITSRLEPDCAYVYQYQSGSPLTFGGKVEIKR 132

RESULT 11
Q9ER29 PRELIMINARY; PRT; 107 AA.
ID Q9ER29;
AC Q9ER29;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN (2)
RP SEQUENCE FROM N.A.
RX Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun 1 Ta Heueh Heueh Pao 19:373-376(1998).
RN (3)

```

RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.,  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF262753; AAC23804.1; -  
 DR HSSP: P80362; 1WT.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON TER 107  
 SQ SEQUENCE 107 AA; 11784 MW; 2B15EBA604A26C3 CRC64;

Query Match 62.9%; Score 360; DB 11; Length 107;  
 Best Local Similarity 65.4%; Pred. No. 7.1e-32;  
 Matches 70; Conservative 13; Mismatches 18; Indels 6; Gaps 1;

QY 4 MTSPPKFLVSNADRYITCKASQSVSND-----VAMVQKQKSGSPKLMYASRRYGV 57  
 DB 1 MTSPPSLAWSVQKVTMSCKSQSVLSNTQKNTLAWYQKQKSGPBLVYFASVRS 60  
 QY 58 VPDRTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 104  
 DB 61 VPDRTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 107

RESULT 12  
 Q9UL83 PRELIMINARY; PRT; 108 AA.

AC Q9UL83;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (fragment).  
 OS Homo sapiens (Human).  
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9827139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL: AF035031; AAD56267.1; -  
 DR HSSP: P80362; 1WT.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EBA CRC64;

Query Match 62.8%; Score 359; DB 4; Length 108;  
 Best Local Similarity 63.0%; Pred. No. 9.3e-32;  
 Matches 69; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 1 DIQMTSPKFLVSNADRYITCKASQSVSNDVAMVQKQKSGSPKLMYASRRYGV 60  
 DB 1 EIVMTSPKFLVSNADRYITCKASQSVSNDVAMVQKQKSGSPKLMYASRRYGV 60  
 QY 61 RFTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 108  
 DB 61 RFTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 108

RESULT 13  
 Q9NEK1 PRELIMINARY; PRT; 234 AA.  
 AC Q9NEK1;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC030813; AAH30813.1; -  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00407; IGc1\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25530 MW; 6316B8DEF8D132F8 CRC64;

Query Match 62.6%; Score 358; DB 4; Length 234;  
 Best Local Similarity 63.0%; Pred. No. 3.1e-31;  
 Matches 68; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIQMTSPKFLVSNADRYITCKASQSVSNDVAMVQKQKSGSPKLMYASRRYGV 60  
 DB 21 EIVMTSPKFLVSNADRYITCKASQSVSNDVAMVQKQKSGSPKLMYASRRYGV 80  
 QY 61 RFTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 108  
 DB 81 RFTGSGYGTDFFTTISTVQAEDLAVYFCQDYGSPPTFGGKTL 128

RESULT 14  
 Q9IMF8 PRELIMINARY; PRT; 234 AA.

AC Q9IMF8;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Scltognathi; Muridae; Murinae; Mus.  
 OC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC015293; AAH15292.1; -  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR InterPro: IPR001865; Ribosomal\_S2.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR PROSITE: PS00962; RIBOSOMAL\_S2\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25929 MW; B000B0B6EB7812D2 CRC64;

Query Match 61.0%; Score 349; DB 11; Length 234;  
 Best Local Similarity 61.1%; Pred. No. 3e-30;

Matches 66; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Dy 61 RFTSSGCTDPTFITSVQAEADLVAVYCCODYSPPFGSGTLEIKR 108  
Qy 21 DIQTOTTSLSASLGDRTATISCRAGDSINVLNMYQQKRDGVKLIIITYTSLYLIVPS 80

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Dd 81 RFSSGGGTGSLLTISMBOGLAIFYCQGAMTPPFTTGSLYLEVKR 128  
Qd 61 RFTSSGCTDPTFITSVQAEADLVAVYCCODYSPPFGSGTLEIKR 108

**RESULT 15**

ID	PRELIMINARY:	PR:	238 AA.
AC	Q99M37,		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Hypothetical 26.3 kDa protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX	NCBI_TaxID=10090;		

Query Match	60.6%	Score	346.5	DB	11	Length	238
Best Local Similarity	61.9%	Pred.	No. 5.7e-30				
Matches	70	Conservative	15	Mismatches	23	Indels	5
						Gaps	2

Dy  
Dy  
Db  
Dy  
Dy

PIKOTSKRFLVLAAGRGVRITTCASGV--SND---VAAYQQRPKQGSPLTLMYVASNRY 55  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
20 DVNMTGTFPLSPVLSPGLSQASISCRSSSGSIYHNSGNNTLYEATLKRPQSPTLLLYKXSNRF 79

56 TGVPDRRTGSGVGDTFFFTSTVOAEEDLNAVYFCQDYGSGPPTGGCTKLFIKR 108  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
80 SGVDRRSGSSGSDTFDLTKLSRVEAELGVYYCCQGSHVVYTGGSGFKLEIKR 132  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

Search completed: November 7, 2003, 07:34:33  
Job time : 36.7155 secs



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XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX WPI: 2001-290358/30.
XX N-PSDB; AAF30723.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Claim 8; Fig 14; 138pp; English.
XX
XX The present sequence is that of a single chain Fv (scfv) derivative
XX of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain
XX variable regions of 193/AD3 joined by an artificial, flexible linker
XX peptide. The scfv was obtained by PCR amplification of cDNAs from
XX 193/AD3 VH and VL regions and cloning in vector pDAP2. 193/AD3 is
XX an example of anti-human factor IX (FIX)/activated factor IX (FIXa)
XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
XX including scfv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FVIIa inhibitors. This allows for rapid blood coagulation even
XX in the absence of FVIII or FVIIIa, and in the case of FVIII
XX inhibitor patients. The antibodies and derivatives are used in a
XX claimed pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis.
XX
XX Sequence 242 AA;
XX
XX Query Match 100.0%; Score 572; DB 22; Length 242;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-39;
XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DIOMTOSPKFLVNSAGDVRVTTTCRASQSVSNVDVWYQOKPQSPRLMYYASNNRYTGVPDR 60
XX DB 135 DIOMTOSPKFLVNSAGDVRVTTTCRASQSVSNVDVWYQOKPQSPRLMYYASNNRYTGVPDR 194
XX QY 61 FTGSGYGTDFFTFTISTVQAEIDLAVYFCQODYSGSPFTFGGSKLEIKR 108
XX DB 195 FTGSGYGTDFFTFTISTVQAEIDLAVYFCQODYSGSPFTFGGSKLEIKR 242
XX
XX RESULT 2
XX AAR70828
XX ID AAR70828 standard; Protein; 154 AA.
XX
XX AC AAR70828;
XX
XX XX 25-MAR-2003 (updated)
XX DT 31-AUG-1995 (first entry)
XX
XX DE MAb 4197X light chain variable region.
XX
XX XX Immunotoxin; heavy chain; light chain; variable region; antibody;
XX KM ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
XX KM pHb19; 4197X; monoclonal antibody; MAb.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX PH 53..64
XX FT /label= CDR1
XX FT /note= "complementarity determining region 1"
XX FT Region 80..86
XX FT /label= CDR2

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FT Region /note= "complementarity determining region 2"
FT 119..127
FT /label= CDR3
FT /note= "complementarity determining region 3"
XX
XX WO9503828-A1.
XX
XX PD 09-FEB-1995.
XX
XX PF 15-JUL-1994; 94WO-US07919.
XX
XX PR 02-AUG-1993; 93US-0101329.
XX
XX PA (Hous-) HOUSTON BIOTECHNOLOGY INC.
XX
XX PI Gould RM, Kelleher RJ, Wallace TL, Wood MS;
XX
XX WPI: 1995-082036/11.
XX N-PSDB; AAQ85387.
XX
XX New single chain immuno-toxin - binds specifically to epithelial
XX cells, for inhibiting development of sec. cataracts after
XX extra-capsular cataract extraction.
XX
XX Disclosure; Fig.3; 68pp; English.
XX
XX An immunotoxin (given in AAR70827) comprises the heavy (VH) and light
XX chain (VL) variable regions of anti-lens epithelium IgG3 MAb 4197X
XX linked to ricin-A. cDNAs encoding the VL and VH regions of 4197X
XX (AAQ85387-88, respectively) were obtained from hybridoma mRNA,
XX amplified by PCR, and engineered for inclusion in the immunotoxin
XX construct (AAQ85386).
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 154 AA;
XX
XX Query Match 92.5%; Score 529; DB 16; Length 154;
XX Best Local Similarity 93.5%; Pred. No. 6.4e-36;
XX Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 IOMTOSPKFLVNSAGDVRVTTTCRASQSVSNVDVWYQOKPQSPRLMYYASNNRYTGVPDR 61
XX DB 31 IOMTOSPKFLVNSAGDVRVTTTCRASQSVSNVDVWYQOKPQSPRLMYYASNNRYTGVPDR 90
XX QY 62 FTGSGYGTDFFTFTISTVQAEIDLAVYFCQODYSGSPFTFGGSKLEIKR 108
XX DB 91 FTGSGYGTDFFTFTISTVQAEIDLAVYFCQODYSGSPFTFGGSKLEIKR 137
XX
XX RESULT 3
XX AAE29157
XX ID AAE29157 standard; Protein; 128 AA.
XX
XX AC AAE29157;
XX
XX XX 27-JAN-2003 (first entry)
XX DT
XX
XX DE Chimeric 31.1 antibody light chain variable region.
XX
XX KM 31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;
XX KM light chain variable region.
XX
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX PH 1..20
XX FT Peptide
XX FT /label= Signal-peptide
XX FT 21..128
XX FT /note= "31.1 antibody light chain variable region"
XX
XX WO200274251-A2.
XX EN
XX PD 26-SEP-2002.

```

XX 15-MAR-2002; 2002MO-US09193.  
PF 15-MAR-2001; 2001US-276284P.  
PR (ITBI-) INT BIOIMMUNE SYSTEMS INC.  
PA Arlen M, Tang KY;  
PI WPI; 2002-759857/82.  
DR N-PSDB; AAD46727.  
XX  
PT New nucleic acid encoding light and heavy chain variable regions of the  
antibody 31.1, useful for expressing chimerized 31.1 antibodies for  
treating pancreatic cancer or for diagnosing pancreatic carcinoma -  
XX  
PS Claim 4; Fig 2; 40pp; English.  
XX  
CC The present invention relates to novel nucleic acid sequences encoding  
light and heavy chain variable regions of the antibody 31.1. Sequences  
of the invention are useful in expressing chimerized 31.1 antibodies,  
which can be used for treating pancreatic cancer or for diagnosing  
pancreatic carcinoma. They are also used in antibody therapy. The present  
sequence is chimeric 31.1 antibody light chain variable region.  
XX  
SQ Sequence 128 AA;  
Query Match 92.3%; Score 528; DB 23; Length 128;  
Best Local Similarity 93.5%; Pred. No. 6.5e-36;  
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 2 IOWTOSPKFLVLSAGRVTITCKASQSVSNDAWVQKQKSPKILMYASNRVTGVDP 61  
DB 22 IVMOTPKFLVLSAGRVTITCKASQSVSNDAWVQKQKSPKILMYASNRVTGVDP 81  
QY 62 FTGSGYGTDFFTTISTVQAEPLAVVFCQDDYSGSPPTFGSGTKLEIR 108  
DB 82 FTGSGYGTDFFTTISTVQAEPLAVVFCQDDYSGSPPTFGSGTKLEIR 128  
RESULT 4  
AAR39818  
ID AAR39818 standard; Protein; 106 AA.  
XX  
AC AAR39818;  
XX  
DT 25-MAR-2003 (updated)  
DT 11-JAN-1994 (first entry)  
XX  
DB HP1/2 VK.  
XX  
KW Monoclonal antibody; allergen; light chain; asthma; VLA-4;  
KW very late antigen; hypersensitivity.  
XX  
OS Homo sapiens.  
XX  
PN MO9313798-A1.  
XX  
PD 22-JUL-1993.  
XX  
PF 12-JAN-1993; 93WO-US00030.  
XX  
PR 13-JAN-1992; 92US-0821768.  
XX  
PA (BIOJ) BIOGEN INC.  
XX  
PI Lobb RR;  
XX  
DR WPI; 1993-242914/30.  
DR N-PSDB; AAQ47059.  
XX  
PT Use of anti-VLA-4 antibodies e.g. HP1/2, HP2/1, HP2/4, L25 or  
P4C2 antibodies - for inhibiting late phase response to allergens

PT in treating chronic allergen-induced asthma  
XX  
XX Claim 4; Page 29; 40pp; English.  
XX  
CC Asthma is treated by admin. of an anti-VLA (very late antigen)-4  
antibody, esp. monoclonal antibody HP1/2. The antibody is able to  
bind to the alpha 4 subunit of VLA-4 so as to (a) inhibit late phase  
response to an allergen to which the subject is hypersensitive or (b)  
decrease airway hypersensitivity after allergen challenge.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 106 AA;  
Query Match 91.4%; Score 523; DB 14; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IOWTOSPKFLVLSAGRVTITCKASQSVSNDAWVQKQKSPKILMYASNRVTGVDP 61  
DB 2 IVMOTPKFLVLSAGRVTITCKASQSVSNDAWVQKQKSPKILMYASNRVTGVDP 61  
QY 62 FTGSGYGTDFFTTISTVQAEPLAVVFCQDDYSGSPPTFGSGTKLEI 106  
DB 62 FTGSGYGTDFFTTISTVQAEPLAVVFCQDDYSGSPPTFGSGTKLEI 106  
RESULT 5  
AAR39567  
ID AAR39567 standard; Protein; 106 AA.  
XX  
AC AAR39567;  
XX  
DT 25-MAR-2003 (updated)  
DT 08-FEB-1994 (first entry)  
XX  
DB Sequence of the variable region of the light chain of the anti-VLA-4  
monoclonal antibody HP1/2 (HP1/2 V kappa).  
XX  
KW Monoclonal antibody; anti-very late antigen-4; VLA-4; HP1/2;  
KW variable light chain.  
XX  
OS Synthetic.  
XX  
PN MO9315764-A1.  
XX  
PD 19-AUG-1993.  
XX  
PF 02-FEB-1993; 93WO-US00924.  
XX  
PR 12-FEB-1992; 92US-0835139.  
XX  
PA (BIOJ) BIOGEN INC.  
XX  
PI Lobb RR;  
XX  
DR WPI; 1993-272566/34.  
DR N-PSDB; AAQ46080.  
XX  
PT Treatment of inflammatory bowel disease - using anti-very late  
antigen-4 antibody, polypeptide or other molecule recognising  
anti-very late antigen-4, reducing acute inflammation in  
ulcerative colitis, Crohn's disease, etc.  
XX  
PS Disclosure; Page 26; 35pp; English.  
XX  
CC Anti-VLA-4 antibody = anti-very late antigen-4 antibody. One anti-  
VLA-4 monoclonal antibody is designated HP1/2 (obtained from Biogen  
Inc., Cambridge, MA). The variable regions of the heavy and light  
chains of the anti-VLA-4 antibody HP1/2 were cloned, sequenced and  
expressed in combination with constant regions of human  
immunoglobulin heavy and light chains. Such a chimeric HP1/2  
antibody is similar in specificity and potency to the murine HP1/2  
antibody, and may be useful in methods for treating ulcerative

CC colitis, Crohn's disease or an acute flare-up of inflammatory  
CC bowel disease  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 106 AA;  
Query Match 91.4%; Score 523; DB 14; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMQTPEKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
QY 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106  
DB 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106  
RESULT 6  
AAR59937  
ID AAR59937 standard; Protein; 106 AA.  
AC AAR59937;  
XX  
DT 25-MAR-2003 (updated)  
DT 07-MAR-1995 (first entry)  
XX  
DE HP1/2 VK.  
XX Humanised; human; mouse; recombinant; antibody; anti-VLA4; heavy;  
KW light; variable; framework; rAb; monoclonal; CDR; HP1/2; asthma;  
KW complementarity determining region; inflammatory bowel disease.  
XX  
OS Synthetic.  
XX  
PN MO9416094-A2.  
XX  
PD 21-JUL-1994.  
XX  
PF 07-JAN-1994; 94WO-US00266.  
XX  
PR 12-JAN-1993; 93US-0004798.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Carr FJ, Lobb RR, Tempest PR;  
XX WPI; 1994-249240/30.  
DR P-PSDB; AAR59937.  
XX  
PT Recombinant and humanised anti-VLA4 antibodies - contg.  
PT non-human CDRs in their light and heavy chains, used to treat  
PT (non-)specific inflammation, e.g. asthma  
XX  
PS Example 1; Page 78; 140pp; English.  
XX  
XX This sequence represents the HP1/2 antibody kappa chain variable region  
CC (VK). This protein sequence was used in the production of a humanised  
CC recombinant anti-VLA4 antibody (rAb). The humanised rAb comprises  
CC non-human complementarity determining regions at VH positions 31-35  
CC (CDR1), 50-65 (CDR2) and 95-102 (CDR3). It may further comprise non-  
CC human residues at framework positions 27-30, 75, 77-79 or 66-67, or  
CC 66-71 and 69-71, or 84-85, or 38 and 40 or 24. The VL of the rAb has  
CC non-human CDRs at positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3).  
CC It may also have non-human residues at framework positions 60 and 67.  
CC The non-human CDRs are pref. derived from the HP1/2 murine monoclonal  
CC antibody. HP1/2 is a member of Kabat V with no unusual residues. The  
CC rAb can be used to treat inflammation in mammals, esp. asthma or  
CC inflammatory bowel disease.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 106 AA;

Query Match 91.4%; Score 523; DB 15; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMQTPEKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
QY 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106  
DB 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106  
RESULT 7  
AAR58750  
ID AAR58750 standard; Protein; 106 AA.  
AC AAR58750;  
XX  
DT 25-MAR-2003 (updated)  
DT 21-MAR-1995 (first entry)  
XX  
DE Anti-VLA4 Ab HP1/2 V-kappa sequence.  
XX  
KW Chimeric antibody; HP1/2; integrin; VLA4; very late antigen-4;  
KW heavy chain; light chain; constant region; variable region;  
KW antibody engineering; VCAW-1; fibronectin; monoclonal antibody;  
KW insulin-dependent diabetes.  
XX  
OS Mus sp.  
XX  
PN WO9417828-A2.  
XX  
PD 18-AUG-1994.  
XX  
PF 09-FEB-1994; 94WO-US01456.  
XX  
PR 09-FEB-1993; 93US-0029330.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Burkly LC;  
XX  
DR WPI; 1994-279394/34.  
XX  
DR N-PSDB; AAR67344.  
XX  
PT Treatment and prevention of insulin dependent diabetes - by  
PT administering monoclonal antibodies specified for the integrin  
PT VLA4 blocking interactions with VCAW-1 and fibronectin  
XX  
PS Disclosure; Page 54; 73pp; English.  
XX  
XX Chimeric HP1/2 antibody comprises the variable regions of the heavy  
CC and light chains of mouse anti-VLA4 Ab HP1/2 and constant regions of  
CC human heavy and light chains. cDNA encoding the HP1/2 VH and V-  
CC kappa sequences are given in AAR67343-44, and the encoded proteins in  
CC AAR58749-50.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 106 AA;  
Query Match 91.4%; Score 523; DB 15; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMQTPEKFLVLSAGDRVTITCKASQSVSNDAVAVYQKQKPGSPKLLMYASNRRTGVDPDR 61  
QY 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106  
DB 62 FTGSGYGTDFFTTISTVQAEADLAVYFCQDDYSGSPPTFGGRTKEI 106

```

RESULT 8
AAV23985
ID AAV23985 standard; Protein; 106 AA.
XX
AC AAV23985;
XX
DT 20-MAR-2003 (updated)
DT 22-SEP-1999 (first entry)
XX
DE Antibody HP1/2 light chain variable region.
XX
KW light chain variable region; very late antigen-4; VLA-4; antibody HP1/2;
KW inflammatory bowel disease; B1 epitope; B2 epitope; alpha 4 subunit;
KW ulcerative colitis; Crohn's disease.
XX
OS Mus sp.
XX
PN US5932214-A.
XX
PD 03-AUG-1999.
XX
PF 15-OCT-1997; 97US-0950660.
XX
PR 12-MAY-1995; 95US-0456124.
PR 12-FEB-1992; 92US-0835139.
PR 02-FEB-1993; 93WO-US00924.
PR 11-AUG-1994; 94US-0284603.
PR 18-JAN-1995; 95US-0373857.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Burkly LC; Lobb RR;
XX
DR WPI; 1999-443570/37.
DR N-PSDB; AAX86185.
XX
PT Treating inflammatory bowel disease with VLA-4 blockers
XX
PS Disclosure; Columns 25-26; 26pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC murine anti-human very late antigen-4 (VLA-4) monoclonal antibody HP1/2.
CC The protein can be used in the method of the invention. The specification
CC describes methods for treating inflammatory bowel disease with a
CC composition comprising an antibody, or its fragments, able to bind to
CC the B1 or B2 epitope of the alpha 4 subunit of VLA-4. The method is
CC useful for treating ulcerative colitis and Crohn's disease.
CC (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 106 AA;
XX
Query Match 91.4%; Score 523; DB 20; Length 106;
Best Local Similarity 94.3%; Pred. No. 1.4e-35;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 IQMTOSPKFLVSAAGRVITTCASQSYNDVAMVQKQSPKILMYASNRRTGVPR 61
DB 2 IWTOTPKFLVSAAGRVITTCASQSYNDVAMVQKQSPKILMYASNRRTGVPR 61
QY FTGSGYGTDFFTTISTVQAEPLAVVFCQODYSGPPTFGGTTLEI 106
DB 62 FTGSGYGTDFFTTISTVQAEPLAVVFCQODYSGPPTFGGTTLEI 106
XX
RESULT 9
AAV01034
ID AAV01034 standard; Protein; 106 AA.
XX
AC AAV01034;
XX
DT 04-JUN-1999 (first entry)

```

```

XX
DE Anti VLA-4 antibody HP1/2 VK protein sequence.
XX
KW VLA-4; antibody; anti VLA-4 antibody HP1/2; VH chain; alpha 4 subunit;
KW insulin-dependent type I diabetes; very late antigen-4; soluble VCAM-1;
KW vascular cell adhesion molecule-1; insulin-dependent diabetes; therapy.
XX
OS Homo sapiens.
XX
PN US5888507-A.
XX
PD 30-MAR-1999.
XX
PP 22-MAY-1995; 95US-0447118.
XX
PR 22-MAY-1995; 95US-0447118.
PR 09-FEB-1993; 93US-0029330.
PR 09-FEB-1994; 94US-0001456.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Burkly LC;
XX
DR WPI; 1999-24365/20.
DR N-PSDB; AAX27914.
XX
PT Treating insulin-dependent diabetes by blocking VLA-4 antigen
XX
PS Disclosure; Column 27-28; 28pp; English.
XX
CC This sequence is the anti VLA-4 antibody HP1/2 VK chain.
CC The invention relates to a method for the treatment of insulin-dependent
CC type I diabetes, comprising administering to a prediabetic mammal (or one
CC showing partial beta-cell destruction) one or more compositions of an
CC antibody that binds to the alpha 4 subunit of VLA-4 (very late
CC antigen-4); its antigen-binding fragments, or a soluble VCAM-1 (vascular
CC cell adhesion molecule-1) polypeptide that binds to the alpha 4 subunit
CC of VLA-4. The treatment is used to prevent development of
CC insulin-dependent diabetes.
XX
SQ Sequence 106 AA;
XX
Query Match 91.4%; Score 523; DB 20; Length 106;
Best Local Similarity 94.3%; Pred. No. 1.4e-35;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 IQMTOSPKFLVSAAGRVITTCASQSYNDVAMVQKQSPKILMYASNRRTGVPR 61
DB 2 IWTOTPKFLVSAAGRVITTCASQSYNDVAMVQKQSPKILMYASNRRTGVPR 61
QY FTGSGYGTDFFTTISTVQAEPLAVVFCQODYSGPPTFGGTTLEI 106
DB 62 FTGSGYGTDFFTTISTVQAEPLAVVFCQODYSGPPTFGGTTLEI 106
XX
RESULT 10
AAW96742
ID AAW96742 standard; Protein; 106 AA.
XX
AC AAW96742;
XX
DT 20-MAR-2003 (updated)
DT 16-APR-1999 (first entry)
XX
DE Light chain variable region of antibody HP1/2.
XX
KW light chain variable region; antibody HP1/2;
KW alpha 4 beta 1 integrin very late antigen-4; VLA-4;
KW chronic allergen-induced asthma; VLA4-leukocyte migration;
KW leukocyte infiltration; signal transduction inhibition.
XX
OS Mus sp.
XX

```

PN US5871734-A.  
 PF 16-FEB-1999.  
 PD  
 XX  
 XX 21-MAR-1997; 97US-0822830.  
 XX  
 XX 31-MAY-1995; 95US-0456193.  
 PR 13-JAN-1992; 92US-0821768.  
 PR 12-JAN-1993; 93MO-US00030.  
 PR 12-JUL-1994; 94US-0256631.  
 PR 18-JAN-1995; 95US-0374331.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Burklly LC, Lobb RR;  
 XX  
 XX WPI; 1999-166573/14.  
 DR N-PSDB; AAX15094.  
 XX  
 XX Treating allergic asthma with very late antigen-4 binding agent  
 PT to inhibit late phase response and decrease airway hypersensitivity  
 XX  
 PS Disclosure; Columns 23-24; 31pp; English.  
 XX  
 XX The present sequence represents the light chain variable region of  
 CC antibody HPI/2. This antibody binds alpha 4 beta 1 integrin very  
 CC late antigen-4 (VLA-4). The antibody can be used in methods to  
 CC treat chronic allergen-induced asthma. Inhibition of VLA4-leukocyte  
 CC migration prevents secondary effects of leukocyte infiltration  
 CC (release of toxins, inducers of soluble inflammatory cell mediators  
 CC or chemotactic agents) and inhibition of signal transduction causing  
 CC release of such mediators and chemotactic agents.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 106 AA;  
 QY  
 Query Match 91.4%; Score 523; DB 20; Length 106;  
 Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVSNDAVAMYOQKPGQSPKFLMYASNRVTGVPR 61  
 DB 2 IWMQTPKFLVLSAGDRVTITCKASQSVSNDAVAMYOQKPGQSPKFLMYASNRVTGVPR 61  
 QY 62 FTGSGYGTDFFTTISTVQAEEDLAVYFCQODYSSPYTFGGGTLEI 106  
 DB 62 FTGSGYGTDFFTTISTVQAEEDLAVYFCQODYSSPYTFGGGTLEI 106  
 RESULT 11  
 AAB73463  
 ID AAB73463 standard; Protein; 106 AA.  
 XX  
 XX AAB73463;  
 XX  
 DT 02-JUL-2001 (first entry)  
 XX  
 XX Murine anti-VLA-4 monoclonal antibody HPI/2 VL.  
 DE  
 XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;  
 KW very late antigen; monoclonal antibody HPI/2; mouse; murine;  
 KW kidney disease; chronic renal failure; end-stage renal disease;  
 KW chronic diabetic nephropathy; diabetic glomerulopathy;  
 KW diabetic renal hypertrophy; hypertensive nephrosclerosis;  
 KW hypertensive glomerulosclerosis; chronic glomerulonephritis;  
 KW hereditary nephritis; renal dysplasia; nephrotropic;  
 KW light chain variable region; VL.  
 XX  
 OS Mus sp.  
 XX  
 XX W0200119396-A1.  
 PN  
 XX 22-MAR-2001.

XX  
 XX 14-SEP-2000; 2000MO-US25140.  
 PF  
 XX 14-SEP-1999; 99US-0153826.  
 PR  
 XX  
 XX (BIOJ ) BIOGEN INC.  
 PA (UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.  
 XX  
 XX Allen A, Pusey C, Lobb R;  
 PI  
 XX WPI; 2001-273408/28.  
 DR N-PSDB; AAF86602.  
 XX  
 XX Treating a mammal in, or at a risk of developing, chronic renal  
 PT failure, involves administering at least one integrin antagonist to the  
 PT mammal  
 XX  
 XX Claim 12; Page -; 62pp; English.  
 XX  
 XX The invention relates to a method for treating a mammal with,  
 CC or at risk of developing, chronic renal failure, involving the  
 CC administration of at least one integrin antagonist. The integrin  
 CC antagonists that may be used in the method include antagonists of  
 CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-  
 CC containing integrins. In particular, the antagonists are antibodies  
 CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or  
 CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the  
 CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in  
 CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).  
 CC The method of the invention may be used to treat chronic renal failure,  
 CC end-stage renal disease, chronic diabetic nephropathy, diabetic  
 CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,  
 CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary  
 CC nephritis or renal dysplasia. The present sequence represents the light  
 CC chain variable region (VL) of the murine anti-VLA-4 monoclonal antibody  
 CC HPI/2.  
 CC Note: The present sequence is not given in the specification, but  
 CC is given in US5932214, columns 25-26.  
 XX  
 SQ Sequence 106 AA;  
 QY  
 Query Match 91.4%; Score 523; DB 22; Length 106;  
 Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
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 DB 2 IWMQTPKFLVLSAGDRVTITCKASQSVSNDAVAMYOQKPGQSPKFLMYASNRVTGVPR 61  
 QY 62 FTGSGYGTDFFTTISTVQAEEDLAVYFCQODYSSPYTFGGGTLEI 106  
 DB 62 FTGSGYGTDFFTTISTVQAEEDLAVYFCQODYSSPYTFGGGTLEI 106  
 RESULT 12  
 AB008539  
 ID AB008539 standard; Protein; 106 AA.  
 XX  
 XX AB008539;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 XX Mouse anti-VLA-4 antibody HPI/2 kappa chain variable region.  
 DE  
 XX Mouse; antibody; VLA-4; alpha4beta1 integrin; VCAM-1; IBD;  
 KW vascular cell adhesion molecule-1; inflammatory bowel disease;  
 KW ulcerative colitis; Crohn's disease; chronic inflammatory disorder;  
 KW antineur; antiinflammatory; VCAM 2D IgG; kappa chain variable region.  
 XX  
 OS Mus musculus.  
 XX  
 XX US6482409-B1.  
 PN  
 XX

PD 19-NOV-2002.  
 XX 21-SEP-1998; 98US-0157452.  
 XX 31-MAY-1995; 95US-0456124.  
 PR 15-OCT-1997; 97US-0950660.  
 PR 02-FEB-1993; 93US-0835139.  
 PR 02-FEB-1993; 93MO-US00924.  
 PR 11-AUG-1994; 94US-0284603.  
 XX 18-JAN-1995; 95US-0373857.  
 XX (BIOI ) BIOGEN INC.  
 PI Lobb RR, Burckly LC;  
 DR WPI; 2003-340372/32.  
 DR N-PSDB; ABX93815.  
 XX  
 XX Treating inflammatory bowel disease, comprises administering a  
 PT composition comprising a vascular cell adhesion  
 PT molecule-1/immunoglobulin G fusion protein -  
 PS Disclosure; Column 23-24; 28pp; English.  
 XX The invention relates to treating inflammatory bowel disease (IBD),  
 CC comprising administering to a mammal suffering from IBD a composition  
 CC comprising a vascular cell adhesion molecule (VCAM)-1/immunoglobulin G  
 CC (193) fusion protein in an amount effective to provide relief to the  
 CC mammal. Antibodies against VLA-4 (alpha4beta1 integrin, a binding partner  
 CC for VCAM-1) may also be effective in treating IBD. The method is useful  
 CC for treating inflammatory bowel disease in a mammal, preferably a human  
 CC suffering from ulcerative colitis or Crohn's disease (both are chronic  
 CC inflammatory diseases). The composition is administered during an acute  
 CC flare-up of the inflammatory bowel disease. The fusion protein is  
 CC termed VCAM 2D IgG and comprises 2 N-terminal domains of VCAM-1 fused to  
 CC the human IgG heavy chain constant regions, hinge CH2 and CH3.  
 CC The present sequence represents the kappa chain variable regions of a  
 CC mouse monoclonal antibody HPI/2 which recognises VLA-4 and may be of  
 CC use as a treatment for IBD.  
 XX  
 XX Sequence 106 AA;  
 SQ  
 Query Match 91.4%; Score 523; DB 24; Length 106;  
 Best Local Similarity 94.3%; Pred. No. 1.4e-35;  
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IQMTQSPKFLVLSAGDRVITTCASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 61  
 DB 2 IVMTQTPKFLVLSAGDRVITTCASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 61  
 QY 62 FTGSGYGTDFPTFTISTVQAEIDLAVYFCQDDYSGPPTFGGSKLEI 106  
 DB 62 FTGSGYGTDFPTFTISTVQAEIDLAVYFCQDDYSGPPTFGGSKLEI 106  
 RESULT 13  
 AARS8612  
 ID AARS8612 standard; Protein; 246 AA.  
 XX  
 XX AARS8612;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 28-APR-1995 (first entry)  
 XX  
 XX 11-6 binding inhibitor.  
 DE  
 XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
 KW septic shock; multiple myeloma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN BB617126-A2.  
 XX

PD 28-SEP-1994.  
 XX  
 XX 16-FEB-1994; 94EP-0102346.  
 XX  
 XX 17-FEB-1993; 93JP-0028173.  
 XX  
 XX (AJIN ) AJINOMOTO KK.  
 XX  
 XX Hamuro J, Nakazawa H, Shimamura T;  
 PI WPI; 1994-295777/37.  
 DR N-PSDB; AAQ70612.  
 XX  
 XX Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
 PT its receptor - useful for treating autoimmune disease induced  
 PT or aggravated by IL-6  
 XX  
 XX Claim 5; Page 18; 26pp; English.  
 PS  
 XX AAQ70612 codes for human interleukin-6 binding inhibitor, the  
 CC polypeptide described in AARS8612. This polypeptide inhibits the  
 CC binding of human IL-6 to its receptor, and can therefore be  
 CC useful in the treatment of a variety of autoimmune diseases;  
 CC specifically in the treatment of rheumatoid arthritis, septic  
 CC shock due to bacterial infection and multiple myeloma.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 246 AA;  
 SQ  
 Query Match 90.7%; Score 519; DB 15; Length 246;  
 Best Local Similarity 92.5%; Pred. No. 6.6e-35;  
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPKFLVLSAGDRVITTCASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 60  
 DB 2 DILNQSPKFLVLSAGDRVITTCASQSVSNDAVWYQKPGQSPKLLMYASNRRTGVDP 61  
 QY 61 RFTGSGYGTDFPTFTISTVQAEIDLAVYFCQDDYSGPPTFGGSKLEI 107  
 DB 62 RFTGSGYGTDFPTFTISTVQAEIDLAVYFCQDDYSGPPTFGGSKLEI 108  
 RESULT 14  
 AAR70827  
 ID AAR70827 standard; Protein; 554 AA.  
 XX  
 XX AAR70827;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 31-AUG-1995 (first entry)  
 XX  
 XX Anti-cataract immunotoxin.  
 DE  
 XX Immunotoxin; heavy chain; light chain; variable region; antibody;  
 KW ricin-A; cytotoxic; cataract; lens opacification; epithelial cell;  
 KW PHB19; 4197X; monoclonal antibody; Mab.  
 XX  
 OS Synthetic.  
 XX  
 XX Key  
 FH Location/Qualifiers  
 FH 1..27  
 FH Peptide  
 FT /label= Sig\_peptide  
 FT /note= "phoa signal sequence"  
 FT 28..145  
 FT Domain  
 FT /label= HEAVY  
 FT /note= "MAB 4197X heavy chain"  
 FT 148..166  
 FT Peptide  
 FT /label= LINKER  
 FT 169..274  
 FT Domain  
 FT /label= LIGHT  
 FT /note= "MAB 419X light chain"  
 FT 276..544  
 FT Domain  
 FT /label= RICIN-A



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Run on: November 7, 2003, 07:30:19 ; Search time 94.7343 Seconds  
(without alignment)  
195.799 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	91.4	106	US-10-428-662-10	Sequence 10, Appl
2	523	91.4	106	US-10-095-496-2	Sequence 2, Appl
3	523	91.4	106	US-10-252-978-4	Sequence 4, Appl
4	512	89.5	107	US-10-422-049-17	Sequence 17, Appl
5	507	88.6	107	US-10-422-049-13	Sequence 13, Appl
6	498	87.1	107	US-10-283-838-6	Sequence 6, Appl
7	490	85.7	124	US-09-900-766-1	Sequence 1, Appl
8	479	83.7	124	US-10-428-662-1	Sequence 71, Appl
9	479	83.7	128	US-10-428-662-67	Sequence 67, Appl
10	466	81.5	128	US-10-428-662-63	Sequence 63, Appl
11	461	80.6	128	US-10-428-662-31	Sequence 31, Appl
12	448	78.3	108	US-10-422-049-18	Sequence 18, Appl
13	445	77.8	128	US-10-010-729-72	Sequence 72, Appl
14	442	77.3	108	US-10-422-049-14	Sequence 14, Appl
15	442	77.3	128	US-08-779-784-36	Sequence 36, Appl

16	442	77.3	333	US-10-059-261-61	Sequence 61, Appl
17	439	76.7	107	US-09-509-098-130	Sequence 130, App
18	439	76.7	131	US-09-269-921-104	Sequence 104, App
19	439	76.7	131	US-09-509-098-2	Sequence 2, Appl
20	439	76.7	131	US-10-218-253-104	Sequence 104, App
21	437	76.4	131	US-10-059-261-169	Sequence 169, App
22	435	76.0	250	US-09-887-853-2	Sequence 2, Appl
23	431	75.3	107	US-09-509-098-134	Sequence 134, App
24	430	75.2	109	US-09-811-123-4	Sequence 4, Appl
25	427	74.7	107	US-09-566-2064-79	Sequence 79, Appl
26	427	74.7	127	US-09-956-2064-49	Sequence 49, Appl
27	425	74.3	107	US-10-268-501-1	Sequence 1, Appl
28	424	74.1	133	US-09-874-141-45	Sequence 45, Appl
29	424	74.1	133	US-09-874-141-51	Sequence 51, Appl
30	423	74.0	106	US-09-824-286-4	Sequence 4, Appl
31	423	74.0	107	US-09-956-2064-81	Sequence 81, Appl
32	423	74.0	127	US-09-956-2064-65	Sequence 65, Appl
33	422.5	73.9	213	US-10-281-479A-76	Sequence 76, Appl
34	422.5	73.9	213	US-10-275-180A-76	Sequence 76, Appl
35	422.5	73.9	213	US-10-286-132A-76	Sequence 76, Appl
36	422.5	73.9	234	US-10-281-479A-24	Sequence 24, Appl
37	422.5	73.9	234	US-10-275-180A-24	Sequence 24, Appl
38	422.5	73.9	234	US-10-286-132A-24	Sequence 24, Appl
39	421	73.6	126	US-09-760-723-6	Sequence 6, Appl
40	421	73.6	126	US-09-355-925-6	Sequence 6, Appl
41	421	73.6	126	US-09-269-921-106	Sequence 106, App
42	421	73.6	126	US-09-509-098-12	Sequence 12, Appl
43	421	73.6	126	US-10-428-085-6	Sequence 6, Appl
44	421	73.6	126	US-10-315-125-6	Sequence 6, Appl
45	421	73.6	126	US-10-218-253-106	Sequence 106, App

#### ALIGNMENTS

RESULT 1

US-10-428-662-10

Sequence 10, Application US/10428662

Publication No. US20030185819A1

GENERAL INFORMATION:

APPLICANT: Lobb, Roy R.

APPLICANT: Carr, Frank J.

TITLE OR INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES

FILE REFERENCE: 10274-007001

CURRENT APPLICATION NUMBER: US/10/428, 662

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US/08/454, 899G

PRIOR FILING DATE: 1995-05-31

PRIOR APPLICATION NUMBER: US 08/004, 798

PRIOR FILING DATE: 1993-01-12

PRIOR APPLICATION NUMBER: PCT/US94/00266

PRIOR FILING DATE: 1994-01-07

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 106

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: light chain variable region

US-10-428-662-10

Query Match 91.4%; Score 523; DB 12; Length 106;

Best Local Similarity 94.3%; Pred. No. 9.4e-44;

Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOWTQSKFLVNSAGRVTVTTCASQSVNDVAMVYQCKPQSPRLMTVYNSNRYGVGPR 61

DB 2 IOWTQSKFLVNSAGRVTVTTCASQSVNDVAMVYQCKPQSPRLMTVYNSNRYGVGPR 61

QY 62 FTGSGYGTDFTFITSTVQADLAIVYFCQDDYSGPPIFGGCTKLEI 106

```
DB      62 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 106
;
; ORGANISM: Mus musculus
; US-10-252-978-4
;
; RESULT 2
; US-10-095-496-2
; Sequence 2, Application US/10095496
; Publication No. US20030007969A1
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy
; APPLICANT: Allen, Andrew
; APPLICANT: Pussey, Charles
; APPLICANT: Biogen, Inc.
; APPLICANT: Imperial College of Science, Technology and Medicine
; TITLE OF INVENTION: Therapies for Chronic Renal Failure
; TITLE OF INVENTION: Using One or More Integrin Antagonists
; FILE REFERENCE: A082 US
; CURRENT APPLICATION NUMBER: US/10/095,496
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US00/25140
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/153,826
; PRIOR FILING DATE: 1998-03-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPI/2 light chain variable region
; US-10-095-496-2
;
; Query Match
; Best Local Similarity 91.4%; Score 523; DB 15; Length 106;
; Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
;
; QY      2 IOMTOSPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLMYASNRRTGVPDR 61
; DB      2 IVMOTPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLIYASNRRTGVPDR 61
;
; QY      62 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 106
; DB      62 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 106
;
; RESULT 3
; US-10-252-978-4
; Sequence 4, Application US/10252978
; Publication No. US20030095969A1
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Burkly, Linda C.
; TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
; FILE REFERENCE: 10274-004003
; CURRENT APPLICATION NUMBER: US/10/252,978
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/157,452
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US 08/950,660
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 08/373,857
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/284,603
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: PCT/US93/00924
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: US 07/835,139
; PRIOR FILING DATE: 1992-02-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
;
; QY      1 DIOMTOSPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLMYASNRRTGVPD 60
; DB      1 NIWMTQPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLIYASNRRTGVPD 60
;
; QY      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
; DB      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
;
; RESULT 5
; US-10-422-049-13
; Sequence 13, Application US/10422049
; Publication No. US20030199679A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John Robert
; APPLICANT: Adair, John Robert
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Emwage, John Spencer
; APPLICANT: Bodmer, Mark William
; TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
; FILE REFERENCE: CARP0063
; CURRENT APPLICATION NUMBER: US/10/422,049
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/09/267,281
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 08/456,418
; PRIOR FILING DATE: 1995-06-01
; PRIOR APPLICATION NUMBER: 06/373,882
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 07/920,378
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Murine
; US-10-422-049-17
;
; Query Match
; Best Local Similarity 89.5%; Score 512; DB 12; Length 107;
; Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
;
; QY      1 DIOMTOSPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLMYASNRRTGVPD 60
; DB      1 NIWMTQPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLIYASNRRTGVPD 60
;
; QY      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
; DB      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
;
; RESULT 4
; US-10-422-049-17
; Sequence 17, Application US/10422049
; Publication No. US20030199679A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John Robert
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Emwage, John Spencer
; APPLICANT: Bodmer, Mark William
; TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
; FILE REFERENCE: CARP0063
; CURRENT APPLICATION NUMBER: US/10/422,049
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/09/267,281
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 08/456,418
; PRIOR FILING DATE: 1995-06-01
; PRIOR APPLICATION NUMBER: 06/373,882
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 07/920,378
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Murine
; US-10-422-049-17
;
; Query Match
; Best Local Similarity 87.9%; Score 512; DB 12; Length 107;
; Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
;
; QY      1 DIOMTOSPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLMYASNRRTGVPD 60
; DB      1 NIWMTQPKFLVLSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLIYASNRRTGVPD 60
;
; QY      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
; DB      61 FTGSGYGTDFFTISTVQAEADLAVYFCQDDYSSPYTFGGGTGKLEI 107
;
; RESULT 5
; US-10-422-049-13
; Sequence 13, Application US/10422049
; Publication No. US20030199679A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John Robert
; APPLICANT: Adair, John Robert
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Emwage, John Spencer
; APPLICANT: Bodmer, Mark William
; TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
; FILE REFERENCE: CARP0063
; CURRENT APPLICATION NUMBER: US/10/422,049
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/09/267,281
; PRIOR FILING DATE: 1999-03-12
```

PRIOR APPLICATION NUMBER: 08/456,418  
PRIOR FILING DATE: 1995-06-01  
PRIOR APPLICATION NUMBER: 08/373,882  
PRIOR FILING DATE: 1995-01-17  
PRIOR APPLICATION NUMBER: 07/920,378  
PRIOR FILING DATE: 1993-09-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 13  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Murine  
US-10-422-049-13

Query Match 88.6%; Score 507; DB 12; Length 107;  
Best Local Similarity 90.6%; Pred. No. 3,4e-42;  
Matches 96; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IOMTSPKFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 61  
DB 2 IVMYQTPFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 61  
QY 62 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 107  
DB 62 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 107

## RESULT 6

US-10-283-838-6  
Sequence 6, Application US/10283838  
Publication No. US20030092894A1

## GENERAL INFORMATION:

APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,  
Johan Hansson, Terje Kalland, Lars  
Aabrahmsen and Goran Forsberg  
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pravel, Hewitt, Kimball & Krieger  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77027-9095

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/283,838  
FILING DATE: 30-Oct-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/695,692  
FILING DATE: August 12, 1996  
APPLICATION NUMBER: 9601245-5  
FILING DATE: March 29, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Krieger, Paul E.  
REGISTRATION NUMBER: 25,886  
REFERENCE/DOCKET NUMBER: 41986/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-283-838-6

Query Match 87.1%; Score 498; DB 15; Length 107;  
Best Local Similarity 87.9%; Pred. No. 2.6e-41;  
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTSPKFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 60  
DB 1 DAVMTQTPFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 60  
QY 61 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 107  
DB 61 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 107

## RESULT 7

US-09-900-766-1  
Sequence 1, Application US/09900766  
Publication No. US20030039655A1

## GENERAL INFORMATION:

APPLICANT: FORSBERG, GORAN  
APPLICANT: ERLANDSSON, EVA  
APPLICANT: ANTONSSON, PER  
APPLICANT: MALSE, BJORN  
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY  
FILE REFERENCE: P0218800/10104199  
CURRENT APPLICATION NUMBER: US/09/900,766  
CURRENT FILING DATE: 2001-07-06  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent In Version 3.0  
SEQ ID NO 1  
LENGTH: 672  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(672)  
OTHER INFORMATION: Conjugate protein  
US-09-900-766-1

Query Match 85.7%; Score 490; DB 11; Length 672;  
Best Local Similarity 86.9%; Pred. No. 1.1e-39;  
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 IOMTSPKFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 61  
DB 460 IVMYQTPFLVSAADRVITTCASQSVNDVAMVYQKPGSPKLIYASNRRTGVDR 519  
QY 62 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 108  
DB 520 FTGSGYGTDFFTITSTVQAEADLAVYFCQDDYSGSPPTFGGKLEIK 566

## RESULT 8

US-10-428-662-71  
Sequence 71, Application US/10428662  
Publication No. US20030185819A1

## GENERAL INFORMATION:

APPLICANT: Lobb, Roy R.  
APPLICANT: Carr, Frank J.  
APPLICANT: Tempest, Philip R.  
TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES  
FILE REFERENCE: 10274-007001  
CURRENT APPLICATION NUMBER: US/10/428,662  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: US/08/454,899G  
PRIOR FILING DATE: 1995-05-31  
PRIOR APPLICATION NUMBER: US 08/004,798  
PRIOR FILING DATE: 1993-01-12  
PRIOR APPLICATION NUMBER: PCT/US94/00266  
PRIOR FILING DATE: 1994-01-07  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0

```
/ SEQ ID NO 71
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain variable region
US-10-428-662-71
```

```
Query Match      83.7%; Score 479; DB 12; Length 124;
Best Local Similarity 85.7%; Pred. No. 2,1e-39;
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 2 IOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 61
DB 20 IOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 79
QY 62 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 106
DB 80 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 124
```

RESULT 9

```
US-10-428-662-67
/ Sequence 67, Application US/10428662
/ Publication No. US20030185819A1
/ GENERAL INFORMATION:
/ APPLICANT: Lobb, Roy R.
/ APPLICANT: Carr, Frank J.
/ APPLICANT: Tempest, Philip R.
/ TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
/ FILE REFERENCE: 10274-007001
/ CURRENT APPLICATION NUMBER: US/10/428,662
/ CURRENT FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US/08/454,899G
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/004,798
/ PRIOR FILING DATE: 1993-01-12
/ PRIOR APPLICATION NUMBER: PCT/US94/00266
/ PRIOR FILING DATE: 1994-01-07
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain variable region
US-10-428-662-67
```

```
Query Match      83.7%; Score 479; DB 12; Length 128;
Best Local Similarity 81.5%; Pred. No. 2,2e-39;
Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 DIOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 60
DB 20 DIOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 79
QY 61 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 108
DB 80 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 127
```

RESULT 10

```
US-10-428-662-63
/ Sequence 63, Application US/10428662
/ Publication No. US20030185819A1
/ GENERAL INFORMATION:
/ APPLICANT: Lobb, Roy R.
/ APPLICANT: Carr, Frank J.
/ APPLICANT: Tempest, Philip R.
/ TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
/ FILE REFERENCE: 10274-007001
/ CURRENT APPLICATION NUMBER: US/10/428,662
```

```
/ CURRENT FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US/08/454,899G
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/004,798
/ PRIOR FILING DATE: 1993-01-12
/ PRIOR APPLICATION NUMBER: PCT/US94/00266
/ PRIOR FILING DATE: 1994-01-07
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain variable region
US-10-428-662-63
```

```
Query Match      81.5%; Score 466; DB 12; Length 128;
Best Local Similarity 80.4%; Pred. No. 4,1e-38;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 2 IOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 61
DB 21 IOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 80
QY 62 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 108
DB 81 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 127
```

RESULT 11

```
US-10-428-662-31
/ Sequence 31, Application US/10428662
/ Publication No. US20030185819A1
/ GENERAL INFORMATION:
/ APPLICANT: Lobb, Roy R.
/ APPLICANT: Carr, Frank J.
/ APPLICANT: Tempest, Philip R.
/ TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
/ FILE REFERENCE: 10274-007001
/ CURRENT APPLICATION NUMBER: US/10/428,662
/ CURRENT FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US/08/454,899G
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/004,798
/ PRIOR FILING DATE: 1993-01-12
/ PRIOR APPLICATION NUMBER: PCT/US94/00266
/ PRIOR FILING DATE: 1994-01-07
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain variable region
US-10-428-662-31
```

```
Query Match      80.6%; Score 461; DB 12; Length 128;
Best Local Similarity 78.7%; Pred. No. 1,3e-37;
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1 DIOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 60
DB 20 DIOWTQSPKFLVSAAGDRTVITTCASQSVSNDAVWYQKFGQSPKLTMYASNRRTGVDPDR 79
QY 61 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 108
DB 80 FTGSGGYGDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEIKR 127
```

RESULT 12

US-10-422-049-18

```
Sequence 18, Application US/10422049
; Publication No. US20030199679A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John Robert
; APPLICANT: Ahtwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; APPLICANT: Bodmer, Mark William
; TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
; FILE REFERENCE: CARP0063
; CURRENT APPLICATION NUMBER: US/10/422,049
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/09/267,281
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 08/456,418
; PRIOR FILING DATE: 1995-06-01
; PRIOR APPLICATION NUMBER: 08/373,882
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 07/920,378
; PRIOR FILING DATE: 1992-09-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; US-10-422-049-18

Query Match
Best Local Similarity 78.3%; Score 448; DB 12; Length 108;
Matches 83; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 60
DB 1 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 60
QY 61 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 108
DB 61 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 108

RESULT 13
US-10-010-729-72
; Sequence 72, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 128
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TYPE: PRT
; ORGANISM: Mus musculus
; US-10-010-729-72

Query Match
Best Local Similarity 77.8%; Score 445; DB 12; Length 128;
Matches 86; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 60
DB 21 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 80
QY 61 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 108
DB 81 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 128

RESULT 14
US-10-422-049-14
; Sequence 14, Application US/10422049
; Publication No. US20030199679A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John Robert
; APPLICANT: Ahtwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; APPLICANT: Bodmer, Mark William
; TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
; FILE REFERENCE: CARP0063
; CURRENT APPLICATION NUMBER: US/10/422,049
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US/09/267,281
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 08/456,418
; PRIOR FILING DATE: 1995-06-01
; PRIOR APPLICATION NUMBER: 08/373,882
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 07/920,378
; PRIOR FILING DATE: 1992-09-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; US-10-422-049-14

Query Match
Best Local Similarity 77.3%; Score 442; DB 12; Length 108;
Matches 82; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 60
DB 1 DIOMTQSPKFLVNSAGRVITTCASQSVNDVAMVYQKQKQSPKLTMYASNRVTGVPD 60
QY 61 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 108
DB 61 RFTSGSGGTDTFTFTISSVQAEADLAIVYCCQDDYSSPFTFGGTGLKLTIR 108

RESULT 15
US-08-779-784-36
; Sequence 36, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
```

1 CORRESPONDENCE ADDRESS: 2  
3 ADDRESSEE: David A. Jackson, Esq.  
4 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
5 STREET: Floor  
6 CITY: Hackensack  
7 STATE: New Jersey  
8 COUNTRY: USA  
9 ZIP: 07601  
10  
11 COMPUTER READABLE FORM:  
12 MEDIUM TYPE: Floppy disk  
13 COMPUTER: IBM PC compatible  
14 OPERATING SYSTEM: PC-DOS/MS-DOS  
15 SOFTWARE: Patentin Release #1.0, Version #1.30  
16  
17 CURRENT APPLICATION DATA:  
18 APPLICATION NUMBER: US/08/779,784  
19 FILING DATE: 07-JAN-1997  
20 CLASSIFICATION: 424  
21  
22 PRIOR APPLICATION DATA:  
23 APPLICATION NUMBER: US 08/692,084  
24 FILING DATE: 08-AUG-1996  
25  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER: US 08/236,520  
28 FILING DATE: 29-APR-1994  
29  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: Jackson Esq., David A.  
32 REGISTRATION NUMBER: 26,742  
33 REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
34 TELECOMMUNICATION INFORMATION:  
35 TELEPHONE: 201-487-5800  
36 TELEFAX: 201-343-1684  
37  
38 INFORMATION FOR SEQ ID NO: 36:  
39 SEQUENCE CHARACTERISTICS:  
40 LENGTH: 128 amino acids  
41 TYPE: amino acid  
42 STRANDEDNESS: single  
43 TOPOLOGY: linear  
44 MOLECULE TYPE: protein  
45  
46 HYPOTHETICAL: NO  
47 FRAGMENT TYPE: N-terminal  
48  
49 ORIGINAL SOURCE:  
50 ORGANISM: Mus musculus  
51  
52 US-08-779-784-36

	Query Match	77.3%	Score 442;	DB 8;	Length 128;
	Blast Local Similarity	79.7%	Pred. No. 6;gc-36;		
Matches	85;	Conservative	8;	Mismatches 15;	Indels 0;
	Gaps				0;
QY	1 D I Q M T G S K F L N A G D E V T I T C R K S O S V S D V A Y W Q Q P R O S P E L I A M W Y S A N R T Y G P D	60			
Dd	21   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :	80			
QY	61 R F T G S G Y G I D F T I T S T Y Q A B D P L A Y F C O O D Y G S P P T T G G G T K L E I K R	108			
Dd	81 R F T G S G S I D F F T I T S S V Q A E D L A Y Y C O O H T T Y L T T R Q A G T R L E I K R	128			

Search completed: November 7, 2003, 08:16:51  
Job time : 95.7343 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 15.8611 Seconds  
(without alignments)  
288,098 Million cell updates/sec

Title: US-09-661-992b-82\_COPY\_135\_242

Perfect score: 572  
Sequence: 1 DIQMTQSPKRLVSAGDRAVT.....QQDYGSPPTFGGTYKLEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310658 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	523	91.4	106	2	US-08-822-830B-4 Sequence 4, Appli
2	523	91.4	106	2	US-08-950-660-4 Sequence 4, Appli
3	523	91.4	106	4	US-09-157-452B-4 Sequence 4, Appli
4	523	91.4	106	5	PCT-US93-00030-4 Sequence 4, Appli
5	523	91.4	106	5	PCT-US93-00924-4 Sequence 4, Appli
6	519	90.7	246	1	US-08-197-834-7 Sequence 7, Appli
7	498	87.1	107	4	US-08-695-632B-6 Sequence 6, Appli
8	474	82.9	105	3	US-09-065-059-17 Sequence 17, Appli
9	466	81.5	128	1	US-08-463-128-10 Sequence 10, Appli
10	466	81.5	128	2	US-08-463-298-10 Sequence 10, Appli
11	466	81.5	128	2	US-08-436-339A-10 Sequence 10, Appli
12	461	80.6	128	1	US-08-463-128-6 Sequence 6, Appli
13	461	80.6	128	2	US-08-463-298-6 Sequence 6, Appli
14	461	80.6	128	1	US-08-436-339A-6 Sequence 6, Appli
15	443	77.4	109	2	US-07-934-373C-5 Sequence 5, Appli
16	443	77.4	109	3	US-08-437-642B-5 Sequence 5, Appli
17	443	77.4	109	4	US-08-146-206C-5 Sequence 5, Appli
18	443	77.4	109	5	PCT-US93-07932-5 Sequence 5, Appli
19	437	76.4	530	4	US-08-840-713-2 Sequence 2, Appli
20	437	76.4	615	4	US-08-840-713-35 Sequence 35, Appli
21	437	76.4	617	1	US-08-840-713-37 Sequence 37, Appli
22	437	76.4	637	1	US-08-235-838-14 Sequence 14, Appli
23	437	76.4	637	2	US-08-465-473B-14 Sequence 14, Appli
24	437	76.4	711	1	US-08-235-838-7 Sequence 7, Appli
25	437	76.4	711	2	US-08-465-473B-7 Sequence 7, Appli
26	435	76.0	250	1	US-08-133-804-2 Sequence 2, Appli
27	435	76.0	250	1	US-08-461-184-8 Sequence 8, Appli

28	435	76.0	250	1	US-08-463-675-8 Sequence 8, Appli
29	435	76.0	250	1	US-08-464-589-8 Sequence 8, Appli
30	435	76.0	250	1	US-08-461-838-2 Sequence 2, Appli
31	435	76.0	250	2	US-08-461-386-2 Sequence 2, Appli
32	432	75.5	241	1	US-08-235-838-5 Sequence 5, Appli
33	432	75.5	241	2	US-08-465-473B-5 Sequence 5, Appli
34	427	74.7	107	4	US-08-525-539A-79 Sequence 79, Appli
35	427	74.7	126	2	US-08-822-028-28 Sequence 28, Appli
36	427	74.7	126	3	US-08-479-285-28 Sequence 28, Appli
37	427	74.7	127	4	US-08-525-539A-49 Sequence 49, Appli
38	423	74.0	106	4	US-09-189-129-4 Sequence 4, Appli
39	423	74.0	107	4	US-08-525-539A-81 Sequence 81, Appli
40	423	74.0	127	4	US-08-525-539A-65 Sequence 65, Appli
41	421	73.6	126	4	US-09-355-925-6 Sequence 6, Appli
42	420.5	73.5	124	3	US-08-466-151-4 Sequence 4, Appli
43	420.5	73.5	124	4	US-08-466-163B-4 Sequence 4, Appli
44	419	73.3	107	3	US-08-554-840-1 Sequence 1, Appli
45	419	73.3	107	4	US-08-925-339-1 Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-08-822-830B-4  
Sequence 4, Application US/08822830B  
Patent No. 5871734  
GENERAL INFORMATION:  
APPLICANT: Lobb, Roy R.; Burkly, Linda C.  
TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking  
TITLE OF INVENTION: Agents  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,830B  
FILING DATE: 03-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/456,193  
FILING DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/374,331  
FILING DATE: 18-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/256,631  
FILING DATE: 12-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00030  
FILING DATE: 12-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/821,768  
FILING DATE: 13-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: BGP-021USCN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-822-830B-4

Query Match 91.4%; Score 523; DB 2; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.3e-46;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOMTOSPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMOTPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61  
QY 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106  
DB 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106

## RESULT 2

US-08-950-660-4  
Sequence 4, Application US/08950660  
Patent No. 5932214

## GENERAL INFORMATION:

APPLICANT: Lobb, Roy R.; Burkly, Linda C.  
TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,660  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/456,124  
FILING DATE:  
APPLICATION NUMBER: US 08/373,857  
FILING DATE: 18-JAN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/284,603  
FILING DATE: 11-AUG-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/000924  
FILING DATE: 02-FEB-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/835,139  
FILING DATE: 12-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: BGP-031USCP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-950-660-4

Query Match 91.4%; Score 523; DB 2; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.3e-46;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOMTOSPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMOTPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61

QY 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106  
DB 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106

## RESULT 3

US-09-157-452B-4  
Sequence 4, Application US/09157452B  
Patent No. 6482409

## GENERAL INFORMATION:

APPLICANT: Burkly, Linda C.  
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE  
FILE REFERENCE: 10274-004003  
CURRENT APPLICATION NUMBER: US/09/157,452B  
CURRENT FILING DATE: 1998-09-21  
PRIORITY APPLICATION NUMBER: US 08/950,660  
PRIORITY FILING DATE: 1997-10-15  
PRIORITY APPLICATION NUMBER: US 08/373,857  
PRIORITY FILING DATE: 1995-01-18  
PRIORITY APPLICATION NUMBER: US 08/284,603  
PRIORITY FILING DATE: 1994-08-11  
PRIORITY APPLICATION NUMBER: PCT/US93/000924  
PRIORITY FILING DATE: 1993-02-02  
PRIORITY APPLICATION NUMBER: US 07/835,139  
PRIORITY FILING DATE: 1992-02-12  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-157-452B-4

Query Match 91.4%; Score 523; DB 4; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1.3e-46;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0

QY 2 IOMTOSPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61  
DB 2 IVMOTPKFLVSAAGRWITTCASQSVSNDAVAMYOQKPGQSPKLLMYASNRRTGVDPDR 61  
QY 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106  
DB 62 FTSGGYGDTFTTISTVQAEADLAVYFCQODYGSPPFTGGGTKLEI 106

## RESULT 4

PCT-US93-00030-4  
Sequence 4, Application PC/TUS9300030

## GENERAL INFORMATION:

APPLICANT: Lobb, Roy R.  
TITLE OF INVENTION: Treatment for Asthma  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Wilcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00030  
FILING DATE: 19930112

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-00924-4

Query Match 91.4%; Score 523; DB 5; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1,3e-46;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61  
DB 2 IVMOTPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61

QY 62 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 106  
DB 62 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 106

## RESULT 5

PCT-US93-00924-4  
Sequence 4, Application PC/TUS9300924  
GENERAL INFORMATION:

APPLICANT: Lobd, Roy R.  
TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00924  
FILING DATE: 19930202  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-00924-4

Query Match 91.4%; Score 523; DB 5; Length 106;  
Best Local Similarity 94.3%; Pred. No. 1,3e-46;  
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOMTQSPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61  
DB 2 IVMOTPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61

DB 2 IVMOTPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61  
QY 62 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 106  
DB 62 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 106

RESULT 6  
US-08-197-834-7  
Sequence 7, Application US/08197834  
Patent No. 5639455

GENERAL INFORMATION:  
APPLICANT: SHIMAMURA, TOSHIRO  
APPLICANT: NAKAZAWA, HARUMI  
APPLICANT: HAMURO, JUNJI  
TITLE OF INVENTION: IMMUNOSUPPRESSANT  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,834  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 028173/1993  
FILING DATE: 17-FEB-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Obion, No. 5639455man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-661-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 246 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-197-834-7

Query Match 90.7%; Score 519; DB 1; Length 246;  
Best Local Similarity 92.5%; Pred. No. 9e-46;  
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTQSPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 60  
DB 2 DIOMTQSPKFLVLSAGDRVTITCKASQSVNDVANYQQRPGSPKLLMYASNRRTGVDR 61

QY 61 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 107  
DB 62 FTGSGYGTDFTTISTVQAEADLAVYFCQDDYRSPPTFGGTXLEI 108

## RESULT 7

US-08-695-692B-6  
Sequence 6, Application US/08695692B  
Patent No. 6514498

GENERAL INFORMATION:  
APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,  
APPLICANT: Johan Hansson, Terje Kalland, Lars

```

1  APPLICANT: Abrahamson and Goren Forsberg
2  TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERNATIGENS
3  TITLE OF INVENTION: AND THEIR USE
4  NUMBER OF SEQUENCES: 24
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
7  STREET: 1177 West Loop South, 10th floor
8  CITY: Houston
9  STATE: TX
10 COUNTRY: USA
11 ZIP: 77027-9095
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/695,692B
19 FILING DATE: August 12, 1996
20 CLASSIFICATION: 530
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 9601245-5
23 FILING DATE: March 29, 1996
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Krieger, Paul E.
26 REGISTRATION NUMBER: 25,886
27 REFERENCE/DOCKET NUMBER: 41986/1
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 713-850-0909
30 TELEFAX: 713-850-0165
31 INFORMATION FOR SEQ ID NO: 6:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 107 amino acids
34 TYPE: amino acid
35 TOPOLOGY: linear
36 MOLECULE TYPE: peptide
37 US-08-695-692B-6
38
39 Query Match 87.1%; Score 498; DB 4; Length 107;
40 Best Local Similarity 87.9%; Pred. No. 5e-44;
41 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
42
43 QY 1 DIGNTOSKPLFLVAGSDRVTTCRASQSVSNDVAMYQOKPGSPPLMYASRYGVDP 60
44 DB 1 DAVNTQPTFLVLSAGDRVITTCRASQSVSNDVAMYQOKPGSPPLLSYSSRYAGVDP 60
45 QY 61 RFTSGGVGTDFFTISTVQAEIDLAVYFCQDYGSPPRTGGGKLEIK 107
46 DB 61 RFTSGGVGTDFFTISTVQAEIDLAVYFCQDYNSPPRTGGGKLEIK 107
47
48 RESULT 8
49 US-09-065-059-17
50 Sequence 17, Application US/09065059
51 Patent No. 6068841
52 GENERAL INFORMATION:
53 APPLICANT: SEINO, Ken-ichi
54 APPLICANT: KAYAGAKI, No. 6068841uniko
55 APPLICANT: YAGITA, Hideo
56 APPLICANT: OKUMURA, KO
57 APPLICANT: NAKAYA, Motomi
58 TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
59 NUMBER OF SEQUENCES: 18
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: Medemott, Will & Emery
62 STREET: 99 Canal Center Plaza
63 CITY: Alexandria
64 STATE: Virginia
65 COUNTRY: USA
66 ZIP: 22314
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: Floppy disk
69 COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-17

Query Match      82.9%; Score 474; DB 3; Length 105;
Best Local Similarity 84.8%; Pred. No. 1,4e-41;
Matches 89; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Cy 1 DIQWTSRPFLLVNSAGDRTVITCKASQSVSNDVAMYQKQSGQSPKLLMAYASNRVTGVPD 60
Db 1 DVMTQTPKPLPVSAGRTVMTCKASQSVGNANVAMYQKQSGSKLLIYTSNRYTGVPD 60
Cy 61 RFTGSGYGTDTFTFTISVQAEIDLAVYFCQGDYSGSPPTFGGATKLE 105
Db 61 RFTGSGSGTDTFTFTISSVQVEDLAVYFCQGHYSSPYTFGSGTKLE 105

RESULT 9
US-08-463-128-10
; Sequence 10, Application US/08463128
; Patent No. 5695755
; GENERAL INFORMATION:
; APPLICANT: Papayannopoulou, Thalia (USA only)
; APPLICANT: Board of Regents, U
; APPLICANT: Washington (except USA)
; TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,128
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11060
; FILING DATE: 11-11-1993
; APPLICATION NUMBER: US 07/977,702
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B173C1P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000

```

TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-463-128-10

Query Match 81.5%; Score 466; DB 1; Length 128;  
Best Local Similarity 80.4%; Pred. No. 1.2e-40;  
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 IGMTQSPKFLVLSAGDRVTITCKASQSVSNDAVYQOKPGQSPKLLMTYASNRVTGVDR 61  
DB 21 IVMTQSPSSLASVGDVTVITCKASQSVTNDVAVYQOKPGKAPKLLIYASNRVTGVDR 80  
QY 62 FTGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 108  
DB 81 FSGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 127

## RESULT 10

US-08-463-298-10  
; Sequence 10, Application US/08463298  
; Patent No. 5624304

GENERAL INFORMATION:  
; APPLICANT: Papayannopoulos, Thalia (USA only)

APPLICANT: Board of Regents, U.

TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463.298

FILING DATE: 05-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11060

FILING DATE: 11-NOV-1993

APPLICATION NUMBER: US 07/977,702

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B173CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-463-298-10

Query Match 81.5%; Score 466; DB 2; Length 128;  
Best Local Similarity 80.4%; Pred. No. 1.2e-40;  
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 IGMTQSPKFLVLSAGDRVTITCKASQSVSNDAVYQOKPGQSPKLLMTYASNRVTGVDR 61  
DB 21 IVMTQSPSSLASVGDVTVITCKASQSVTNDVAVYQOKPGKAPKLLIYASNRVTGVDR 80  
QY 62 FTGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 108  
DB 81 FSGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 127

## RESULT 11

US-08-436-339A-10  
; Sequence 10, Application US/08436339A  
; Patent No. 5843438

GENERAL INFORMATION:

APPLICANT: Papayannopoulos, Thalia (USA only)

APPLICANT: Board of Regents, U.

TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436.339A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/463,128

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: PCT/US93/11060

FILING DATE: 11-11-1993

APPLICATION NUMBER: US 07/977,702

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B173CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-339A-10

Query Match 81.5%; Score 466; DB 2; Length 128;  
Best Local Similarity 80.4%; Pred. No. 1.2e-40;  
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 IGMTQSPKFLVLSAGDRVTITCKASQSVSNDAVYQOKPGQSPKLLMTYASNRVTGVDR 61  
DB 21 IVMTQSPSSLASVGDVTVITCKASQSVTNDVAVYQOKPGKAPKLLIYASNRVTGVDR 80  
QY 62 FTGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 108  
DB 81 FSGSGYGTDFFTTISTVOAEDLAVYFCQODYGSPPFTFGGSKTKEIKR 127

RESULT 12

US-08-463-128-6

Sequence 6, Application US/08463128  
Patent No. 5695755  
GENERAL INFORMATION:  
APPLICANT: Papayannopoulou, Thalia (USA only)  
APPLICANT: Board of Regents, U  
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM  
NUMBER OF SEQUENCES: 10  
CURRENT APPLICATION DATA:  
ADDRESS: c/o FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,128  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11060  
FILING DATE: 11-11-1993  
APPLICATION NUMBER: US 07/977,702  
FILING DATE: 13-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B173CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-128-6

Query Match 80.6%; Score 461; DB 1; Length 128;  
Best Local Similarity 78.7%; Pred. No. 3.7e-40;  
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIQNTOSPKFLVLSAGDRVTITCKASQSVSNDAVWYQKQKPGOSPLMLVYASNRITGVDP 60  
DB 20 DIQNTOSPKFLVLSAGDRVTITCKASQSVSNDAVWYQKQKPGOSPLMLVYASNRITGVDP 79  
QY 61 RFTSGGYGTDFTFTISTVQAEPLAVYFCQDDYSGPPTFGGTTKEIKR 108  
DB 80 RFTSGGYGTDFTFTISTVQAEPLAVYFCQDDYSGPPTFGGTTKEIKR 127

RESULT 13  
US-08-463-298-6  
Sequence 6, Application US/08463298  
Patent No. 5824304  
GENERAL INFORMATION:  
APPLICANT: Papayannopoulou, Thalia (USA only)  
APPLICANT: Board of Regents, U  
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM  
NUMBER OF SEQUENCES: 10  
CURRENT APPLICATION DATA:  
ADDRESS: c/o FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,298  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11060  
FILING DATE: 11-NOV-1993  
APPLICATION NUMBER: US 07/977,702  
FILING DATE: 13-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B173CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-298-6

Query Match 80.6%; Score 461; DB 2; Length 128;  
Best Local Similarity 78.7%; Pred. No. 3.7e-40;  
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIQNTOSPKFLVLSAGDRVTITCKASQSVSNDAVWYQKQKPGOSPLMLVYASNRITGVDP 60  
DB 20 DIQNTOSPKFLVLSAGDRVTITCKASQSVSNDAVWYQKQKPGOSPLMLVYASNRITGVDP 79  
QY 61 RFTSGGYGTDFTFTISTVQAEPLAVYFCQDDYSGPPTFGGTTKEIKR 108  
DB 80 RFTSGGYGTDFTFTISTVQAEPLAVYFCQDDYSGPPTFGGTTKEIKR 127

RESULT 14  
US-08-436-339A-6  
Sequence 6, Application US/08436339A  
Patent No. 5843438  
GENERAL INFORMATION:  
APPLICANT: Papayannopoulou, Thalia (USA only)  
APPLICANT: Board of Regents, U  
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM  
NUMBER OF SEQUENCES: 10  
CURRENT APPLICATION DATA:  
ADDRESS: c/o FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,339A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 15.6702 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_1\_121

Sequence: 1 EVQLVESGGGLVKGPGSLKLT.....KGYGSSFDYWGQGITLTIVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	86.6	122	2 E27888	Ig heavy chain V r
2	546.5	85.0	119	2 F27888	Ig heavy chain V r
3	542	84.3	152	2 B26471	Ig heavy chain pre
4	535.5	83.3	118	2 PH0097	Ig heavy chain V r
5	531	82.6	120	2 S55536	Ig heavy chain V r
6	530.5	82.5	121	2 H27888	Ig heavy chain V r
7	529.5	82.3	118	2 PH0096	Ig heavy chain V r
8	528.5	82.2	121	2 I27887	Ig heavy chain V r
9	524	81.5	120	2 S55537	Ig heavy chain V r
10	518	80.6	120	2 S55539	Ig heavy chain V r
11	515.5	80.2	119	2 B27889	Ig heavy chain V r
12	512.5	79.7	123	2 G27888	Ig heavy chain V r
13	509.5	79.2	254	2 B31790	Ig heavy chain V r
14	508	79.0	119	2 B34352	anti-peptide Fab'
15	508	79.0	119	2 PH0098	Ig heavy chain V r
16	508	79.0	124	2 C27888	Ig heavy chain V r
17	507.5	78.9	123	2 S63597	Ig heavy chain V r
18	507	78.8	120	2 S55538	Ig heavy chain V r
19	506	78.7	138	2 S09258	Ig heavy chain V r
20	504.5	78.5	119	2 D27889	Ig heavy chain V r
21	504.5	78.5	121	2 A27888	Ig heavy chain V r
22	504.5	78.5	139	2 S38808	Ig heavy chain V r
23	503.5	78.3	121	2 H27887	Ig heavy chain V r
24	501.5	78.0	548	2 S38864	Ig epsilon chain C
25	500.5	77.8	121	2 D27888	Ig heavy chain V r
26	498.5	77.5	121	2 B27888	Ig heavy chain V r
27	498	77.4	124	2 I27888	Ig heavy chain V r
28	497.5	77.4	112	2 A27889	Ig heavy chain V r
29	493.5	77.1	121	2 S55540	Ig heavy chain V r

30	492	76.5	117	2 P10249	Ig heavy chain V r
31	490	76.2	119	2 C36005	Ig heavy chain V r
32	490	76.2	119	2 A43413	Ig heavy chain V r
33	488.5	76.0	108	2 PH1010	Ig heavy chain V r
34	488	75.9	118	2 S20641	Ig heavy chain V r
35	487.5	75.8	122	2 PH1537	Ig heavy chain V r
36	485.5	75.5	108	2 P10248	Ig heavy chain V r
37	485	75.4	111	2 PH1007	Ig heavy chain V r
38	485	75.4	117	2 P10252	Ig heavy chain V r
39	484	75.3	142	2 C34903	Ig heavy chain pre
40	483.5	75.2	112	2 S26327	Ig heavy chain V r
41	482	75.0	119	2 S31107	Ig heavy chain V r
42	477	74.2	118	2 E27889	Ig heavy chain V r
43	476	74.0	98	1 HVM596	Ig heavy chain V r
44	474.5	73.8	113	2 S26468	Ig heavy chain V r
45	473.5	73.6	119	2 PH1531	Ig H chain V regio

## ALIGNMENTS

### RESULT 1

E27888

Ig heavy chain V region (H35-C6) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: E27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A>Title: Structural and functional implications of a restricted antibody response

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: E27888

A:Molecule type: DNA

A:Residues: 1-122 <CAT>

A:Experimental source: strain Balb/c

A>Note: This sequence was determined from the germline gene

C:Superfamily: Immunoglobulin V region, immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 557; DB 2; Length 122;

Best Local Similarity 87.7%; Pred. No. 1.5e-41;

Matches 107; Conservative 8; Mismatches 5; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVKGPGSLKLTSCAASGFTFTYTWGVRQTEKLEWVATISSGGSYTY 60

DB 1 DVQLVESGGGLVKGPGSLKLTSCAASGFTFTYTWGVRQTEKLEWVATISSGGSYTY 60

QY 61 PDSVRCGRFTISRDNKNTLYIQMSLSKSEDTAMTYCTPQGSGYRDVAMDYWGQSVT 118

DB 61 PDSVRCGRFTISRDNKNTLYIQMSLSKSEDTAMTYCTPQGSGYRDVAMDYWGQSVT 120

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

QY 119 VS 120

DB 121 VS 122

C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 546.5; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 1.2e-40;  
Matches 105; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 EVQLVSGGGLVPGGSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYTY 60  
DB 1 DVKLVSAGGLVPGGSLKLSCAASGFTSSYMSWVRQTPKRLKLEWVAITSSGGSYTY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCHGYGSSFPYWGQITLV 120  
DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCHGYGSSFPYWGQITLV 119

## RESULT 3

B26471

Ig heavy chain precursor V region (MAK33) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 05-Jun-1988 #sequence\_rev1501 05-Jun-1988 #text\_change 23-Jul-1999

C/Accession: B26471, S70410

R/Bachkel, P.; Huhner-Parajsz, C.; Mattee, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A/Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creating

A/Reference number: A91572; MID:87248058; PMID:3110009

A/Accession: B26471

A/Molecule type: mRNA

A/Residues: 1-152 &lt;BUC&gt;

A/Cross-references: GB:M16163; NID:g195405; PIDN:AAA8292.1; PID:g195406

R/Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 172, 1717-1727, 1990

A/Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary

A/Reference number: S70410; MID:91079775; PMID:2258702

A/Accession: S70410

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-19 &lt;LEB&gt;

A/Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

C/Genetics:

A/Intons: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-152/Product: Ig heavy chain V region MAK33 #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 84.3%; Score 542; DB 2; Length 152;  
Best Local Similarity 84.6%; Pred. No. 3.7e-40;  
Matches 104; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLVSGGGLVPGGSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYTY 60  
DB 20 EVQGVSGGLVPGGSLKLSCAASGFTSDYMWVRQTPKRLKLEWVAITSSGGSYTY 79  
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCH--GYGSSFPYWGQITLV 118  
DB 80 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCARDAVYGYGADAMVWGQITV 139  
QY 119 VSS 121  
DB 140 VSS 142

## RESULT 4

PH0097

Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 15-Jan-1993 #sequence\_rev1501 15-Jan-1993 #text\_change 16-Aug-1996

C/Accession: PH0097

R/Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V

MOL. Immunol. 27, 1029-1038, 1990  
A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporin  
A/Reference number: PH0087; MID:91042649; PMID:2122240

A/Accession: PH0097

A/Molecule type: mRNA

A/Residues: 1-118 &lt;SCH&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F:31-35/Region: complementarity-determining 1

F:50-66/Region: complementarity-determining 2

F:99-105/Region: complementarity-determining 3

Query Match 83.3%; Score 535.5; DB 2; Length 118;  
Best Local Similarity 86.0%; Pred. No. 1e-39;  
Matches 104; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVQLVSGGGLVPGGSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYTY 60  
DB 1 DVKLVSAGGLVPGGSLKLSCAASGFTSSYMSWVRQTPKRLKLEWVAITSSGGSYTY 60

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCHGYGSSFPYWGQITLV 120  
DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCHGYGSSFPYWGQITLV 115

QY 121 S 121  
DB 116 S 116

## RESULT 5

S55536

Ig heavy chain V region pe20 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_rev1501 03-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S55536

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies

A/Reference number: S55528; MID:95239763; PMID:7536850

A/Accession: S55536

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 &lt;BOB&gt;

A/Cross-references: EMBL:X82589; NID:9854304; PIDN:CAA57925.1; PID:9854305

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 82.6%; Score 531; DB 2; Length 120;  
Best Local Similarity 86.7%; Pred. No. 2.6e-39;  
Matches 104; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 VOLVSGGGLVPGGSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYTY 61  
DB 1 VOLVSGGGLVPGGSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYTY 60  
QY 62 DSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCTRDGCHGYGSSFPYWGQITLV 121  
DB 61 DSVGRFTISRDNKNTLYLQMSLSKSEPTAMYYCARLYDYDPVMDYWGQITV 120

## RESULT 6

H27888

Ig heavy chain V region (H37-40) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_rev1501 15-Dec-1988 #text\_change 16-Aug-1996

C/Accession: H27888

R/Caton, A.O.; Brownlee, G.G.; Staudt, L.M.; Gearhart, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response

A/Reference number: A91043; MID:86300658; PMID:2427335

A/Accession: H27888  
A/Molecule type: DNA  
A/Residues: 1-121 <CAT>  
A/Experimental source: strain Balb/c  
A/Note: this sequence was determined from the germ-line gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 530.5; DB 2; Length 121;  
Best Local Similarity 83.6%; Pred. No. 2.9e-39;  
Matches 102; Conservative 9; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 60  
DB 1 EVOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 118  
DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 118  
QY 119 VS 120  
DB 120 VS 121

## RESULT 7

PH0096  
Ig heavy chain V region (anti-cyclosporin A) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996  
C/Accession: PH0096  
R/Schmitter, D.; Pech, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V  
Kotl. Immunol. 27, 1029-1038, 1990  
A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
A/Reference number: PH0087; MUID:91042649; PMID:2122240  
A/Accession: PH0096  
A/Molecule type: mRNA  
A/Residues: 1-118 <SCH>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-66/Region: complementarity-determining 2  
F:99-105/Region: complementarity-determining 3

Query Match 82.3%; Score 529.5; DB 2; Length 118;  
Best Local Similarity 83.5%; Pred. No. 3.4e-39;  
Matches 101; Conservative 10; Mismatches 5; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 60  
DB 1 DVKLVESGGGLVYKPGGSLKLSCAASRFTFTSSISMSWRQTEPEKRLWVATISSGGSYYTY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 120  
DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 118  
QY 121 S 121  
DB 116 S 116

## RESULT 8

127887  
Ig heavy chain V region (H37.45) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C/Accession: 127887  
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A/Title: Structural and functional implications of a restricted antibody response to a d

A/Reference number: A91043; MUID:86300658; PMID:2427335  
A/Accession: 127887  
A/Molecule type: DNA  
A/Residues: 1-121 <CAT>  
A/Experimental source: strain Balb/c  
A/Note: this sequence was determined from the germ-line gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 528.5; DB 2; Length 121;  
Best Local Similarity 82.9%; Pred. No. 4.3e-39;  
Matches 102; Conservative 7; Mismatches 9; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 60  
DB 1 EVOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 117  
DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 118  
QY 118 TVS 120  
DB 119 TVS 121

## RESULT 9

S55537  
Ig heavy chain V region pe21 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S55537  
R/Boettger, V.; Boettger, A.; Lane, B.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antipep  
tides in the variable region genes.  
A/Reference number: S55528; MUID:95239763; PMID:7536850  
A/Accession: S55537  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-120 <BOB>  
C/Cross-references: EMBL:X82590; NID:9854306; PIDN:CAAS7926.1; PID:9854307  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 524; DB 2; Length 120;  
Best Local Similarity 85.8%; Pred. No. 1e-38;  
Matches 103; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 2 VOLVESGGGLVYKPGGSLKLSCAASGFTFTYMSWRQTEPEKRLWVATISSGGSYYTY 61  
DB 1 VOLVESGGGLVYKPGGSLKLSCAASRFTFTSSISMSWRQTEPEKRLWVATISSGGSYYTY 60  
QY 62 DSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 121  
DB 61 DSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLT 120

## RESULT 10

S55539  
Ig heavy chain V region pe24 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S55539  
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antipep  
tides in the variable region genes.  
A/Reference number: S55528; MUID:95239763; PMID:7536850  
A/Accession: S55539

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
A:Cross-references: EMBL:X82593; NID:g854312; PIRN:CAA57929.1; PID:g854313  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 518; DB 2; Length 120;  
Best Local Similarity 84.2%; Pred. No. 3.5e-38;  
Matches 101; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 2 VOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 61  
DB 1 VOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
QY 62 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 121  
DB 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 120

## RESULT 11

B27889  
Ig heavy chain V region (H146-2483) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: B27889  
R:Atton, A.U.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986

A>Title: Structural and functional implications of a restricted antibody response to a  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: B27889  
A:Molecule type: DNA  
A:Residues: 1-119 <CAT>

A:Experimental source: strain Balb/c  
A>Note: this sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 515.5; DB 2; Length 119;  
Best Local Similarity 83.6%; Pred. No. 5.7e-38;  
Matches 102; Conservative 3; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
DB 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
QY 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 118  
DB 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 117

QY 119 VS 120  
DB 118 VS 119

## RESULT 12

G27888  
Ig heavy chain V region (H28-A2) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: G27888  
R:Atton, A.U.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A>Title: Structural and functional implications of a restricted antibody response to a  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: G27888  
A:Molecule type: DNA  
A:Residues: 1-123 <CAT>

A:Experimental source: strain Balb/c  
A>Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 512.5; DB 2; Length 123;  
Best Local Similarity 79.7%; Pred. No. 1.1e-37;  
Matches 98; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
DB 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
QY 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 117  
DB 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 120  
QY 118 TVS 120  
DB 121 TVS 123

## RESULT 13

B31780  
Ig heavy chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-May-1997  
C:Accession: B31780  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson  
J. Biol. Chem. 263, 17100-17105, 1988  
A>Title: Preliminary crystallographic data, primary sequence, and binding data f  
A:Reference number: A92686; MUID:89034213; PMID:3162835  
A:Accession: B31780  
A:Molecule type: mRNA  
A:Residues: 1-254 <SCH>

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 509.5; DB 2; Length 254;  
Best Local Similarity 81.0%; Pred. No. 4.2e-37;  
Matches 98; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
DB 1 EVOLVESGGGLVPRGSSLKLSCAASGFTFTYMSWRQTPERLEWATISSGGSYYTP 60  
QY 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 120  
DB 61 PSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGSHGYSFDPYWGQGTTLTVS 119

QY 121 S 121  
DB 120 A 120

## RESULT 14

B34353  
anti-peptide Fab' B3132 heavy chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 23-Jul-1999  
C:Accession: B34353  
R:Stura, E.A.; Stanfield, R.L.; Fleiser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner  
U. Biol. Chem. 264, 15721-15725, 1989  
A>Title: Preliminary crystallographic data and primary sequence for anti-peptide  
A:Reference number: A34353; MUID:89359424; PMID:2504725  
A:Accession: B34353  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <STU>

A:Cross-references: GB:M29252; NID:g195657; PIRN:AAA38388.1; PID:g195658  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 508; DB 2; Length 119;  
 Best Local Similarity 81.8%; Pred. No. 2.5e-37;  
 Matches 101; Conservative 6; Mismatches 9; Indels 8; Gaps 2;

```

QY      1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSMVRQTPKRLKLEWYATISGGSYTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLVESGGDLVPGGSLKLSCAASGFTSRCAASGFTSRQTPKRLKLEWYAGISGGSYTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 PDVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYGSS--FDYWGQGTTL 117
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 PDVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYGSS--FDYWGQGTTL 115
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      118 TVSS 121
        |||
Db      116 TVSS 119
        |||

```

## RESULT 15

PH0098

Ig heavy chain V region (anti-cyclosporin G) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996

C/Accession: PH0098

R/Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Queheniaux, V.F.J.; V

Mol. Immunol. 27, 1029-1038, 1990

A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.

A/Reference number: PH0087; MUID:91042649; PMID:2122240

A/Accession: PH0098

A/Molecule type: mRNA

A/Residues: 1-119 &lt;SCH&gt;

A/Note: the authors translated the codon GNG for residue 104 as Gly

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F/31-35/Region: complementarity-determining 1

F/50-66/Region: complementarity-determining 2

F/99-106/Region: complementarity-determining 3

## Query Match

79.0%; Score 508; DB 2; Length 119;

Best Local Similarity 81.8%; Pred. No. 2.5e-37;

Matches 99; Conservative 7; Mismatches 11; Indels 4; Gaps 1;

```

QY      1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSMVRQTPKRLKLEWYATISGGSYTY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 DVKHMESGGGLVPGGSLKLSCAASGFTSTYTMVMVRQTPKRLKLEWYATISTGDSITY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 PDVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYGSSFDYWGQGTTL 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 PDVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYGSSFDYWGQGTTL 116
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 $ 121
        |
Db      117 $ 117

```

Search completed: November 7, 2003, 07:36:19  
 Job time : 15.7702 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 8.72363 Seconds  
(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_1\_121

Perfect score: 643  
Sequence: 1 EVQLVESGGGLVPGGSLKL.....HGVGSSFDVWGQITLVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	476	74.0	98 1 HV57_MOUSE	P18528 mus musculus
2	466	72.5	117 1 HV55_MOUSE	P18526 mus musculus
3	462.5	71.9	136 1 HV16_MOUSE	P01783 mus musculus
4	461	71.7	117 1 HV54_MOUSE	P18525 mus musculus
5	461	71.7	117 1 HV56_MOUSE	P18529 mus musculus
6	457.5	71.2	97 1 HV58_MOUSE	P18527 mus musculus
7	441.5	68.7	126 1 HV3K_HUMAN	P01772 homo sapien
8	437	68.0	117 1 HV59_MOUSE	P18530 mus musculus
9	430.5	67.0	122 1 HV3G_HUMAN	P01768 homo sapien
10	430	66.9	117 1 HV53_MOUSE	P18524 mus musculus
11	424	65.9	121 1 HV3F_HUMAN	P01771 homo sapien
12	415.5	64.6	119 1 HV38_MOUSE	P01808 mus musculus
13	414	64.4	118 1 HV39_MOUSE	P01809 mus musculus
14	410.5	63.8	116 1 HV3I_HUMAN	P01781 homo sapien
15	407.5	63.4	111 1 HV35_MOUSE	P01804 mus musculus
16	407	63.3	117 1 HV3C_HUMAN	P01764 homo sapien
17	405.5	63.1	122 1 HV3A_HUMAN	P01762 homo sapien
18	402.5	62.6	122 1 HV3H_HUMAN	P01769 homo sapien
19	402	62.5	115 1 HV3F_HUMAN	P01767 homo sapien
20	401.5	62.4	119 1 HV37_MOUSE	P01807 mus musculus
21	400.5	62.3	114 1 HV3B_HUMAN	P01801 mus musculus
22	400	62.2	144 1 HV26_MOUSE	P01795 mus musculus
23	398	61.9	115 1 HV32_MOUSE	P01801 mus musculus
24	398	61.9	117 1 HV02_CANFA	P01785 canis fam1
25	397	61.7	123 1 HV25_MOUSE	P01794 mus musculus
26	395	61.4	117 1 HV41_MOUSE	P01811 mus musculus
27	393.5	61.2	116 1 HV05_CARAU	P19181 carassius a
28	393	61.1	119 1 HV3I_HUMAN	P01770 homo sapien
29	392	61.0	115 1 HV3D_HUMAN	P01765 homo sapien
30	391.5	60.9	119 1 HV40_MOUSE	P01810 mus musculus
31	391	60.8	113 1 HV27_MOUSE	P01796 mus musculus
32	391	60.8	113 1 HV30_MOUSE	P01793 mus musculus
33	391	60.8	123 1 HV24_MOUSE	P01793 mus musculus

34	390	60.7	115 1 HV33_MOUSE	P01802 mus musculus
35	390	60.7	120 1 HV3E_HUMAN	P01766 homo sapien
36	389	60.5	123 1 HV18_MOUSE	P01787 mus musculus
37	388	60.3	113 1 HV31_MOUSE	P01800 mus musculus
38	387.5	60.3	119 1 HV3M_HUMAN	P01774 homo sapien
39	387.5	60.3	122 1 HV20_MOUSE	P01789 mus musculus
40	385	59.9	113 1 HV28_MOUSE	P01797 mus musculus
41	385	59.9	123 1 HV19_MOUSE	P01788 mus musculus
42	385	59.9	123 1 HV23_MOUSE	P01792 mus musculus
43	384.5	59.8	122 1 HV21_MOUSE	P01790 mus musculus
44	384	59.7	119 1 HV3L_HUMAN	P01773 homo sapien
45	382.5	59.5	120 1 HV3U_HUMAN	P01782 homo sapien

## ALIGNMENTS

## RESULT 1

ID	HV57_MOUSE	STANDARD;	PRT;	98 AA.
AC	P18528;			
DT	01-NOV-1990 (Rel. 16, Created)			
DR	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V region 6.96.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/CJ;			
RX	MEDLINE=89279149; PubMed=2499654;			
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;			
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";			
RT	J. Exp. Med. 169:2007-2019(1989).			
CC	-1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; J070501; HVMS96.			
DR	HSSP; P01772; 2F84.			
DR	InterPro; IPR007110; IG-1like.			
DR	InterPro; IPR003006; IG-MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; 1g; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG-LIKE; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 >98 IG-LIKE.			
FT	NON TER 98			
SQ	SEQUENCE 98 AA; 11007 MW; B8644FFP2F8F95B CRC64;			
Query Match				
Best Local Similarity 92.9%; Pred. No. 1.2e-40;				
Matches 91; Conservative 1; Mismatches 6; Indels 0; Gaps 0;				
Qy	1 EVQLVESGGGLVPGGSLKSCASGFFPSYTMNQOTPEKRLKEMVATISGGSYTY 60			
Db	1 EVQLVESGGGLVPGGSLKSCASGFFPSYTMNQOTPEKRLKEMVATISGGSYTY 60			
Qy	61 PDSVGRFTISRDNAKNTLYIQMSISKEPDAMYYCTR 98			
Db	61 PDSVGRFTISRDNAKNTLYIQMSISKEPDAMYYCAR 98			
RESULT 2				
ID	HV55_MOUSE	STANDARD;	PRT;	117 AA.
AC	P18526;			
DT	01-NOV-1990 (Rel. 16, Created)			
DR	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region 345 precursor.			

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA MEDLINE=88279149; PubMed=2499654;
RX Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
FT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J05052; HVMS34.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627AC9A99A CRC64;

Query Match 72.5%; Score 466; DB 1; Length 117;
Best Local Similarity 90.8%; Pred. No. 1,4e-39;
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLKSCASGFTSTYMSWVRQTPKRLKLEWVAITISGGSSTYY 60
DB 20 EVQLVESGGGLVPGGSLKSCASGFTSTYMSWVRQTPKRLKLEWVAITISGGSSTYY 79
QY 61 PDVVRGFTISRDNKNTLYLQMSLSKSEDTAMYYCTR 98
DB 80 PDVVRGFTISRDNKNTLYLQMSLSKSEDTAMYYCAR 117

RESULT 3
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB 15-SEP-2003 (Rel. 42, Last annotation update)
DB 15 heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA MEDLINE=81234548; PubMed=6788376;
RX Bochsweil A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
FT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN 12
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adelhubo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----

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CC -----
DR EMBL: J05222; AAD15290.1; -.
DR PIR: E90809; GIMS21.
DR PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 1
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAD (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A9EBDBF016 CRC64;

Query Match 71.9%; Score 462.5; DB 1; Length 136;
Best Local Similarity 73.6%; Pred. No. 3,6e-39;
Matches 89; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKSCASGFTSTYMSWVRQTPKRLKLEWVAITISGGSSTYY 60
DB 17 EVQLVESGGGLVPGGSLKSCASGFTSTYMSWVRQTPKRLKLEWVAITISGGSSTLYH 76
QY 61 PDVVRGFTISRDNKNTLYLQMSLSKSEDTAMYYCTRQGHGSSPDYWGQGTLLTVS 120
DB 77 ADTVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARAGNVPY-YADYWGQGTSTVTS 135
QY 121 S 121
DB 136 S 136

RESULT 4
HV54_MOUSE STANDARD; PRT; 117 AA.
ID HV54_MOUSE
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB 15-JUL-1999 (Rel. 38, Last annotation update)
DB 15 heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RX Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
FT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; Ig_LIKE: 1.
KW Immunoglobulin V region; signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 71.7%; Score 461; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 4.3e-39;
Matches 87; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 60
DB 20 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 79
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTR 98
DB 80 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCAR 117

RESULT 5
HV56 MOUSE STANDARD; PRT; 117 AA.
ID HV56_MOUSE
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RT J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC PIR: J0506; HYMS57.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_1-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; Ig_LIKE: 1.
KW Immunoglobulin V region; signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 71.7%; Score 461; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 4.3e-39;
Matches 87; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 1 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 60
DB 20 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 79
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTR 98
DB 80 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCAR 117

RESULT 6
HV56 MOUSE STANDARD; PRT; 97 AA.
ID HV56_MOUSE
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RT J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC PIR: J0504; HYMS91.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_1-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; Ig_LIKE: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 IG-LIKE.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 71.2%; Score 457.5; DB 1; Length 97;
Best Local Similarity 89.8%; Pred. No. 7.8e-39;
Matches 88; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 60
DB 1 EVQLVESGGGLVPGGSLKLTSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSYYTY 59
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTR 98
DB 60 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCAR 97

RESULT 7
HV3K HUMAN STANDARD; PRT; 126 AA.
ID HV3K_HUMAN
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;

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CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUM.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 67.0%; Score 430.5; DB 1; Length 122;
Best Local Similarity 66.4%; Pred. No. 4.9e-36;
Matches 81; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 60
DB 1 QVBLVESGGGVAVZQSRSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 60
QY 61 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTRDG-GHGSGSPDYWGQGTLLTV 119
DB 61 ABSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTRDG-GHGSGSPDYWGQGTLLTV 120
QY 120 SS 121
DB 121 SS 122

RESULT 10
HV3J_MOUSE STANDARD; PRT; 117 AA.
ID HV3J_MOUSE
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S.; Malipiero U.V.; LeDeque S.G.; Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC PIR; J10503; HWSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

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FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 66.9%; Score 430; DB 1; Length 117;
Best Local Similarity 64.7%; Pred. No. 5.2e-36;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 60
DB 20 DVTLVESGGGLVLTGGSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 79
QY 61 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTR 98
DB 61 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTR 117
QY 80 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTR 117
DB 80 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTR 117

RESULT 11
HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HIL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H.; Lopez de Castro J.A.; Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT B-lymphocyte immunoglobulin IgG H.L."
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02054; G1HUL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC536108F5DAB CRC64;

Query Match 65.9%; Score 424; DB 1; Length 121;
Best Local Similarity 66.1%; Pred. No. 2.1e-35;
Matches 80; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 60
DB 1 QVBLVESGGGVAVZQSRSLKLSCAAGFTSTYMSWVRQPEKRLKLVAVATISSGGSYTY 60
QY 61 PDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTRDG-GHGSGSPDYWGQGTLLTVS 120
DB 61 GDSVKGRTISRDNANKTYLYQMSLSKSEDTAMYCTRDG-GHGSGSPDYWGQGTLLTVS 120
QY 121 S 121
DB 121 S 121

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RESULT 12
HV38 MOUSE STANDARD; PRT; 119 AA.
ID HV38 MOUSE STANDARD; PRT; 119 AA.
AC P01809;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region T501.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02078; AVMS16.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00B8 CRC64;

Query Match 64.4%; Score 415.5; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.5e-34;
Matches 81; Conservative 13; Mismatches 24; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLKSCAASGFTSTYMSWVRQTPKRLKLVATISSGGSITTY 60
DB 1 EVKLLESGGGLVQPGGSLKSCAASGFTSTYMSWVRQTPKRLKLVATISSGGSITTY 60
QY 61 PDVVRGFTISRDNKNTLYLQMSLKSEDTMYCTRDGCHGYGSSFDYWGQGITLTVS 120
DB 61 TPSLKDRTISRDNKNTLYLQMSKVRSEDTALYCARLGYYG---FDYWGAGITVTVS 117
QY 121 S 121
DB 118 S 118

RESULT 13
HV39 MOUSE STANDARD; PRT; 118 AA.
ID HV39 MOUSE STANDARD; PRT; 118 AA.
AC P01809;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region X24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and

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RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; P01394; AVMSX2.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 118
SQ SEQUENCE 118 AA; 13105 MW; BB16A2DB677EF17F CRC64;

Query Match 64.4%; Score 414; DB 1; Length 118;
Best Local Similarity 67.8%; Pred. No. 2.1e-34;
Matches 82; Conservative 12; Mismatches 23; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLKSCAASGFTSTYMSWVRQTPKRLKLVATISSGGSITTY 60
DB 1 EVKLLESGGGLVQPGGSLKSCAASGFTSTYMSWVRQTPKRLKLVATISSGGSITTY 59
QY 61 PDVVRGFTISRDNKNTLYLQMSLKSEDTMYCTRDGCHGYGSSFDYWGQGITLTVS 120
DB 60 TPSLKDRTISRDNKNTLYLQMSKVRSEDTALYCARLGYYG---FDYWGAGITLTVS 116
QY 121 S 121
DB 117 S 117

RESULT 14
HV37 HUMAN STANDARD; PRT; 116 AA.
ID HV37 HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete IgM-molecule."
RT Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; R:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV_1.

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Search completed: November 7, 2003, 07:28:08  
 Job time : 9.72363 secs

DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 116 116  
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAA1282 CRC64;

Query Match 63.4%; Score 410.5; DB 1; Length 116;  
 Best Local Similarity 67.8%; Pred. No. 4.5e-34;  
 Matches 82; Conservative 10; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVKGSGSLKSCAAGFTFTYMSWVRQPEKRLKLEWATISGGSYTY 60  
 DB 1 EVOLVESGGDLVQFGSLRISCASGFBFLQMTWVRQAPGKLEWATIKBGSZBY 60

QY 61 PDSVRGFTISRDNARKTYLQMSLSKSEPTANYCTRDGHHGYSSFDYWGQTLTVS 120  
 DB 61 VDSVGRFTISRDNARKSLYLQMSLSRVEDTALYCARWGSG---DYWGQTLTVS 115

QY 121 S 121  
 DB 116 T 116

RESULT 15  
 HV35 MOUSE STANDARD; PRT; 111 AA.

AC P01804;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG heavy chain V-III region HPC76 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

KN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81013937; Pubmed=6251474;  
 RA Bernard O., Gough N.M.;  
 RT "Nucleotide sequence of immunoglobulin heavy chain joining segments  
 between translocated VH and mu constant regions genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C  
 REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE  
 CC CORRESPONDING PORTION OF THE MOUSE MOPC 104B MU CHAIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region.

FT NON\_TER 1 1  
 FT DOMAIN <1 110 IG-LIKE.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12304 MW; 0ED598EC7348056A CRC64;

Query Match 63.4%; Score 407.5; DB 1; Length 111;  
 Best Local Similarity 66.7%; Pred. No. 8.5e-34;  
 Matches 78; Conservative 17; Mismatches 15; Indels 7; Gaps 2;

QY 6 ESQGGVLRFGSLKSCAAGFTFTYMSWVRQPEKRLKLEWATISGGSY-TYYPDSV 64  
 DB 1 ESQGGVLRFGSLKSCAAGFTFTYMSWVRQPEKRLKLEWATISGGSY-TYYPDSV 60

QY 65 RGRFTISRDNARKTYLQMSLSKSEPTANYCTRDGHHGYSSFDYWGQTLTVS 121  
 DB 61 KGRFTISRDSKSSVYLQMNLAEDTGYYCTRPGVP-----DYWGQTLTVS 111

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 39.9025 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_1\_121

Perfect score: 643

Sequence: 1 EVGLVSSGGGLVPRGSLKSLK.....HGYSSEFDYWGQTTIVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563.5	87.6	487	11	Q99KA4
2	540	84.0	119	11	Q920E7
3	488	75.9	486	11	Q91207
4	474	73.7	479	11	Q91WP5
5	465.5	72.4	473	11	Q91205
6	464	72.2	480	11	Q91XE1
7	462.5	71.9	471	4	Q8TC77
8	454.5	70.7	494	4	Q96KE8
9	452	70.3	116	4	Q9UL93
10	448.5	69.8	597	4	Q96BB9
11	442	68.7	613	4	Q8W0X1
12	439.5	68.4	113	4	Q9UL90
13	437.5	68.0	147	4	Q9Y509
14	432.5	67.3	437	11	Q9UL91
15	431	67.0	121	4	Q9UL94
16					Q9UL71 homo sapien

17	430	66.9	493	4	Q8NCL6	Q8NCL6 homo sapien
18	427	66.4	499	4	Q8N5K4	Q8N5K4 homo sapien
19	426.5	66.3	118	4	Q9UL72	Q9UL72 homo sapien
20	425.5	66.2	122	4	Q9UL84	Q9UL84 homo sapien
21	425.5	66.2	573	4	Q8M038	Q8M038 homo sapien
22	412.5	64.2	112	4	Q9H0C1	Q9H0C1 homo sapien
23	404.5	62.9	469	11	Q8R3V9	Q8R3V9 mus musculus
24	401	62.4	131	4	Q9UL88	Q9UL88 homo sapien
25	396.5	61.7	298	11	Q9QYF0	Q9QYF0 mus musculus
26	390	60.7	95	4	Q9UL86	Q9UL86 homo sapien
27	377.5	58.7	464	11	Q8VBA0	Q8VBA0 mus musculus
28	361	56.1	521	4	Q8N4V9	Q8N4V9 homo sapien
29	356.5	55.4	143	11	Q924F9	Q924F9 mus musculus
30	350	54.4	112	4	Q9UG23	Q9UG23 homo sapien
31	349.5	54.4	124	6	Q9N0W4	Q9N0W4 cryocollagus
32	348.5	54.2	124	4	Q9UL92	Q9UL92 homo sapien
33	346.5	53.9	124	6	Q9N0W6	Q9N0W6 cryocollagus
34	338	52.6	125	4	Q9UL95	Q9UL95 mus musculus
35	335.5	52.2	143	11	Q924Q0	Q924Q0 mus musculus
36	333	51.8	104	4	Q9UL87	Q9UL87 homo sapien
37	333	51.8	481	11	Q91WT1	Q91WT1 mus musculus
38	332	51.6	117	11	Q9QXF0	Q9QXF0 mus musculus
39	332	51.6	146	11	Q924R8	Q924R8 mus musculus
40	329.5	51.2	145	11	Q924O7	Q924O7 mus musculus
41	329	51.2	468	11	Q99L31	Q99L31 mus musculus
42	327.5	50.9	118	11	Q92L04	Q92L04 mus musculus
43	327.5	50.9	482	11	Q8K172	Q8K172 mus musculus
44	327	50.9	473	11	Q9DL14	Q9DL14 mus musculus
45	326	50.7	119	4	Q9UL94	Q9UL94 homo sapien

## ALIGNMENTS

RESULT 1  
Q99KA4 PRELIMINARY; PRT; 487 AA.

AC Q99KA4; 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 52.6 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_taxonomy=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC004786; AAH04786.1; -  
DR HSSP; P01810; 2PB.  
DR InterPro; IPR007110; IG\_11ke.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_4.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00230; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 87.6%; Score 563.5; DB 11; Length 487;  
Best Local Similarity 87.9%; Pred. No. 1e-47;  
Matches 109; Conservative 4; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVGLVSSGGGLVPRGSLKSLKCAAGFTSTYMSVWRPPEKRLMVATISSGGSYTY 60  
DB 20 EVGLVSSGGGLVPRGSLKSLKCAAGFTSTYMSVWRPPEKRLMVATISSGGSYTY 79  
QY 61 PDVSKRFTTISRDNANNTLYLQSSLSKSDTANYCTRD-QGNGYG--SSFDYWGQTT 117  
DB 80 PDVSKRFTTISRDNANNTLYLQSSLSKSDTANYCTRD-QGNGYG--SSFDYWGQTT 139

QY 118 TVSS 121  
Db 140 TVSS 143

## RESULT 2

Q920E7 PRELIMINARY; PRT; 119 AA.

AC Q920E7; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Pterin-mimicking anti-idiotope heavy chain variable region  
DE (fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the idiotope of Pterin-mimicking Antibodies Expressed  
in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB079337; AA09421.1; -  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS00835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 84.0%; Score 540; DB 11; Length 119;  
Best Local Similarity 86.0%; Pred. No. 4e-46; Mismatches 6; Indels 2; Gaps 1;  
Matches 104; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLIKSCAAGFTFTSTYMSWVROTPERLEWVATISSGGSYYT 60  
Db 1 EVOLVESGGDLVPGGSLIKSCAAGFTFTSYGMSWVRQTPERLEWVATISSGGSYYT 60  
QY 61 PSVVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGCGHGXSSPPYMGQTTLVTS 120  
Db 61 PSVVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGHGDYDVG--FAYWQQTGLVTVS 118  
QY 121 S 121  
Db 119 A 119

## RESULT 3

Q91207 PRELIMINARY; PRT; 486 AA.

AC Q91207; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 52.7 KDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010324; AA010324.1; -  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG; 4.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS00835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 2.  
KW Hypothetical protein  
SQ SEQUENCE 486 AA; 52682 MW; 4BFB85125D8A70B CRC64;

Query Match 75.9%; Score 488; DB 11; Length 486;  
Best Local Similarity 77.4%; Pred. No. 3.2e-40; Mismatches 96; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLIKSCAAGFTFTSTYMSWVROTPERLEWVATISSGGSYYT 60  
Db 20 EVOLVESGGGLVPGGSLIKSCVSGFTSYDMSWVRQTPERLEWVAITSGGNTYY 78  
QY 61 PSVVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGDGHG---GSPDYMGQTTLV 117  
Db 79 PSVVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGDGHG---GSPDYMGQTTLV 118  
QY 118 TVSS 121  
Db 139 TVSS 142

## RESULT 4

Q91WPS PRELIMINARY; PRT; 479 AA.

AC Q91WPS; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 51.6 KDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013656; AA013656.1; -  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 4.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS00835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 2.  
KW Hypothetical protein  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match 73.7%; Score 474; DB 11; Length 479;  
Best Local Similarity 75.2%; Pred. No. 7.8e-39; Mismatches 91; Conservative 9; Mismatches 15; Indels 6; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLIKSCAAGFTFTSTYMSWVROTPERLEWVATISSGGSYYT 60  
Db 20 EVOLVESGGGLVPGGSLIKSCAAGFTFTSYGMSWVRQTPERLEWVATISSGGSYYT 79  
QY 61 PSVVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGDGHGSSPDYMGQTTLVTS 120  
Db 80 SDYVRGFTISRDNKNTLYLQMSLSKSDPTMYCTRGDGHGSSPDYMGQTTLVTS 133  
QY 121 S 121  
Db 134 S 134

## RESULT 5

Q91Z05 PRELIMINARY; PRT; 473 AA.

ID Q91Z05;

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DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR WGD; MG1; 214367; AB044919.
DR InterPro; IPR000345; Cytochrome_bind.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match
Best Local Similarity 72.4%; Score 465.5; DB 11; Length 473;
Best Local Similarity 75.2%; Pred. No. 5.4e-38;
Matches 91; Conservative 10; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKSCAASGFTSTYTWMSWVRQTEPEKRLIEWATISSGGSYYTY 60
DB 20 EVQLVESGGGLVPGGSLKSCAASGFTSDYGMHWRAPEKGLIEWATISSGGSYYTY 79
QY 61 PDVYRGFTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 120
DB 80 ADVYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 136
QY 121 S 121
DB 137 S 137

RESULT 6
Q91XEL PRELIMINARY; PRT; 480 AA.
ID Q91XEL;
AC Q91XEL;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Unknown (Protein for IMAGE:4224494) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010798; AAH10798.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW NON TER
SQ
SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match
Best Local Similarity 72.2%; Score 464; DB 11; Length 480;

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Best Local Similarity 75.2%; Pred. No. 7.8e-38;
Matches 91; Conservative 13; Mismatches 13; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKSCAASGFTSTYTWMSWVRQTEPEKRLIEWATISSGGSYYTY 60
DB 19 DVKLVESGGGLVPGGSLKSCAASGFTFSYSWVRQTEPEKRLIEWATISSGGSYYTY 78
QY 61 PDVYRGFTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 120
DB 79 PDSMKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 134
QY 121 S 121
DB 135 S 135

RESULT 7
Q8TC77 PRELIMINARY; PRT; 471 AA.
ID Q8TC77;
AC Q8TC77;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

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Query Match
Best Local Similarity 71.9%; Score 462.5; DB 4; Length 471;
Best Local Similarity 71.2%; Pred. No. 1.1e-37;
Matches 89; Conservative 16; Mismatches 13; Indels 7; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKSCAASGFTSTYTWMSWVRQTEPEKRLIEWATISSGGSYYTY 60
DB 20 EVQLVESGGGLVPGGSLKSCAASGFTFSYSWVRQTEPEKRLIEWATISSGGSYYTY 79
QY 61 PDVYRGFTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 116
DB 80 ADVYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGYSFDPYMGQGTTLTVS 136
QY 117 LTSS 121
DB 137 VTSS 141

RESULT 8
Q96K68 PRELIMINARY; PRT; 494 AA.
ID Q96K68;
AC Q96K68;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Iosgai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Wakamabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,  
 RA Ninomiya K., Iwayanagi T.;  
 RT "MEDO human cDNA sequencing project";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK027379; BAB55072.1; -.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_4.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AE85AE4C0E CRC64;

Query Match 70.3%; Score 454.5; DB 4; Length 494;  
 Best Local Similarity 71.8%; Pred. No. 7.1e-37;  
 Matches 89; Conservative 13; Mismatches 17; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLKLSCAASGFTSTYTMWVRQTPKRLKLEWVATISSGGSYYTP 60  
 DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTSTYAMNVRQAPGKLEWVATISSGGSYYTP 79  
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHG---YGSSEPDYWGCGTTL 117  
 DB 80 RDSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHG---YGSSEPDYWGCGTTL 137  
 QY 118 TVSS 121  
 DB 138 TVSS 141

RESULT 9  
 Q9UL93 PRELIMINARY; PRT; 116 AA.  
 ID Q9UL93;  
 AC Q9UL93;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=98277139; Pubmed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035021; AAD56257.1; -.  
 DR HSP; P01772; 3F84.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IgV\_1.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1  
 FT NON\_TER 116  
 SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 70.3%; Score 452; DB 4; Length 116;  
 Best Local Similarity 73.3%; Pred. No. 2.2e-37;  
 Matches 88; Conservative 10; Mismatches 18; Indels 4; Gaps 1;

QY 2 VOLVSSGGGLVPGGSLKLSCAASGFTSTYTMWVRQTPKRLKLEWVATISSGGSYYTP 61  
 DB 1 VOLVSSGGGLVPGGSLRLSCAASGFTSTYAMNVRQAPGKLEWVATISSGGSYYTP 60  
 QY 62 DSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHGYSFPYWGCGTTLTVSS 121  
 DB 61 DSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHGYSFPYWGCGTTLTVSS 116

RESULT 10  
 Q96BB9 PRELIMINARY; PRT; 597 AA.  
 ID Q96BB9;  
 AC Q96BB9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=B-cell;  
 RA Strassberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015760; AAH15760.1; -.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65039 MW; 4PCA3AD8ECE263D9 CRC64;

Query Match 70.3%; Score 452; DB 4; Length 597;  
 Best Local Similarity 68.3%; Pred. No. 1.6e-36;  
 Matches 86; Conservative 18; Mismatches 16; Indels 6; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLKLSCAASGFTSTYTMWVRQTPKRLKLEWVATISSGGSYYTP 60  
 DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTSTYAMNVRQAPGKLEWVATISSGGSYYTP 79  
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHGYS---FDYWGCGT 115  
 DB 80 ADSVGRFTISRDNKNTLYLQMSLSKSEDTMYCTRDGCHGYS---FDYWGCGT 138  
 QY 116 TVSS 121  
 DB 139 TVSS 144

RESULT 11  
 Q8WUK1 PRELIMINARY; PRT; 613 AA.  
 ID Q8WUK1;  
 AC Q8WUK1;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;

RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020240; AAH20240.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 5.  
DR PROSITE; PSS0290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match  
Best Local Similarity 69.8%; Score 448.5; DB 4; Length 613;  
Matches 86; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLKLSGASGFTSTYMSWVRQPEKLEWVAITSSGGSYYT 60  
DB 20 QVQLVSGGAVVQPGSRSLRLSCAASGFTSSYGMHWRAQKGLWVAIVSYGSSNRY 79  
QY 61 PDSVGRFTISRDNKNTLYLQMSLKSEDTAMYYCTRDGHHGSGSFDYWGQGITLTVS 120  
DB 80 ADSVKGRTISRDNKNTLYLQMSLSRAEDTAVYYCAKDNBSGV-ETFDIWGQGITLTVS 138  
QY 121 S 121  
DB 139 S 139

RESULT 12  
Q9UL90 PRELIMINARY; PRT; 113 AA.

ID Q9UL90  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035024; AADS6260.1; -  
DR HSSP; P01772; 2PB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 113 AA; 12437 MW; ED57DD19086D07F CRC64;

Query Match  
Best Local Similarity 68.7%; Score 442; DB 4; Length 113;  
Matches 85; Conservative 13; Mismatches 15; Indels 8; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLKLSGASGFTSTYMSWVRQPEKLEWVAITSSGGSYYT 60  
DB 1 EVOLVESGGGAVVQPGSRSLRLSCAASGFTSSYGMHWRAQKGLWVAIVSYGSSNRY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLKSEDTAMYYCTRDGHHGSGSFDYWGQGITLTVS 120  
DB 80 ADSVKGRTISRDNKNTLYLQMSLSRAEDTAVYYCAKDNBSGV-ETFDIWGQGITLTVS 138

DB 61 ADSVKGRTISRDNKNTLYLQMSLSRAEDTAVYYCAKDNBSGV-ETFDIWGQGITLTVS 112  
QY 121 S 121  
DB 113 S 113

RESULT 13  
Q9Y509 PRELIMINARY; PRT; 147 AA.

ID Q9Y509  
AC Q9Y509;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE VHA protein (Fragment).  
GN VHA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96071149; PubMed=7475288;  
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,  
RA Lichtenstein A.K., Berenson J.R.,  
RA "A CD10-positive subset of malignant cells is identified in multiple  
RT myeloma using PCR with patient-specific immunoglobulin gene primers";  
RL Leukemia 9:1948-1953(1995).  
DR EMBL; S80860; AAD14339.1; -  
DR HSSP; P01772; 2PB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER  
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match  
Best Local Similarity 68.4%; Score 439.5; DB 4; Length 147;  
Matches 85; Conservative 14; Mismatches 22; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLKLSGASGFTSTYMSWVRQPEKLEWVAITSSGGSYYT 60  
DB 1 QVQLVSGGAVVQPGSRSLRLSCAASGFTSTYMSWVRQKGLWVAIVSYGSSNRY 60  
QY 61 PDSVGRFTISRDNKNTLYLQMSLKSEDTAMYYCTRDGHHGSGSFDYWGQGIT 115  
DB 61 AGSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAKDNBSGVYAGIDYWGQIT 120  
QY 116 TLTVSS 121  
DB 121 LVTYSS 126

RESULT 14  
Q9UL91 PRELIMINARY; PRT; 118 AA.

ID Q9UL91  
AC Q9UL91;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035023; AAD56259.1; -.  
DR HSSP: P01772; 2F84.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00406; IGV: 1.  
DR PROSITE: PS50835; Ig\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 118  
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 68.0%; Score 437.5; DB 11; Length 118;  
Best Local Similarity 70.8%; Pred. No. 6, 1e-36;  
Matches 85; Conservative 14; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVQLVDSGGGLVPGGSLKSCAAGFTFTSTYMSWVRQPEKRLKLEWVATISGGGSYYT 60  
DB 1 EVQLVDSGGGLVPGGSLKSCAAGFTFTSTYMSWVRQPEKRLKLEWVATISGGGSYYT 60  
QY 61 PSYVGRFTISRDNKNTLYLQMSLSKSDPTAMYCTPDGCHGIGSSFDYWGQTTLVSS 120  
DB 61 ADSYKGRFTISRDNKNTLYLQMSLSKSDPTAMYCTPDGCHGIGSSFDYWGQTTLVSS 117

## RESULT 15

ID Q9RI14 PRELIMINARY; PRT; 437 AA.

AC Q9RI14;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Gamma1 heavy chain of Mab7 (Fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv)."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF152372; AAD40243.1; -.  
DR HSSP: P01842; 7F8B.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig: 4.  
DR SMART: SM00406; IGV: 1.  
DR PROSITE: PS50835; Ig\_LIKE; 4.  
DR PROSITE: PS00290; Ig\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 67.3%; Score 432.5; DB 11; Length 437;  
Best Local Similarity 72.5%; Pred. No. 9, 4e-35;  
Matches 87; Conservative 8; Mismatches 18; Indels 7; Gaps 2;

QY 2 VOLVDSGGGLVPGGSLKSCAAGFTFTSTYMSWVRQPEKRLKLEWVATISGGGSYYT 61  
DB 1 VOLVDSGGGLVPGGSLKSCAAGFTFTSTYMSWVRQPEKRLKLEWVATISGGGSYYT 59  
QY 63 DSYKGRFTISRDNKNTLYLQMSLSKSDPTAMYCTPDGCHGIGSSFDYWGQTTLVSS 121

DB 60 DSYKGRFTISKDRNITLSQMSLSRSEDPTAMYCAR-----GDYSAYWGPGTLVTVSA 113  
Search completed: November 7, 2003, 07:34:35  
Job time : 41.0025 secs



XX PF 13-SEP-2000; 2000MO-EP08936.  
 XX PR 14-SEP-1999; 99AT-0001576.  
 XX PA (BAXT) BAXTER AG.  
 XX PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 DR WPI: 2001-290358/30.  
 DR N-PSDB; AAF30724.  
 XX PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Claim 10; Fig 15; 138pp; English.  
 XX  
 CC The present sequence is that of a single chain Fv (scFv) derivative  
 CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain  
 CC variable regions of 193/K2 joined by an artificial, flexible linker  
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
 CC 193/K2 VH and VL regions and cloning in vector pDAP2. 193/K2 is  
 CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)  
 CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,  
 CC including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIIa inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis.  
 XX  
 SQ Sequence 249 AA;  
 Query Match 100.0%; Score 643; DB 22; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVOLVESGGGLVPRGSGSLKSCAASGFTSTYMSWVRPERKLEAVATISSGGSTYY 60  
 DB 1 EVOLVESGGGLVPRGSGSLKSCAASGFTSTYMSWVRPERKLEAVATISSGGSTYY 60  
 QY PDSVGRFTISRDAKNTLYLQMSLSSEDTAMVYCTRDSGEGSGSPDYWGQGITLVTS 120  
 DB 61 PDSVGRFTISRDAKNTLYLQMSLSSEDTAMVYCTRDSGEGSGSPDYWGQGITLVTS 120  
 QY 121 S 121  
 DB 121 S 121  
 QY 121 S 121  
 DB 121 S 121  
 RESULT 2  
 AAU76122 standard; Protein; 140 AA.  
 ID AAU76122;  
 AC AAU76122;  
 XX  
 DT 08-MAY-2002 (first entry)  
 DE Mouse monoclonal antibody 26-2F heavy chain variable region.  
 XX  
 KW Mouse; monoclonal antibody; heavy chain variable region;  
 KW VH; angiotensin; 26-2F; angiotensin; tumour; cancer; retinopathy;  
 KW ocular neovascular disease; vitamin A deficiency; syphilis;  
 KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;  
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;  
 KW osteoarthritis; graft versus host disease; autoimmune disease;  
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
 KW myasthenia gravis.  
 XX

OS Mus sp.  
 XX  
 FH Key 1.19 Location/Qualifiers  
 FT Peptide /label= Signal\_peptide  
 FT Protein 20..140 /label= Signal\_peptide  
 FT Region 50..54 /label= Mature\_VH  
 FT /note= Complementarity determining region  
 FT /note= "This region is specifically claimed in claim 3"  
 FT Region 69..85 /label= Complementarity determining region  
 FT /note= "This region is specifically claimed in claim 3"  
 FT /note= "This region is specifically claimed in claim 3"  
 FT /note= "This region is specifically claimed in claim 3"  
 XX  
 PN US2002010320-A1.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 05-APR-1999; 99US-0286240.  
 XX  
 PR 05-APR-1999; 99US-0286240.  
 XX  
 PA (FETT/) FETT J W.  
 XX  
 PI FETT JW;  
 XX  
 DR WPI: 2002-187790/24.  
 DR N-PSDB; ABK15270.  
 XX  
 PT New antibody immunologically reactive to angiotensin useful for  
 PT inhibiting angiogenesis and for treating conditions associated with  
 PT abnormal angiogenesis e.g. cancer, ocular neovascular disease,  
 PT rheumatoid arthritis  
 XX  
 PS Claim 6; Page 14; 20pp; English.  
 XX  
 CC The invention relates to an antibody immunologically reactive to  
 CC angiotensin or a fragment of angiotensin comprising light and heavy chain  
 CC nonhuman-derived complementarity determining regions having a binding  
 CC affinity to the angiotensin or its fragment in combination with human  
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F).  
 CC Also included are an expression vector comprising a nucleic acid  
 CC encoding the antibody and a host cell transformed with the vector.  
 CC The antibody or its fragment is useful for inhibiting the angiogenic  
 CC activity of angiotensin. The antibody is useful for treating a tumour in  
 CC humans, by inhibiting, prohibiting, reducing or eliminating a tumour  
 CC growth, or inhibiting the ability of circulating tumour cell to form a  
 CC vascularised tumour mass. The antibody is useful for treating a mammary  
 CC with abnormal or unwanted angiogenesis, including cancer, and other  
 CC diseases mediated by angiogenesis, including ocular neovascular disease,  
 CC diabetic retinopathy, retinopathy of prematurity, corneal graft  
 CC rejection, neovascular glaucoma and retrolental fibroplasia, and other  
 CC diseases associated with corneal neovascularisation including epidemic  
 CC keratoconjunctivitis, vitamin A deficiency, contact lens overwear,  
 CC atopic keratitis, superior limbic keratitis, syphilis, mycobacteria  
 CC infections, lipid degeneration, chemical burns, bacterial ulcers,  
 CC fungal ulcers, herpes simplex infections, herpes zoster infections,  
 CC protozoan infections, Kaposi's sarcoma, Mooren ulcer, rheumatoid  
 CC arthritis, polyarteritis, trauma, Wegner's sarcoidosis, scleritis,  
 CC Steven Johnson's disease, and corneal graft rejection. Diseases  
 CC associated with retinal/choroidal neovascularisation include macular  
 CC degeneration, sickle cell anaemia, sarcoïd, Paget's disease,  
 CC mycobacterial infections, Behcet's disease, trauma, osteoarthritis,  
 CC Osler-Weber-Rendu disease, graft versus host disease, transplant  
 CC rejection, autoimmune diseases such as type I diabetes, multiple  
 CC sclerosis, systemic lupus erythematosus, and myasthenia gravis. The  
 CC present sequence is the heavy chain variable region of mouse  
 CC monoclonal antibody 26-2F.  
 XX  
 SQ Sequence 140 AA;

Query Match 85.8%; Score 552; DB 23; Length 140;  
 Best Local Similarity 86.0%; Pred. No. 3e-44;  
 Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVPGGSLKLSGASGFTSTYMSWVRQTPKRLKLEWATISSGGSYTY 60  
 |||  
 DB 20 EMLVSGGGLVPGGSLKLSGASGFTSTYMSWVRQTPKRLKLEWATISSGGSYTY 79  
 |||  
 QY 61 PDSVKGFTISRDNKNTLYLQMSLKSSEDNTAMYYCTRDGHHGYS--SFDYGGGTTL 120  
 |||  
 DB 80 PDSVKGFTISRDNKNTLYLQMSLKSSEDNTALYYCTRLGPGYAYTMDYGGGTSVTS 139  
 |||  
 QY 121 S 121  
 |||  
 DB 140 S 140  
 |||

## RESULT 3

ABP7295  
 ID ABP7295 standard; Protein, 144 AA.

XX AC ABB79730;  
 XX DT 29-OCT-2002 (first entry)

XX DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.

XX KW Streptococcus mutans; monoclonal antibody; MAb; mouse;  
 XX KW chimeric antibody; antibody; anticaries; transgenic plant;  
 XX KW transgenic animal; caries; immunotherapy; therapy.

XX OS Mus musculus.

XX PN US2002068066-A1.

XX PD 06-JUN-2002.

XX PF 15-JUN-2001; 2001US-0881823.

XX PR 20-AUG-1999; 99US-0378577.

XX PA (SHIM/) SHI W.  
 (MORR/) MORRISON S. L.

XX PA (TRINH/) TRINH K.

XX PA (WIMS/) WIMS L.

XX PA (CHEN/) CHEN L.

XX PA (ANDE/) ANDERSON M. H.

XX PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX PR WPI; 2002-565838/60.

XX DR N-PSDB; ABN84611.

XX PT Treatment and prevention of dental caries in mammals, in particular

XX PT humans by orally administering genetically engineered or purified

XX PT antibodies that bind to surface antigens of cariogenic organisms -

XX PS Claim 14; Fig 3B; 30pp; English.

XX The present sequence is the protein sequence of the heavy chain  
 CC variable region (VH) of the murine monoclonal antibody SWLA3 (Tg9),  
 CC which binds specifically to the surface antigens of cariogenic type  
 CC c Streptococcus mutans (ATCC 25175). The monoclonal antibody is  
 CC produced by SWLA3 (ATCC HB 12558) hybridoma cells. In an example  
 CC from the invention, chimeric monoclonal antibody Tg9 was produced  
 CC comprising SWLA3 variable regions and human antibody constant  
 CC regions. Such chimeric monoclonal antibodies can be used to  
 CC prevent or treat dental caries in humans. The antibodies engage  
 CC the effector apparatus of the human immune system when they bind  
 CC cariogenic organisms, resulting in their destruction. The chimeric  
 CC antibodies may be produced in edible plants, in transgenic animals,  
 CC or in chicken eggs for oral ingestion.

XX SQ Sequence 144 AA;

Query Match 85.7%; Score 551; DB 23; Length 144;  
 Best Local Similarity 84.7%; Pred. No. 3.9e-44;  
 Matches 105; Conservative 11; Mismatches 4; Indels 4; Gaps 2;

QY 1 EVLVESGGGLVPGGSLKLSGASGFTSTYMSWVRQTPKRLKLEWATISSGGSYTY 60  
 |||  
 DB 20 DVKLVEGGGLVPGGSLKLSGASGFTSTYMSWVRQTPKRLKLEWATISSGGSYTY 79  
 |||  
 QY 61 PDSVKGFTISRDNKNTLYLQMSLKSSEDNTAMYYCTRDGHHGYS--SFDYGGGTTL 117  
 |||  
 DB 80 PDSVKGFTISRDNKNTLYLQMSLKSSEDNTAMYYCTRDG--SYGSSYYAMDYGGGTSV 138  
 |||  
 QY 118 TVSS 121  
 |||  
 DB 139 TVSS 142  
 |||

## RESULT 4

ABP72295  
 ID ABP72295 standard; Protein, 155 AA.

XX AC ABB72295;  
 XX DT 08-MAY-2003 (first entry)

XX DE Chimeric construct comprising dhvart fusion to SWLA3 VH.

XX KW Dhvart; SWLA3; antibody; antimicrobial; antibacterial; anticaries.

XX OS Unidentified.

XX PN NO2003007989-A1.

XX PD 30-JAN-2003.

XX PF 17-JUL-2002; 2002WO-US22695.

XX PR 19-JUL-2001; 2001US-0910358.

XX PA 14-FEB-2002; 2002US-0077624.

XX PA (WASH-) WASHINGTON DENTAL SERVICE.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH, Qi F;

XX PR WPI; 2003-229542/22.

XX DR N-PSDB; ABZ58398.

XX PT A composition comprising a targeting moiety and an anti-microbial

XX PT peptide moiety, useful for treating microbial infections, e.g. on

XX PT mucosal surfaces, caused by bacteria, rickettsia, fungi, yeasts,

XX PT protozoa, or parasites -

XX PS Example 1; Fig 4; 53pp; English.

XX The present sequence is that of a chimeric construct composed of  
 CC the antimicrobial peptide dhvart (see also ABP72291) joined via  
 CC a peptide linker to the heavy chain variable region of SWLA3, a  
 CC monoclonal antibody made against the cariogenic organism,  
 CC Streptococcus mutans. The chimeric construct shows antimicrobial  
 CC activity toward S. mutans strains ATCC 25175, LM7 and OM2175, but  
 CC not against a range of other oral bacterial strains. It is an



PA (FERT/) FERT J W.

XX Fect JW;

XX WPI; 2002-187790/24.

PT New antibody immunologically reactive to angiogenin useful for  
PT inhibiting angiogenesis and for treating conditions associated with  
PT abnormal angiogenesis e.g. cancer, ocular neovascular disease,  
PT rheumatoid arthritis

PS Claim 10; Page -; 20pp; English.

XX The invention relates to an antibody immunologically reactive to  
XX angiogenin or a fragment of angiogenin comprising light and heavy chain  
XX nonhuman-derived complementarity determining regions having a binding  
XX affinity to the angiogenin or its fragment in combination with human  
XX derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F).  
XX Also included are an expression vector comprising a nucleic acid  
XX encoding the antibody and a host cell transformed with the vector.  
XX The antibody or its fragment is useful for inhibiting the angiogenic  
XX activity of angiogenin. The antibody is useful for treating a tumour in  
XX humans, by inhibiting, prohibiting, reducing or eliminating a tumour  
XX growth, or inhibiting the ability of circulating tumour cell to form a  
XX vascularised tumour mass. The antibody is useful for treating a mammal  
XX with abnormal or unwanted angiogenesis, including cancer, and other  
XX diseases mediated by angiogenesis, including ocular neovascular disease,  
XX diabetic retinopathy, retinopathy of prematurity, corneal graft  
XX rejection, neovascular glaucoma and retrolental fibroplasia, and other  
XX diseases associated with corneal neovascularisation including epidemic  
XX keratoconjunctivitis, vitamin A deficiency, contact lens overwear,  
XX atopic keratitis, superior limbic keratitis, syphilis, mycobacteria  
XX infections, lipid degeneration, chemical burns, bacterial ulcers,  
XX fungal ulcers, herpes simplex infections, herpes zoster infections,  
XX protozoan infections, Kaposi's sarcoma, Mooren ulcer, rheumatoid  
XX arthritis, polyarteritis, trauma, Wegener's sarcoidosis, Scleritis,  
XX Steven Johnson's disease, and corneal graft rejection. Diseases  
XX associated with retinal/choroidal neovascularisation include macular  
XX degeneration, sickle cell anaemia, sarcoid, Paget's disease,  
XX mycobacterial infections, Bechet's disease, trauma, osteoarthritis,  
XX Osler-Weber-Rendu disease, graft versus host disease, transplant  
XX rejection, autoimmune diseases such as type I diabetes, multiple  
XX sclerosis, systemic lupus erythematosus, and myasthenia gravis. The  
XX present sequence represents the M100Y mutant of the mouse monoclonal  
XX antibody 26-2F light chain variable region.  
XX Note: The present sequence is not shown in the specification but was  
XX created by the indexer using the sequence appearing as AAU76122 and the  
XX information in the claims.

XX Sequence 140 AA;

XX Query Match 85.1%; Score 547; DB 23; Length 140;

XX Best Local Similarity 85.1%; Pred. No. 8.9e-44;

XX Matches 103; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

XX 1 EVOLVESGGGLVTPGGSLKLSCAAGFTSTYMSVWVQTPBKRLKLEWATISSGGSYTY 60

XX 20 EVMVLESGGGLVTPGGSLKLSCAAGFTSTYMSVWVQTPBKRLKLEWATISSGGSYTY 79

XX 61 PDSVKGRTTISRDNAKNTLYLQMSLSKSEDTAMVYCTRDGHHGSSGSPDYGQCTTLTVS 120

XX 80 PDSVKGRTTISRDNAKNTLYLQMSLSKSEDTALYCTRLGDYGVATMDYMGQCTTLTVS 139

XX 121 S 121

XX 140 S 140

XX RESULT 7

XX AAU72814

XX AAU72814 standard; Protein; 119 AA.

XX 26-FEB-2002 (first entry)

XX Humanised mouse TRA-8 anti-human DR5 antibody #4.

XX Tumor necrosis factor-related apoptosis-inducing ligand receptor;

XX TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;

XX autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;

XX rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;

XX Addison disease; scleroderma; Goodpasture's syndrome; sterility;

XX myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;

XX allergy; arteriosclerosis; myocarditis; cardiomyopathy;

XX glomerular nephritis; cancer; antibody; chromosome 9p21-22; TRA-8.

XX Synthetic.

XX WO200183560-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14151.

XX 02-MAY-2000; 2000US-201344P.

XX (UABR-) UAB RES FOUND.

XX Zhou T, Ichikawa K, Kimberly RE, Koopman WJ;

XX WPI; 2002-049336/06.

XX Novel antibody specific for tumour necrosis factor-related

XX apoptosis-inducing ligand, useful for inhibiting cell proliferation in

XX cancer -

XX Example 26; Page 212-213; 229pp; English.

XX The invention describes a novel antibody which recognizes a tumour

XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor

XX DR5 (located on chromosome 9p21-22). The antibody has apoptosis-inducing

XX activity to a cell expressing DR5 in vitro. It is also useful for

XX preparing a therapeutic for selective apoptosis of abnormal or

XX dysregulated cells, and for inhibiting cell proliferation in a cell,

XX preferably a human breast, ovary, colon, hematopoietic, prostate,

XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may

XX also be administered e.g. paclitaxel, taxol or cycloheximide. The

XX antibody is used to treat an autoimmune disease, systemic lupus

XX erythematosus, Hashimoto's disease, rheumatoid arthritis,

XX graft-versus-host disease, Sjogren's syndrome, Chron's disease,

XX pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,

XX autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple

XX sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,

XX allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,

XX glomerular nephritis, hypoplastic anaemia, rejection after organ

XX transplantation, and numerous malignancies of lung, prostate, liver,

XX ovary, lymphatic or breast tissue. This sequence shows one of the

XX humanised anti-DR5 antibodies described in the method of the invention.

XX Sequence 119 AA;

XX Query Match 84.8%; Score 545; DB 23; Length 119;

XX Best Local Similarity 87.6%; Pred. No. 1.1e-43;

XX Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

XX 1 EVOLVESGGGLVTPGGSLKLSCAAGFTSTYMSVWVQTPBKRLKLEWATISSGGSYTY 60

XX 1 EVMVLESGGGLVTPGGSLKLSCAAGFTSTYMSVWVQTPBKRLKLEWATISSGGSYTY 60

XX 61 PDSVKGRTTISRDNAKNTLYLQMSLSKSEDTAMVYCTRDGHHGSSGSPDYGQCTTLTVS 120

XX 61 PDSVKGRTTISRDNAKNTLYLQMSLSKSEDTALYCTRLGDYGVATMDYMGQCTTLTVS 118

XX 121 S 121

Db 119 S 119

RESULT 8  
ABP60555  
ID ABP60555 standard; protein; 134 AA.

XX ABP60555;

DT 21-MAR-2003 (first entry)

DE Murine antibody 14F3 heavy chain variable region.

XX Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;  
XX antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;  
KW neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;  
KW bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;  
KW insulin-dependent diabetes; inflammatory bowel disease;  
KW multiple sclerosis; heavy chain variable region;  
KW complementary determining region; CDR.

XX Mus musculus.

OS Key Location/Qualifiers  
FH Region 31..35  
FT /label= CDR1

FT Region 50..66  
FT /label= CDR2

FT Region 99..110  
FT /label= CDR3

XX WO200295012-A1.

XX 28-NOV-2002.

XX 03-MAY-2002; 2002WO-US14246.

XX 18-MAY-2001; 2001US-292031P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Sweet RW, Tornetta MA, Wattam TA;

XX WPI; 2003-156758/15.  
DR N-PSDB; ABV99887.

XX New monoclonal antibody having the characteristics of a monoclonal  
PT antibody 14F3, useful for treating or preventing osteopathic diseases,  
PT e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.  
PT psoriasis, or diabetes -

PS Disclosure; Page 8; 51pp; English.

XX The invention relates to a novel monoclonal antibody having the  
CC identifying characteristics of, or that is a monoclonal antibody 14F3.  
CC An antibody of the invention has osteopathic, antirheumatic,  
CC antiarthritic, antiinflammatory, cytostatic, antipsoriatic, antidiabetic,  
CC and neuroprotective activity. The polynucleotides encoding the antibodies  
CC of the invention may have a use in gene therapy. The antibodies and  
CC polypeptides are useful for treating or preventing osteopathic diseases,  
CC such as rheumatoid arthritis, osteoporosis, metastatic and primary bone  
CC cancer, wear debris induced osteolysis or osteoarthritis, and immune  
CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory  
CC bowel disease or multiple sclerosis. The present sequence represents the  
CC heavy chain variable region of the murine monoclonal antibody 14F3 of the  
CC invention. The sequence contains three complementary determining regions  
CC (CDR's).

XX Sequence 134 AA;

Query Match 84.8%; Score 545; DB 24; Length 134;  
Best Local Similarity 86.8%; Pred. No. 1.3e-43;

Matches 105; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPRGSGSLKLTSCAAGFTFTSTMSWVRQTPERKLEWATISSGGSYTTY 60  
DB 1 EVOLVESGGGLVPRGSGSLKLTSCAAGFTFTSTMSWVRQTPERKLEWATISSGGSYTTY 60

QY 61 PDSVGRFTTISRDAKNTLYLQWSSLKSEDTNMYCTRDGSGHGSFDMGQGITLTIVS 120  
DB 61 PDSVGRFTTISRDAKNTLYLQWSSLKSEDTNMYCTRDGSGHGSFDMGQGITLTIVS 120

QY 121 S 121  
DB 121 S 121

RESULT 9  
AAU76133  
ID AAU76133 standard; Protein; 140 AA.

XX AAU76133;

DT 08-MAY-2002 (first entry)

DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy;  
KW ocular neovascular disease; vitamin A deficiency; syphilis;  
KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;  
KW sickle cell anaemia; Paget's disease; mycobacterial infection;  
KW osteoarthritis; graft versus host disease; autoimmune disease;  
KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
KW myasthenia gravis; mutant; murine monoclonal antibody; 26-2F;  
KW heavy chain variable region; E59Y.

XX Mus sp.  
OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19  
FT /label= Signal\_peptide

FT Protein 20..140  
FT /label= Mature\_VH

FT Misc-difference 59 /note= "Wild-type Glu substituted by Tyr"

XX US2002010320-A1.

XX 24-JAN-2002.

XX 05-APR-1999; 99US-0286240.

XX 05-APR-1999; 99US-0286240.

XX (FERT/) FERT J W.

XX Felt JW;

XX WPI; 2002-187790/24.

XX New antibody immunologically reactive to angiogenin useful for  
PT inhibiting angiogenesis and for treating conditions associated with  
PT abnormal angiogenesis e.g. cancer, ocular neovascular disease,  
PT rheumatoid arthritis -

XX Claim 11; Page -; 20pp; English.

XX The invention relates to an antibody immunologically reactive to  
CC angiogenin or a fragment of angiogenin comprising light and heavy chain  
CC nonhuman-derived complementarily determining regions having a binding  
CC affinity to the angiogenin or its fragment in combination with human  
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F).  
CC Also included are an expression vector comprising a nucleic acid  
CC encoding the antibody and a host cell transformed with the vector.

CC The antibody or its fragment is useful for inhibiting the angiogenic  
 CC activity of angiogenin. The antibody is useful for treating a tumour in  
 CC humans, by inhibiting, prohibiting, reducing or eliminating a tumour  
 CC growth, or inhibiting the ability of circulating tumour cell to form a  
 CC vascularised tumour mass. The antibody is useful for treating a mammary  
 CC with abnormal or unwanted angiogenesis, including cancer, and other  
 CC diseases mediated by angiogenesis, including ocular neovascular disease,  
 CC diabetic retinopathy, retinopathy of prematurity, corneal graft  
 CC rejection, neovascular glaucoma and retrolental fibroplasia, and other  
 CC diseases associated with corneal neovascularisation including epidemic  
 CC keratoconjunctivitis, vitamin A deficiency, contact lens overwear,  
 CC atopic keratitis, superior limbic keratitis, syphilis, mycobacteria  
 CC infections, lipid degeneration, chemical burns, bacterial ulcers,  
 CC fungal ulcers, herpes simplex infections, herpes zoster infections,  
 CC protozoan infections, Kaposi's sarcoma, Mooren ulcer, rheumatoid  
 CC arthritis, polyarteritis, trauma, Wegener's sarcoidosis, Scleritis,  
 CC Steven Johnson's disease, and corneal graft rejection. Diseases  
 CC associated with retinal/choroidal neovascularisation include macular  
 CC degeneration, sickle cell anaemia, sarcoid, Paget's disease,  
 CC mycobacterial infections, Bechet's disease, trauma, osteoarthritis,  
 CC Osler-Weber-Rendu disease, graft versus host disease, transplant  
 CC rejection, autoimmune diseases such as type 1 diabetes, multiple  
 CC sclerosis, systemic lupus erythematosus, and myasthenia gravis. The  
 CC present sequence represents the E59Y mutant of the mouse monoclonal  
 CC antibody 26-2F light chain variable region.  
 CC Note: The present sequence is not shown in the specification but was  
 CC created by the indexer using the sequence appearing as AAU76122 and the  
 CC information in the claims.

CC Sequence 140 AA;

Query Match 84.8%; Score 545; DB 23; Length 140;  
 Best Local Similarity 85.1%; Pred. No. 1,4e-43;  
 Matches 103; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTYTMQWVRQPEKRLKLEWATISSGGSYTY 60  
 DB 20 EVMALVESGGGLVPGGSLKLSCAASGFTFTYTMQWVRQPEKRLKLEWATISSGGSYTY 79  
 QY 61 PDSVKGRTISRDKAKNTLYLQWSSLKSEPTAMYYCTRDGGHGYSSTDYWGQGTITLV 120  
 DB 80 PDSVKGRTISRDKAKNTLYLQWSSLKSEPTALYYCTRLGDYGYATMDYWGQGTITLV 139  
 QY 121 S 121  
 DB 140 S 140

RESULT 10

AAU72801  
 ID AAU72801 standard; Protein; 464 AA.

AC AAU72801;

DF 26-FEB-2002 (first entry)

DE TRA-8 heavy chain.

KV Tumour necrosis factor-related apoptosis-inducing ligand receptor;  
 KV TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;  
 KV autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
 KV rheumatoid arthritis; Sjogren's syndrome; Chiron's disease; anaemia;  
 KV Addison disease; scleroderma; Goodpasture's syndrome; sterility;  
 KV myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
 KV allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KV glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.

OS Mus musculus.

FN WO200183560-A1.

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14151.  
 XX  
 XX 02-MAY-2000; 2000US-201344P.  
 XX  
 XX (UABR-) UAB RES FOUND.  
 XX  
 XX Zhou T, Ichikawa K, Kimberly RP, Koopman WT;  
 XX  
 XX WPI; 2002-043338/06.  
 DR N-P5DB; AAS97062.

PT Novel antibody specific for tumour necrosis factor-related  
 PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in  
 PT cancer -

PS Claim 26; Page 198-199; 229pp; English.

CC The invention describes a novel antibody which recognizes a tumour  
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
 CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
 CC activity to a cell expressing DR5 in vivo. It is also useful for  
 CC preparing a therapeutic for selective apoptosis of abnormal or  
 CC dysregulated cells, and for inhibiting cell proliferation in a cell,  
 CC preferably a human breast, ovary, colon, hematopoietic, prostate,  
 CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may  
 CC also be administered e.g. paclitaxel, taxol or cycloheximide. The  
 CC antibody is used to treat an autoimmune disease, systemic lupus  
 CC erythematosus, Hashimoto's disease, rheumatoid arthritis,  
 CC pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,  
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple  
 CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,  
 CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, hypoplastic anaemia, rejection after organ  
 CC transplantation, and numerous malignancies of lung, prostate, liver,  
 CC ovary, lymphatic or breast tissue. Peptides used to design primers for  
 CC isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and  
 CC AAU72802), TRA-8 are shown in AAU72799 and AAU72800.

CC Sequence 464 AA;

Query Match 84.8%; Score 545; DB 23; Length 464;  
 Best Local Similarity 87.6%; Pred. No. 5.3e-43;  
 Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTYTMQWVRQPEKRLKLEWATISSGGSYTY 60  
 DB 20 EVMALVESGGGLVPGGSLKLSCAASGFTFTYTMQWVRQPEKRLKLEWATISSGGSYTY 79  
 QY 61 PDSVKGRTISRDKAKNTLYLQWSSLKSEPTAMYYCTRDGGHGYSSTDYWGQGTITLV 120  
 DB 80 PDSVKGRTISRDKAKNTLYLQWSSLKSEPTAMYYCARQDSMT-TTDYWGQGTITLV 137  
 QY 121 S 121  
 DB 138 S 138

RESULT 11

AAB20436  
 ID AAB20436 standard; Protein; 249 AA.

AC AAB20436;

DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 198/A1 scFv.

KV Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;  
 KV Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KV haemorrhagic diathesis; haemostatic; antidolytic; therapy; mouse.  
 OS Chimeric - Mus musculus.

```

OS Chimeric - Synthetic.
XX
FH Key Location/Qualifiers
FT Protein 1..122
FT /label= VH
FT Region 99..111
FT /label= CDR3
FT Peptide 123..136
FT /label= Linker
FT Protein 137..249
FT /label= VL
FT Region 230..238
FT /label= CDR3
FT Misc-difference 142
FT /note= "encoded by ACN"
FT Misc-difference 224
FT /note= "encoded by GCN"
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX WPI, 2001-290358/30.
XX N-PSDB; AAF30726.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Example 10; Fig 17; 138pp; English.
XX
XX The present sequence is that of a single chain Fv (scFv) derivative
XX of antibody 198/A1, comprising the heavy (VH) and light (VL) chain
XX variable regions of 198/A1 joined by an artificial, flexible linker
XX peptide. The scFv was obtained by PCR amplification of cDNAs for
XX 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is
XX an example of anti-human factor IX (FIX)/activated factor IX (FIXa)
XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
XX including scFv and CDR3 fragments, have factor VIIIa (FVIIIa) cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FVIIIa inhibitors. This allows for rapid blood coagulation even
XX in the absence of FVIII or FVIIIa, and in the case of FVIII
XX inhibitor patients. The antibodies and derivatives are used in a
XX claimed pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis.
XX
XX Sequence 249 AA:
SQ
Query Match 84.7%; Score 544.5; DB 22; Length 249;
Best Local Similarity 87.7%; Pred. No. 2.9e-43;
Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
QY 1 EVQLQESGGGLVPRGSKLKSCAASGFTFSYTMHWKQPEKRLMWATISSGSSITY 60
DB 1 EVQLQESGGGLVPRGSKLKSCAASGFTFSYTMHWKQPEKRLMWATISSGSSITY 60
QY 1 PDSEVGRFTISRDAKNTLYLQMSLKSEPTANYYCTRDGSHGYGS-SFDYWGQQTLLTV 119
DB 61 PDSEVGRFTISRDAKNTLYLQMSLKSEPTANYYCTRDGSHGYGS-SFDYWGQQTLLTV 120
QY 120 SS 121
DB 121 SS 122

```

```

RESULT 12
AAB20442
ID AAB20442 standard; Protein; 294 AA.
XX
XX AAB20442;
XX
XX 21-JUN-2001 (first entry)
XX
XX Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
XX
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX myc-tag.
XX
XX Chimeric - Mus musculus.
OS Chimeric - Synthetic.
OS Chimeric - Escherichia coli.
XX
XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..294
FT /label= Mature_protein
FT Protein 23..271
FT /label= scFv
FT Region 23..144
FT /label= VH
FT Misc-difference 76
FT /note= "encoded by GCN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..274
FT /label= Spacer
FT Protein 275..286
FT Peptide 287..288
FT /label= Myc_tag
FT Peptide 289..294
FT /label= His_tag
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX WPI, 2001-290358/30.
XX N-PSDB; AAF30732.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Example 18; Fig 34; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a FcB
XX leader; a single chain Fv (scFv) derivative of antibody 198/B1
XX comprising the heavy (VH) and light (VL) chain variable regions of
XX 198/B1 joined by an artificial, flexible linker peptide; a spacer;
XX a myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.
XX 198/B1 is an example of anti-human factor IX (FIX)/activated factor
XX IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and

```

CC their derivatives, including scfv fragments, have FVIII cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIII inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor  
 CC patients. The antibodies and derivatives are used in a claimed  
 CC pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis. The scfv-myc-tag fusion was expressed in E. coli. It  
 CC exhibited FVIII-like activity.

XX Sequence 294 AA;

Query Match 84.7%; Score 544.5; DB 22; Length 294;  
 Best Local Similarity 86.2%; Pred. No. 3.5e-43;  
 Matches 106; Conservative 9; Mismatches 5; Indels 3; Gaps 2;

QY 1 EVQLVESGGGLVPRGSSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSSTYY 60  
 DB 23 EVKLIVSGGGLVPRGSSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSSTYY 82

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGHHGSS--PDYWGQGTTLT 118  
 DB 83 PDSVGRFTISRDNKNTLYLQMSLSRSEDTAMYCTREGG-GFTVMWYFDVWAGAGTSVT 141

QY 119 VSS 121  
 DB 142 VSS 144

RESULT 13

AA20438 ID AAB20438 standard; Protein; 325 AA.

AA20438; 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.

XX Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;  
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;  
 KW bivalent antibody; plasmid pZlp-198AB2#102.

OS Chimeric - Mus musculus.

OS Chimeric - Synthetic.

OS Chimeric - Escherichia coli.

XX Key Location/Qualifiers

FT 1..22 /label= Signal\_peptide

FT /note= "Peib leader"

FT 23..325 /label= Mature\_protein

FT 23..271 /label= scFv

FT 23..144 /label= VH

FT /label= VH

FT /note= "encoded by GGN"

FT 145..159 /label= Linker

FT 160..271 /label= VL

FT 166 /note= "encoded by TNF"

FT 181 /note= "encoded by TGN"

FT 272..274 /note= "encoded by TGN"

FT 275..284 /label= Spacer

FT 275..284 /label= Hinge

FT Protein 285..319  
 FT /label= Helix  
 FT Peptide 320..325  
 FT /label= His\_tag

XX MO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000MO-EP08936.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT) BAXTER AG.

XX Schefflinger F, Kerschbaumer R, Falkner F, Dornier F;

XX NPI; 2001-290356/30.

XX N-PSDB; AAF30728.

PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX Example 16; Fig 28; 138pp; English.

CC The present sequence is that of a bivalent miniantibody comprising  
 CC a Peib leader peptide, the single chain Fv (scFv) fragment of  
 CC antibody 198/B1 (subclone AB2), an amphipathic helical structure  
 CC and a C-terminal 6His tag. The protein was expressed in  
 CC Escherichia coli from plasmid pZlp198AB2#102 (see AAF30728).  
 CC Antibody 198/B1 is an example of anti-human Factor IX  
 CC (FIX)/activated Factor IX (FIXa) antibodies of the invention.  
 CC Anti-FIX/FIXa antibodies and their derivatives have FVIII cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIII inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis. The bivalent miniantibody exhibited FVIII-like  
 CC activity.

XX Sequence 325 AA;

Query Match 84.7%; Score 544.5; DB 22; Length 325;  
 Best Local Similarity 86.2%; Pred. No. 3.9e-43;  
 Matches 106; Conservative 9; Mismatches 5; Indels 3; Gaps 2;

QY 1 EVQLVESGGGLVPRGSSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSSTYY 60  
 DB 23 EVKLIVSGGGLVPRGSSLKLSCAASGFTSTYMSWVRQTPKRLKLEWVAITSSGGSSTYY 82

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGHHGSS--PDYWGQGTTLT 118  
 DB 83 PDSVGRFTISRDNKNTLYLQMSLSRSEDTAMYCTREGG-GFTVMWYFDVWAGAGTSVT 141

QY 119 VSS 121  
 DB 142 VSS 144

RESULT 14

AA20437 ID AAB20437 standard; Protein; 732 AA.

AA20437;

XX 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.

KM Factor IX; FIX; Factor IXa; scFv; antibody; procoagulant;  
 KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KM haemorrhagic diathesis; haemostatic; amidolytic therapy; mouse;  
 KM alkaline phosphatase.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Synthetic.  
 OS Chimeric - Escherichia coli.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..22  
 FT /label= Signal\_peptide  
 FT 23..732  
 FT /label= Mature\_protein  
 FT 23..271  
 FT /label= scFv  
 FT 23..144  
 FT /label= VH  
 FT Misc-difference 76  
 FT /note= "encoded by GGN"  
 FT Peptide 145..159  
 FT /label= Linker  
 FT 160..271  
 FT /label= VL  
 FT 272..275  
 FT /label= Spacer  
 FT 276..725  
 FT /label= Alkaline\_phosphatase  
 FT 726..732  
 FT /label= His\_tag  
 XX  
 XX MO200119992-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 13-SEP-2000; 2000MO-BE08936.  
 XX  
 PR 14-SEP-1999; 99AT-0001576.  
 XX  
 PA (BAXT ) BAXTER AG.  
 XX  
 XX Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 XX WPI; 2001-290358/30.  
 DR N-PSDB; AAB30727.  
 XX  
 XX New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Example 16; Fig 26; 138pp; English.  
 XX  
 XX The present sequence is that of a fusion protein comprising: a PelB  
 CC leader; a single chain Fv (scFv) derivative of antibody 198/B1  
 CC comprising the heavy (VH) and light (VL) chain variable regions of  
 CC 198/B1 joined by an artificial, flexible linker peptide; a spacer;  
 CC Escherichia coli alkaline phosphatase; and a C-terminal 6His  
 CC affinity tag. 198/B1 is an example of anti-human factor IX  
 CC affinity tail. 198/B1 is an example of anti-human factor IX  
 CC (FIX)/activated factor IX (FIXa) antibodies of the invention.  
 CC Anti-FIX/FIXa antibodies and their derivatives, including scFv  
 CC fragments, have FVIII cofactor activity or FIXa activating  
 CC activity. Administration leads to an increase in the procoagulant  
 CC activity of FIXa, even in the presence of FVIII inhibitors. This  
 CC allows for rapid blood coagulation even in the absence of FVIII or  
 CC FVIII, and in the case of FVIII inhibitor patients. The  
 CC antibodies and derivatives are used in a claimed pharmaceutical  
 CC composition for treating patients with blood coagulation disorders,  
 CC especially haemophilia A and haemorrhagic diathesis. The  
 CC scFv-alkaline phosphatase was expressed in E. coli. It exhibited  
 CC FVIII-like activity.  
 XX  
 SQ Sequence. 732 AA;

Query Match 84.7%; Score 544.5; DB 22; Length 732;  
 Best Local Similarity 86.2%; Pred. No. 9.8e-43;  
 Matches 106; Conservative 9; Mismatches 5; Indels 3; Gaps 2;  
 OY 1 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWRQTPKRLKLEWATISGGSYTY 60  
 DB 23 EVKLVESGGGLVPRGSGSLKISCAASGFTSTYMSWRQTPKRLKLEWATISGGSYTY 82  
 OY 61 PDSVGRFTISRDAKNTLYLQNSLSKEDPTAMYYCTRDGSHGYGSS--FDYWGQGTTLT 118  
 DB 83 PDSVGRFTISRDAKNTLYLQNSLSKEDPTAMYYCTRDGSHGYGSS--FDYWGQGTTLT 141  
 OY 119 VSS 121  
 DB 142 VSS 144  
 RESULT 15  
 ID AAY51266 standard; peptide; 123 AA.  
 AC AAY51266;  
 DE 14-APR-2000 (first entry)  
 DE Monoclonal antibody MAK 33 heavy chain variable region peptide.  
 KW Framework region; monoclonal antibody; variable domain; detection;  
 KW immunotherapy; MAK 33.  
 OS unidentified.  
 OS  
 OS DE19828466-A1.  
 PD 30-DEC-1999.  
 PF 26-JUN-1998; 98DE-1028466.  
 PR 26-JUN-1998; 98DE-1028466.  
 PA (HOPF ) ROCHE DIAGNOSTICS GMBH.  
 PA Nussbaum S, Moessner E, Lenz H, Praest G;  
 PI WPI; 2000-107255/10.  
 DR  
 XX  
 PT Suppressor peptides derived from antibodies for use in immunoassays  
 PS Disclosure; Page 18; 20pp; German.  
 XX  
 CC This invention describes novel peptides derived from a framework region  
 CC of the variable domain of an antibody for detection, immunotherapy or  
 CC for scintigraphs. The peptides of the invention are used in a method to  
 CC detect analytes in a sample by eliminating interference in the sample.  
 CC AAY51254-Y51267 represent peptides derived from the framework regions of  
 CC the variable domain of an antibody which are used to illustrate the  
 CC method of the invention.  
 XX  
 SQ Sequence 123 AA;  
 Query Match 84.3%; Score 542; DB 21; Length 123;  
 Best Local Similarity 84.6%; Pred. No. 2.3e-43;  
 Matches 104; Conservative 5; Mismatches 12; Indels 2; Gaps 1;  
 OY 1 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWRQTPKRLKLEWATISGGSYTY 60  
 DB 1 EVQGVESGGGLVPRGSGSLKISCAASGFTSDYMYWVRQTPKRLKLEWATISGGSYTY 60  
 OY 61 PDSVGRFTISRDAKNTLYLQNSLSKEDPTAMYYCTRDGSH--GYGSSFDYWGQGTTLT 118  
 DB 61 PDSVGRFTISRDAKNTLYLQNSLSKEDPTAMYYCTRDGSH--GYGSSFDYWGQGTTLT 120  
 OY 119 VSS 121

Fri Nov 7 09:40:20 2003

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Page 11

Db 121 VSS 123

Search completed: November 7, 2003, 07:27:02  
Job time : 53.1802 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 / Search time 106.138 Seconds

(Without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992B-84\_COPY\_1\_121

Perfect score: 643

Sequence: 1 EVQIVSGGGGLVKGSGSLK.....HGYSSEFDYWGQCTTLTVSS 121

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	85.8	140	9	US-09-286-240-4
2	551	85.7	144	9	US-09-881-823-12
3	551	85.7	155	12	US-10-077-624-7
4	551	85.7	165	12	US-10-077-624-7
5	545	84.8	119	12	US-10-281-479A-61
6	545	84.8	119	12	US-10-275-180A-61
7	545	84.8	119	12	US-10-286-132A-61
8	545	84.8	119	12	US-10-281-479A-23
9	545	84.8	119	12	US-10-286-132A-23
10	545	84.8	119	12	US-10-286-132A-23
11	532.5	81.9	118	10	US-09-144-886-63
12	526.5	81.9	118	10	US-09-144-886-63
13	523.5	81.4	118	10	US-09-423-800-46
14	523.5	81.4	118	12	US-10-337-981-46
15	523.5	81.4	118	15	US-10-182-018-46

16	523.5	81.4	118	15	US-10-169-003-46	Sequence 46, Appl
17	523.5	81.4	137	10	US-09-423-800-76	Sequence 76, Appl
18	523.5	81.4	137	12	US-10-337-981-76	Sequence 76, Appl
19	522	81.2	119	12	US-10-281-479A-60	Sequence 60, Appl
20	522	81.2	119	12	US-10-275-180A-60	Sequence 60, Appl
21	522	81.2	119	12	US-10-286-132A-60	Sequence 60, Appl
22	521	81.0	123	10	US-09-144-886-60	Sequence 60, Appl
23	518.5	80.6	124	11	US-09-518-737-2	Sequence 60, Appl
24	516	80.2	140	14	US-10-006-773-4	Sequence 2, Appl
25	513.5	79.9	120	12	US-10-229-335-3	Sequence 4, Appl
26	512	79.6	121	12	US-10-300-215-90	Sequence 3, Appl
27	511	79.5	121	12	US-10-300-215-133	Sequence 90, Appl
28	508.5	79.1	118	10	US-09-144-886-64	Sequence 133, App
29	507	78.8	119	15	US-10-305-268-2	Sequence 64, Appl
30	506	78.7	123	10	US-09-144-886-61	Sequence 2, Appl
31	505	78.5	119	12	US-10-281-479A-56	Sequence 61, Appl
32	505	78.5	119	12	US-10-275-180A-56	Sequence 56, Appl
33	505	78.5	119	12	US-10-286-132A-56	Sequence 56, Appl
34	503	78.2	119	12	US-10-281-479A-59	Sequence 56, Appl
35	503	78.2	119	12	US-10-275-180A-59	Sequence 59, Appl
36	503	78.2	119	12	US-10-286-132A-59	Sequence 59, Appl
37	502.5	78.1	118	10	US-09-144-886-65	Sequence 59, Appl
38	502.5	78.1	443	9	US-09-917-410-4	Sequence 65, Appl
39	500	77.8	119	12	US-10-281-479A-31	Sequence 4, Appl
40	500	77.8	119	12	US-10-275-180A-31	Sequence 31, Appl
41	500	77.8	119	12	US-10-286-132A-31	Sequence 31, Appl
42	500	77.8	121	12	US-10-300-215-113	Sequence 31, Appl
43	499	77.6	117	12	US-10-078-757B-56	Sequence 113, App
44	498	77.4	98	10	US-09-840-459-39	Sequence 56, Appl
45	498	77.4	125	12	US-10-169-351-31	Sequence 39, Appl

## ALIGNMENTS

RESULT 1  
US-09-286-240-4  
Sequence 4, Application US/09286240  
Patent No. US20020010320A1  
GENERAL INFORMATION:  
APPLICANT: Fect, James W  
TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin  
FILE REFERENCE: 10/98/74073  
CURRENT APPLICATION NUMBER: US/09/286, 240  
CURRENT FILING DATE: 1999-04-05  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 4  
LENGTH: 140  
TYPR: PRT  
ORGANISM: Mus musculus  
US-09-286-240-4

Query Match 85.8%; Score 552; DB 9; Length 140;  
Best Local Similarity 86.0%; Pred. No. 8.6e-44;  
Matches 104; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY	1	EVQIVSGGGGLVKGSGSLKSCASGFTFTYTWNSWVROTEKLEFWATISGGSSTYY	60
DB	20	EVMLVSGGGGLVKGSGSLKSCASGFTFTYTWNSWVROTEKLEFWATISGGSSTYY	79
QY	61	PDSVKGFTTSRDNAKNTLYLQNSLSSEDTAMTYCRDGGHGYSDFYWGQCTTLTVS	120
DB	80	PDSVKGFTTSRDNAKNTLYLQNSLSSEDTALYYCTRLDYGAYTMDYWGQCTTVTS	139
QY	121	S 121	
DB	140	S 140	

RESULT 2  
US-09-881-823-12  
Sequence 12, Application US/09881823



```

; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THEM
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US2003013932A1e = Synthe
US-10-281-479A-61

Query Match
Best Local Similarity 84.8%; Score 545; DB 12; Length 119;
Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
QY 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
DB 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
QY 121 S 121
DB 119 S 119

RESULT 6
US-10-275-180A-61
; Sequence 61, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
US-10-275-180A-61

Query Match
Best Local Similarity 84.8%; Score 545; DB 12; Length 119;
Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
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Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
QY 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
DB 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
QY 121 S 121
DB 119 S 119

RESULT 7
US-10-286-132A-61
; Sequence 61, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e =
US-10-286-132A-61

Query Match
Best Local Similarity 84.8%; Score 545; DB 12; Length 119;
Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWVRQTEPKRELEWVAITISSGGSYYTY 60
QY 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
DB 61 PDVSRGRTISRDNKNTLYLQMSLSKSDPTAMYYCTRDGSHGSGSPDYWGQGTTLTVS 120
QY 121 S 121
DB 119 S 119

RESULT 8
US-10-281-479A-23
; Sequence 23, Application US/10281479A
; Publication No. US2003013932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
```

```

1  APPLICANT: Oshumi, Jun
2  APPLICANT: Lobuglio, Albert S.
3  APPLICANT: Buchsbaum, Donald J.
4  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
5  TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
6  TITLE OF INVENTION: AGENTS
7  FILE REFERENCE: 21085, 002906
8  CURRENT APPLICATION NUMBER: US/10/281,479A
9  CURRENT FILING DATE: 2003-01-28
10 PRIOR APPLICATION NUMBER: 60/391,478
11 PRIOR FILING DATE: 2002-06-24
12 PRIOR APPLICATION NUMBER: 60/346,402
13 PRIOR FILING DATE: 2001-11-01
14 PRIOR APPLICATION NUMBER: PCT/US01/14151
15 PRIOR FILING DATE: 2001-05-02
16 PRIOR APPLICATION NUMBER: 60/201,344
17 PRIOR FILING DATE: 2000-05-02
18 NUMBER OF SEQ ID NOS: 102
19 SOFTWARE: Patentin version 3.0
20 SEQ ID NO 23
21 LENGTH: 462
22 TYPE: PRT
23 ORGANISM: artificial sequence
24 FEATURE:
25 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
26 US-10-281-479A-23

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Query Match	84.8%	Score 545	DB 12	Length 462
Best Local Similarity	87.6%	Pred. No. 1.4e-42		
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Db	20	EVMLVESGGGLVKKPGGSILKSCAASGFFSTVTMSVRQTPKRLLEWVAITISSGGSITYY	79	
QY	61	PDSVARGRTTISRDNAKNTLYIQMSSLSKSEDTAMYCTRDGGHGYSFPDYQGGSITLYIS	120	
Db	80	PDSVARGRTTISRDNAKNTLYIQMSSLSRSEDTAMYCCARRGDSMI--TTDYMQGGITLYIS	137	
QY	121	\$ 121		
Db	138	\$ 138		

RESULT 9  
US-10-286-132A-23  
Sequence 23, Application US/10286132A  
Publication No. US20030198637A1  
GENERAL INFORMATION:  
APPLICANT: Zhou, Tong  
APPLICANT: Kimberly, Robert P.  
APPLICANT: Koopman, William J.  
APPLICANT: Lobuglio, Albert S.  
APPLICANT: Buchsbaum, Donald J.  
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
FILE REFERENCE: 21085\_002907  
CURRENT APPLICATION NUMBER: US/10/286,132A  
CURRENT FILING DATE: 2003-01-22  
PRIOR APPLICATION NUMBER: US 60/346,402  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/14151  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/201,344  
PRIOR FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 23  
LENGTH: 462  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe

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US-10-286-132A-23

Query Match      84.8%; Score 545; DB 12; Length 462;
Best Local Similarity 87.6%; Pred. No. 1,4e-42;
Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY      1 EVLVESGGGLVNRKGGSLKLSCAASGTFSTYMSWVROTPEKRLBWAATISSGGSTYY 60
Db      20 EVMLVBSGGGLVNRKGGSLKLSCAASGTFSTYSYMSWVRQPEKRLBWAATISSGGSTYY 79

QY      61 PDSYRGFFTSRDNAKNTLYLQWSSLKSEPTAMYYCTRDGGHGYSFDMGGCTTLTVS 120
Db      80 PDSYRGFFTSRDNAKNTLYLQWSSLSEBPTAMYYCARRDSMI--TTDYGQGGCTTLTVS 137

QY      121 S 121
Db      138 S 138

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? RESULT 10
? US-10-275-180A-23
? Sequence 23, Application US/10275180A
? Publication NO. US20030190687A1
? GENERAL INFORMATION:
? APPLICANT: The Uab Research Foundation
? APPLICANT: Zhou, Tony
? APPLICANT: Ichikawa, Kimhisa
? APPLICANT: Kimberly, Robert P.
? APPLICANT: Koopman, William J.
? TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
? TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
? FILE REFERENCE: 21085.0029U5
? CURRENT APPLICATION NUMBER: US/10/275,180A
? CURRENT FILING DATE: 2002-10-31
? NUMBER OF SEQ ID NOS: 102
? SOFTWARE: Patentin version 3.0
? SEQ ID NO 23
? LENGTH: 464
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
? US-10-275-180A-23

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Query Match      84.8%; Score 545; DB 12; Length 464;
Best Local Similarity 87.6%; Pred. No. 1,4e-42;
Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

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DB      20  EVMVLVESGGGLVKGKGLKLSCAASGFTFTSYWSWVROTPEKRLKLEWVAITSSGGSYTTY 79

QY      61  PDSVKGFTTISRDAKNTLYILOMSLSKSEPTNANYTCRRDGHGYSFDTWGQTTITVS 120
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      80  PDSVKGFTTISRDAKNTLYILOMSLSKSEPTNANYTCRRDGSMTTDTYWGQTTITVS 137

QY      121  $ 121
      ||  ||
DB     138  $ 138

RESULT 11
US-09-144-886-63
; Sequence 63, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886

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;; CURRENT FILING DATE: 1998-08-31  
;; NUMBER OF SEQ ID NOS: 98  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 63  
;; LENGTH: 118  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE: Description of Artificial Sequence: BONT/A clone  
;; OTHER INFORMATION: C25 region VH epitope 2  
US-09-144-886-63

Query Match 82.8%; Score 532.5; DB 10; Length 118;  
Best Local Similarity 84.3%; Pred. No. 4,6e-42;  
Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

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DB 1 QVQLQESGGGLVYPGSGSLKLSCAASGFTSDYMWVWRQTPKRLKLEWVATISSGGSYTY 60  
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTRDGCHGSGSPDYWGQGTTLTVS 120  
DB 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCSR---YRYDDAMDYWGQGTTLTVS 117  
QY 121 S 121  
DB 118 S 118

RESULT 12  
US-09-144-886-62  
; Sequence 62, Application US/09144886  
; Patent No. US2002015514A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: C39 region VH epitope 2  
US-09-144-886-62

Query Match 81.9%; Score 526.5; DB 10; Length 118;  
Best Local Similarity 83.5%; Pred. No. 1,6e-41;  
Matches 101; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

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DB 1 QVQLQESGGGLVYPGSGSLKLSCAASGFTSDYMWVWRQTPKRLKLEWVATISSGGSYTY 60  
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTRDGCHGSGSPDYWGQGTTLTVS 120  
DB 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCVR---YRYDEGSDYWGQGTTLTVS 117  
QY 121 S 121  
DB 118 S 118

RESULT 13  
US-09-423-800-46  
; Sequence 46, Application US/09423800  
; Patent No. US20020165363A1

;; GENERAL INFORMATION:  
;; APPLICANT: SATO, KOH  
;; APPLICANT: TSUNENARI, TOSHIKI  
;; APPLICANT: ISHII, KIMIE  
;; TITLE OF INVENTION: CACHEXIA REMEDY  
;; FILE REFERENCE: 04853-0036  
;; CURRENT APPLICATION NUMBER: US/09/423,800  
;; CURRENT FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: JP 125505/1997  
;; PRIOR FILING DATE: 1997-05-15  
;; PRIOR APPLICATION NUMBER: JP 194445/1997  
;; PRIOR FILING DATE: 1997-07-18  
;; NUMBER OF SEQ ID NOS: 87  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 46  
;; LENGTH: 118  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-423-800-46

Query Match 81.4%; Score 523.5; DB 10; Length 118;  
Best Local Similarity 83.5%; Pred. No. 3,1e-41;  
Matches 101; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVYPGSGSLKLSCAASGFTFTYMSVWRQTPKRLKLEWVATISSGGSYTY 60  
DB 1 EVOLVESGGGLVYPGSGSLKLSCAASGFTFSYGMVWRQTPKRLKLEWVATISSGGSYTY 60  
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCTRDGCHGSGSPDYWGQGTTLTVS 120  
DB 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYYCARQTTMTY---FAVWGQGTTLTVS 117  
QY 121 S 121  
DB 118 A 118

RESULT 14  
US-10-337-981-46  
; Sequence 46, Application US/10337981  
; Publication No. US20030138424A1  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUNENARI, TOSHIKI  
; APPLICANT: ISHII, KIMIE  
; TITLE OF INVENTION: CACHEXIA REMEDY  
; FILE REFERENCE: 04853-0036  
; CURRENT APPLICATION NUMBER: US/10/337,981  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 125505/1997  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: JP 194445/1997  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-337-981-46

Query Match 81.4%; Score 523.5; DB 12; Length 118;  
Best Local Similarity 83.5%; Pred. No. 3,1e-41;  
Matches 101; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVYPGSGSLKLSCAASGFTFTYMSVWRQTPKRLKLEWVATISSGGSYTY 60  
DB 1 EVOLVESGGGLVYPGSGSLKLSCAASGFTFSYGMVWRQTPKRLKLEWVATISSGGSYTY 60



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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 17.7704 Seconds  
(without alignments)  
288.098 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_1\_121

Perfect score: 643  
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Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/ECTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	542	84.3	123	4	US-09-344-587-13 Sequence 13, Appl
2	531.5	82.7	135	3	US-08-579-378A-16 Sequence 16, Appl
3	526	81.8	119	4	US-08-875-674A-1 Sequence 1, Appl
4	513.5	79.9	120	4	US-08-435-516-3 Sequence 3, Appl
5	510.5	79.4	123	1	US-08-356-272-3 Sequence 3, Appl
6	507	78.8	247	5	PCT-US94-07659-2 Sequence 2, Appl
7	505.5	78.6	159	4	US-08-653-402B-2 Sequence 2, Appl
8	505	78.5	119	4	US-08-875-674A-3 Sequence 3, Appl
9	505	78.5	239	2	US-08-553-497A-18 Sequence 10, Appl
10	503.5	78.3	118	5	PCT-US93-08435-10 Sequence 18, Appl
11	503	78.2	121	1	US-08-339-582-2 Sequence 2, Appl
12	502.5	78.1	135	3	US-08-579-378A-30 Sequence 20, Appl
13	502.5	78.1	443	5	PCT-US96-13152-4 Sequence 4, Appl
14	500.5	77.8	118	1	US-08-326-362-2 Sequence 2, Appl
15	496	77.1	138	2	US-08-379-057-14 Sequence 14, Appl
16	496	77.1	158	2	US-08-653-402B-6 Sequence 6, Appl
17	496	77.1	158	2	US-08-653-402B-10 Sequence 10, Appl
18	495	77.0	117	3	US-08-752-693A-3 Sequence 3, Appl
19	495	77.0	125	1	US-08-331-398A-65 Sequence 65, Appl
20	495	77.0	125	2	US-08-331-397B-65 Sequence 65, Appl
21	495	77.0	125	2	US-08-739-804A-64 Sequence 64, Appl
22	495	77.0	136	4	US-08-976-183A-31 Sequence 31, Appl
23	495	77.0	136	4	US-08-976-183A-32 Sequence 32, Appl
24	495	77.0	136	4	US-08-976-183A-33 Sequence 33, Appl
25	495	77.0	136	4	US-08-976-183A-34 Sequence 34, Appl
26	495	77.0	239	2	US-07-956-399-4 Sequence 4, Appl
27	495	77.0	245	4	US-09-069-821-5 Sequence 5, Appl

28	494	76.8	117	4	US-09-339-922A-6 Sequence 6, Appl
29	494	76.8	140	3	US-08-836-561-23 Sequence 23, Appl
30	494	76.8	140	4	US-09-434-122-23 Sequence 23, Appl
31	494	76.8	217	5	PCT-US94-14106-59 Sequence 59, Appl
32	494	76.8	237	2	US-08-224-591-16 Sequence 16, Appl
33	494	76.8	237	2	US-08-926-789-16 Sequence 16, Appl
34	494	76.8	241	2	US-08-224-551-18 Sequence 18, Appl
35	494	76.8	241	2	US-08-926-789-18 Sequence 18, Appl
36	494	76.8	265	4	US-09-420-592A-5 Sequence 5, Appl
37	493.5	76.7	354	4	US-09-393-627B-28 Sequence 28, Appl
38	493	76.7	119	2	US-08-475-000-16 Sequence 16, Appl
39	493	76.7	119	2	US-08-484-508-16 Sequence 16, Appl
40	493	76.7	119	2	US-09-316-786-31 Sequence 31, Appl
41	491.5	76.4	167	4	US-08-253-877C-57 Sequence 57, Appl
42	490	76.2	136	2	US-08-452-164A-57 Sequence 57, Appl
43	490	76.1	122	5	PCT-US93-08435-12 Sequence 12, Appl
44	489.5	76.1	122	5	PCT-US93-08435-13 Sequence 13, Appl
45	489.5	76.1	122	5	PCT-US93-08435-43 Sequence 43, Appl

#### ALIGNMENTS

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RESULT 1
US-09-344-587-13
Sequence 13, Application US/09344587
Patent No. 6331402
GENERAL INFORMATION:
APPLICANT: Praest, Gerald
APPLICANT: Nussbaum, Sabine
APPLICANT: Moesener, Ellen
APPLICANT: Lenz, Helmut
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES
FILE REFERENCE: BMID 9928 4897/00/US-1m
CURRENT APPLICATION NUMBER: US/09/344,587
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: DE 19828466.7
EARLIER FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 123
TYPE: PRT
ORGANISM: Mus musculus
US-09-344-587-13

Query Match      84.3%; Score 542; DB 4; Length 123;
Best Local Similarity 84.6%; Pred. No. 4.5e-50;
Matches 104; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLVGGGGLVKGPGSLKLTSCAASGFTFTYTWVWVQTPKRLKLVAVATISGGSYTYX 60
DB 1 EVQVGGGGLVKGPGSLKLTSCAASGFTFTYTWVWVQTPKRLKLVAVATISGGSYTYX 60
QY 61 PDVSRGRTTRDRAKNTVYQMSLSKSEPTAMVYCTRDGH--GYGSSFDYWGQGTTLT 118
DB 61 PDVSRGRTTRDRAKNTVYQMSLSKSEPTAMVYCTRDGH--GYGSSFDYWGQGTTLT 118
QY 119 VSS 121
DB 121 VSS 123

RESULT 2
US-08-579-378A-16
Sequence 16, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 20
```

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CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-16

Query Match      82.7%; Score 531.5; DB 3; Length 135;
Best Local Similarity 85.1%; Pred. No. 6,4e-49;
Matches 103; Conservative 7; Mismatches 6; Indels 5; Gaps 2;

QY 1 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWVRQPEKRLKLEWATISSGGSYTY 60
DB 20 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWVRQPEKRLKLEWATISSGGS- 78
QY 61 PDSVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGSGSPDYWGQGTTLTV 120
DB 79 PDSVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARD---YDGYFPMWGQGTTLTV 134
QY 121 S 121
DB 135 S 135

RESULT 3
US-08-875-674A-1
; Sequence 1, Application US/08875674A
; Patent No. 6572857
; GENERAL INFORMATION:
; APPLICANT: MONTERO CASIMIRO, J. E.
; APPLICANT: LOMBARDO VALLADARES, J.
; APPLICANT: P REZ RODR GUEZ, R.
; APPLICANT: SIERRA BL ZQUEZ, P.
; APPLICANT: TORMO BRAVO, B. R.
; TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

ADDRESSER: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
STREET: One Chase Road
CITY: Scarsdale
STATE: New York
COUNTRY: U.S.A.
ZIP: 10583
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB)
COMPUTER: Compatible PC IBM (80486, 8 M Ram)
OPERATING SYSTEM: Windows 95
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-July-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4301
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 Amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
ORGANISM: Mice Balb/C
INDIVIDUAL ISOLATE: for c1A
TISSUE TYPE: Murine hybridoma
IMMEDIATE SOURCE:
CLONE: Sub-clone for c1A
FEATURE:
IDENTIFICATION METHOD: Experimental.
OTHER INFORMATION: Sequence corresponding to the variable region
OTHER INFORMATION: of the heavy chain of the monoclonal antibody recogn
OTHER INFORMATION: designated as sub-clone for c1A.
US-08-875-674A-1

Query Match      81.8%; Score 526; DB 4; Length 119;
Best Local Similarity 86.1%; Pred. No. 2.1e-48;
Matches 105; Conservative 2; Mismatches 11; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWVRQPEKRLKLEWATISSGGSYTY 60
DB 1 EVQLVESGGGLVPRGSGSLKISCAASGFTSTYMSWVRQPEKRLKLEWATISSGGSYTY 60
QY 61 PDSVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGSHGSGSPDYWGQGTTLTV 119
DB 61 PDSVNRGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARDVDLY---FDWGQGTTLTV 117
QY 120 S 121
DB 118 S 119

RESULT 4
US-08-435-516-3
; Sequence 3, Application US/08435516
; Patent No. 6500951
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR

```

TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384  
FILING DATE: 04-NOV-1992; -02-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Bech E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-435-516-3

Query Match 79.9%; Score 513.5; DB 4; Length 120;  
Best Local Similarity 81.8%; Pred. No. 4.5e-47;  
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLKCAASGFTFSVYTHSWVRQTEPEKRLIEWVAITISGGSYYTY 60  
DB 1 EVQLVESGGGLVQPGGSLRLKCAASGFTFSVYTHSWVRQTEPEKRLIEWVAITISGGSYYTY 60  
QY 61 PDIVRGRTISRDNAKNTLYIQMSSLSKSEPTAMYYCTRDGCHGSGSFDTWGGCTITLV 120  
DB 61 PDIVRGRTISRDNAKNTLYIQMSSLSKSEPTAMYYCTRDGCHGSGSFDTWGGCTITLV 120  
QY 121 S 121  
DB 120 S 120

RESULT 5  
US-08-356-272-3  
Sequence 3, Application US/08356272  
Patent No. 5766946  
GENERAL INFORMATION:  
APPLICANT: Ciantiglia Dr., Maurizio  
TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein P  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Patent and Trademark Department, Sandoz  
ADDRESSER: Corporation  
STREET: 59 Route 10  
CITY: East Hanover  
STATE: N. J.  
COUNTRY: U. S. A.  
ZIP: 07936  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,272  
FILING DATE: 15-DEC-1994  
CLASSIFICATION: 435

CLASSIFICATION: C12N5/20  
CLASSIFICATION: G01N33/574  
CLASSIFICATION: G01N33/577  
CLASSIFICATION: A61K39/295  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT RM92A000457  
FILING DATE: 17-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/BP93/01533  
FILING DATE: 16-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Battle, Carl W.  
REGISTRATION NUMBER: 30,731  
REFERENCE/DOCKET NUMBER: 118-8040  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 503-8177  
TELEFAX: (201) 503-8807  
TELEX: 240867  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-272-3

Query Match 79.4%; Score 510.5; DB 1; Length 123;  
Best Local Similarity 83.7%; Pred. No. 9.6e-47;  
Matches 103; Conservative 6; Mismatches 11; Indels 3; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLKCAASGFTFSVYTHSWVRQTEPEKRLIEWVAITISGGSYYTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLKCAASGFTFSVYTHSWVRQTEPEKRLIEWVAITISGGSYYTY 60  
QY 60 YPDIVRGRTISRDNAKNTLYIQMSSLSKSEPTAMYYCTRDGCHGSGSFDTWGGCTITLV 118  
DB 61 PDIVRGRTISRDNAKNTLYIQMSSLSKSEPTAMYYCTRDGCHGSGSFDTWGGCTITLV 119  
QY 119 VSS 121  
DB 120 VSS 122

RESULT 6  
PCT-US94-07659-2  
Sequence 2, Application PC/TUS9407659  
GENERAL INFORMATION:  
APPLICANT: Young, Peter  
APPLICANT: Gross, Mitchell  
APPLICANT: Jonak, Zdenka L.  
APPLICANT: Theisen, Timothy  
APPLICANT: Hurle, Mark  
APPLICANT: Jackson, Jeffrey R.  
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
TITLE OF INVENTION: Antibodies for treatment of IL-1 Mediated Inflammatory  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SmithKline Beecham Corporation - Corp.  
ADDRESSER: Intellectual Property  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07659-2

Query Match 78.8%; Score 507; DB 5; Length 247;  
Best Local Similarity 82.0%; Pred. No. 5.3e-46;  
Matches 100; Conservative 6; Mismatches 12; Indels 4; Gaps 2;

QY 1 EVLVSSGGGLVPPGSLKLSGASGFTSTYMSWVQTPERLEWVATISGGGTYTY 60  
|||:|||||  
DB 20 EVHLVSSGGGLVPPGSLKLSGASGFTSTYMSWVQTPERLEWVATISGGGTYTY 79  
|||:|||||

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTPDG--HGYGSSFPYMGQTLTV 119  
|||:|||||  
DB 80 PDIYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTPDG--FDVMGAGTIVTV 136  
|||:|||||

QY 120 SS 121  
|||  
DB 137 SS 138

RESULT 7  
US-08-653-402B-2  
Sequence 2, Application US/08653402B  
Patent No. 5969107  
GENERAL INFORMATION:  
APPLICANT: CARCELLER, Ana  
APPLICANT: ROSELL, Elisabeth  
APPLICANT: GOMEZ, Alicia  
APPLICANT: ADEN, Jaume  
APPLICANT: PIJULATS, Jaume  
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,402B  
FILING DATE: 24-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95107967.2  
FILING DATE: 26-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lebovitz, Richard M.  
REGISTRATION NUMBER: 37,067  
REFERENCE/DOCKET NUMBER: MERCK 1781  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-402B-2

Query Match 78.6%; Score 505.5; DB 2; Length 159;  
Best Local Similarity 77.3%; Pred. No. 4.4e-46;  
Matches 99; Conservative 7; Mismatches 13; Indels 9; Gaps 2;

QY 1 EVLVSSGGGLVPPGSLKLSGASGFTSTYMSWVQTPERLEWVATISGGGTYTY 60  
|||:|||||  
DB 20 EVHLVSSGGGLVPPGSLKLSGASGFTSTYMSWVQTPERLEWVATISGGGTYTY 79  
|||:|||||

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTPDG-----HGYGSSFPYMGQ 113  
|||:|||||  
DB 80 PDIYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTPDG-----MDYMGQ 137  
|||:|||||

QY 114 GTTLTVSS 121  
|||:|||||  
DB 138 GTSVTVSS 145

RESULT 8  
US-08-875-674A-3  
Sequence 3, Application US/08875674A  
Patent No. 6572857  
GENERAL INFORMATION:  
APPLICANT: MONTERO CASIMIRO, J. B.  
APPLICANT: LOMBARDO VALADARES, J.  
APPLICANT: P REZ RODR GUEZ, R.  
APPLICANT: SIERRA EL ZOTER, P.  
APPLICANT: TORO BRAVO, B. R.  
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.  
STREET: One Chase Road  
CITY: Scarsdale  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10583

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).  
COMPUTER: Compatible PC IBM (80486, 8 M Ram).  
OPERATING SYSTEM: Windows 95.  
SOFTWARE: Word Perfect 5.0 for Windows 95.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,674A  
FILING DATE: 17-July-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/096/00004  
FILING DATE: 18-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY A. MARZULLO, JR.  
REGISTRATION NUMBER: 20,910  
REFERENCE/DOCKET NUMBER: P-12  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 723-4300  
TELEFAX: (914) 723-4301  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acid residues.  
TYPE: Amino acid.  
STANDEDNESS: Unknown.  
TOPOLOGY: Unknown.  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: -N Terminal fragment.  
ORIGINAL SOURCE:  
TISSUE TYPE: Animal cells  
CELL LINE: NSO " SP 2/0 " CHO  
IMMEDIATE SOURCE:  
CLONE: Sub-clone for t1A  
FEATURE:  
IDENTIFICATION METHOD: By similarity with known sequence.  
OTHER INFORMATION: Sequence corresponding to the humanized  
Patent No. 6572857  
OTHER INFORMATION: variant of sub-clone for t1A recognizing human CD6, particula  
US-08-875-674A-3

Query Match 78.5%; Score 505; DB 4; Length 119;  
Best Local Similarity 82.8%; Pred. No. 3.5e-46;  
Matches 101; Conservative 3; Mismatches 14; Indels 4; Gaps 2;  
DB 1 EVOLVESGGGLVKGPGSLKSCASGFTSTYTMWVROTPKRLKLEWATISSGGSYYTY 60  
1 EVQVHSGGGLVKGPGSLKSCASGFTSTYTMWVROTPKRLKLEWATISSGGSYYTY 60  
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYCT-RDGGHGYGSSFDYWGQGTTLTV 119  
61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYCT-RDGGHGYGSSFDYWGQGTTLTV 117  
DB 120 SS 121  
QY 118 SS 119

## RESULT 9

US-08-553-497A-18  
Sequence 18, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTLEBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSOM, DETLEF  
APPLICANT: ADAM, JADME  
APPLICANT: MITTANS, FRANCESSE  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PIULATS, JADME  
TITLE OF INVENTION: ANTI-BGR SINGLE-CHAIN FVS AND ANTI-BGR  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6

FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-18

Query Match 78.5%; Score 505; DB 2; Length 239;  
Best Local Similarity 82.6%; Pred. No. 8.3e-46;  
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;  
DB 1 EVOLVESGGGLVKGPGSLKSCASGFTSTYTMWVROTPKRLKLEWATISSGGSYYTY 60  
1 EVKQESGGLVKGPGSLKSCASGFTSTYTMWVROTPKRLKLEWATISSGGSYYTY 60  
QY 61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYCTRDGGHGYGSSFDYWGQGTTLTVS 120  
61 PDSVGRFTISRDNKNTLYIQMSLSKSEDTAMYCTRDGGHGYGSSFDYWGQGTTLTVS 118  
DB 121 S 121  
QY 119 S 119

## RESULT 10

PCT-US93-08435-10  
Sequence 10, Application PC/TUS9308435  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham, Corporation  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Navy  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Army  
TITLE OF INVENTION: Novel Antibodies for Confering Passive  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 Norristown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC P50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-08435-10

Query Match 78.3%; Score 503.5; DB 5; Length 118;  
Best Local Similarity 80.5%; Pred. No. 5e-46;  
Matches 95; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 5 VESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 64  
DB 1 LESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 60  
QY 65 RGRFTISRDNKATLYLQMSLSKSEPTAMYYCTRDGHHGYS-SFDPYWGQGTTLTV 121  
DB 61 TGRFTISRDNKATLYLQMSLSKSEPTAMYYCTRDGHHGYS-SFDPYWGQGTTLTV 118

## RESULT 11

US-08-339-582-2  
Sequence 2, Application US/08339582  
Patent No. 5558852  
GENERAL INFORMATION:  
APPLICANT: Bigner, Darrell D.  
APPLICANT: Zalutsky, Michael R.  
TITLE OF INVENTION: METHOD OF TREATMENT  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Kenneth D. Sibley  
STREET: P.O. Drawer 34009  
CITY: Charlotte  
STATE: No. 5558852ch Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/339,582  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/033,864  
FILING DATE: 19-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5405-89  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-339-582-2

Query Match 78.2%; Score 503; DB 1; Length 121;  
Best Local Similarity 83.5%; Pred. No. 5.8e-46;  
Matches 101; Conservative 6; Mismatches 10; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 60  
DB 5 EVQLVESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 63  
QY 61 PDSVGRFTISRDNKATLYLQMSLSKSEPTAMYYCTRDGHHGYS-SFDPYWGQGTTLTV 120

DB 64 PDSVGRFTISRDNKATLYLQMSLSKSEPTAMYYCARGWLHY---FDYGGQGTTLTV 120  
QY 121 S 121  
DB 121 S 121

## RESULT 12

US-08-579-378A-20  
Sequence 20, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: I-Selectin  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebschneitz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-20

Query Match 78.1%; Score 502.5; DB 3; Length 135;  
Best Local Similarity 80.2%; Pred. No. 7.5e-46;  
Matches 97; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 60  
DB 20 EVQLVESGGGLVPGGSLKSCAAGTFTSTYMSVWRQTPPEKLEWVAATISSGGSYTY 78  
QY 61 PDSVGRFTISRDNKATLYLQMSLSKSEPTAMYYCTRDGHHGYS-SFDPYWGQGTTLTV 120  
DB 79 PDSVGRFTISRDNKATLYLQMSLSKSEPTAMYYCTRDGHHGYS-SFDPYWGQGTTLTV 134  
QY 121 S 121

Db 135 S 135

## RESULT 13

PCT-US96-13152-4

Sequence 4, Application PC/TUS9613152

GENERAL INFORMATION:

APPLICANT: Martin, Ulrich, et al.

TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe &amp; Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/13152

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: 27-Dec-95

APPLICATION NUMBER: EP 95 112 895.8

FILING DATE: 17-Aug-95

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Norman D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-13152-4

Query Match

Best Local Similarity 78.1%; Score 502.5; DB 5; Length 443;

Matches 97; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

Db 1 EVOLVESGGGLVPGGSLIKLSCAAGFTFTSTMSWVRQTPKRLKLEWVATISSGGSTYY 60

Db 1 EVOLVESGGGLVPGGSLIKLSCAAGFTFTSTMSWVRQTPKRLKLEWVATISSGGSTYY 60

Db 61 PDSVKGKFTISRDNKNTLYLQMSLKSEPTAMYYCTRDGCHGYGSSPDYWGQGTTLTVS 120

Db 60 PDSVKGKFTISRDNKNTLYLQMSLKSEPTAMYYCTRDGCHGYGSSPDYWGQGTTLTVS 115

QY 121 S 121

Db 116 S 116

## RESULT 14

US-08-326-362-2

Sequence 2, Application US/08326362

Patent No. 5730981

GENERAL INFORMATION:

APPLICANT: Bosslet, Klaus

APPLICANT: Seeman, Gerhard

APPLICANT: Dipold, Wolfgang

TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,

TITLE OF INVENTION: Its Preparation and Use as a Therapeutic Agent

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &amp;

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/326,362

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/032,863

FILING DATE: 17-MAR-1993

APPLICATION NUMBER: DE P 42 08 795.3

FILING DATE: 19-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 02481-1276-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-326-362-2

Query Match

Best Local Similarity 77.8%; Score 500.5; DB 1; Length 118;

Matches 99; Conservative 7; Mismatches 12; Indels 3; Gaps 2;

Db 1 EVOLVESGGGLVPGGSLIKLSCAAGFTFTSTMSWVRQTPKRLKLEWVATISSGGSTYY 60

Db 1 QVQLQESGGGLVPGGSLRLSCAASGFTSTYMSWVRQAPKRLKLEWVATISSGGSTYY 60

QY 61 PDSVKGKFTISRDNKNTLYLQMSLKSEPTAMYYCTRDGCHGYGSSPDYWGQGTTLTVS 120

Db 61 PDSVKGKFTISRDNKNTLYLQMSLKSEPTAMYYCTRDGCHGYGSSPDYWGQGTTLTVS 117

QY 121 S 121

Db 118 S 118

## RESULT 15

US-08-379-057-14

Sequence 14, Application US/08379057

Patent No. 5876950

GENERAL INFORMATION:

APPLICANT: Sladak, Anthony W.

APPLICANT: Hollenbaugh, Diane L.

APPLICANT: Gilliland, Lisa K.

APPLICANT: Gordon, Marcia U.

APPLICANT: Bajorek, Jürgen

APPLICANT: Aruffo, Alejandro A.

TITLE OF INVENTION: Monoclonal Antibodies Specific For

TITLE OF INVENTION: Different Epitopes of Human GP39 and Methods For Their

TITLE OF INVENTION: In Diagnosis and Therapy

NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0133-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-379-057-14

Query Match 77.1%; Score 496; DB 2; Length 138;  
Best Local Similarity 80.3%; Pred. No. 3.8e-45;  
Matches 98; Conservative 9; Mismatches 11; Indels 4; Gaps 3;  
QY 1 EVQLVDSGGGLVPEGGSLKLSGASGFTFTYMSWVQTPKRLKLEWVATISSGGSITYY 60  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 20 EVKLVSAGGLVPEGGSLKLSGASGFTFTYMSWVQTPKRLKLEWVATISSGGSITYY 78  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 PDSVKGRTTISRDNKNTLYLQMSLSKSEDTAMVYCTRDGGHGYGS-SFDYWGQGTTLTV 119  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 79 PDSVKGRTTISRDNKNTLYLQMSLSKSEDTAMVYCANH--YDIDSYAMDYWGQGTSTVTV 136  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 120 SS 121  
||  
Db 137 SS 138

Search completed: November 7, 2003, 07:30:10  
Job time : 18.7704 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 14.6342 Seconds

(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_137\_249

Perfect score: 593

Sequence: 1 QIVLTQSPPLSLPVSIGDQAS.....FQSSHPVMTFGGPKLEIKR 113

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	566	95.4	113	2	anti-DNA autoantib
2	562	94.8	219	2	Ig kappa chain - m
3	559	94.3	219	2	Ig kappa chain (mo
4	556	93.8	131	2	Ig kappa chain pre
5	554	93.4	112	2	Ig kappa chain V r
6	553	93.3	110	2	Ig kappa chain V r
7	551	92.9	118	2	Ig kappa chain V r
8	548	92.4	112	2	Ig kappa chain V r
9	547	92.2	114	2	Ig kappa chain V r
10	546	92.1	131	2	Ig kappa chain V-I
11	543	91.6	112	2	Ig kappa chain pre
12	542	91.4	112	2	Ig kappa chain V r
13	542	91.4	131	2	Ig kappa chain V r
14	541	91.2	219	2	Ig kappa chain pre
15	540	90.9	112	2	Ig kappa chain V r
16	539	90.7	112	2	Ig kappa chain V r
17	538	90.6	114	2	Ig kappa chain V-I
18	537	90.6	112	2	Ig kappa chain V r
19	537	90.6	112	2	Ig kappa chain V r
20	535	90.2	225	2	Ig kappa chain pre
21	532	89.7	112	2	Ig kappa chain pre
22	531	89.5	114	2	Ig kappa chain V r
23	531	89.5	114	2	Ig kappa chain V r
24	530	89.4	113	2	Ig kappa chain V r
25	530	89.4	103	2	Ig kappa chain pre
26	528	89.0	103	2	Ig kappa chain V r
27	528	89.0	112	2	Ig kappa chain pre
28	528	89.0	131	2	Ig kappa chain pre
29	528	89.0	131	2	Ig kappa chain pre

30	528	89.0	131	2	809259	Ig kappa chain pre
31	527	88.9	112	2	B27887	Ig kappa chain V r
32	527	88.9	115	2	S60066	Ig kappa chain V r
33	527	88.9	131	2	D34904	Ig kappa chain pre
34	526	88.7	111	2	PL0257	Ig kappa chain V r
35	526	88.7	219	2	S38865	Ig kappa chain V r
36	525	88.5	111	2	S15673	Ig kappa chain - m
37	525	88.5	112	2	D28195	Ig kappa chain V r
38	525	88.5	113	1	KVMS26	Ig kappa chain V r
39	525	88.5	115	2	S38715	Ig kappa chain V r
40	525	88.5	132	2	PH0106	Ig kappa chain V r
41	520	87.7	131	2	G34803	anti-digoxin trans
42	518	87.4	103	2	PH0442	Ig kappa chain pre
43	517	87.2	113	2	PL0205	Ig kappa chain V r
44	516	87.0	121	2	S67944	anti-DNA autoantib
45	516	87.0	131	2	PT0178	Ig kappa chain pre

## ALIGNMENTS

RESULT 1  
PL0203  
anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_rev150n 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: PL0203  
R/Smith, R.G.; Voss Jr., B.W.  
Mol. Immunol. 27, 463-470, 1990  
A/Title: Variable region primary structures of monoclonal anti-DNA autoantibodi  
A/Reference number: PL0198; MWID:90309768; PMID:2114528  
A/Accession: PL0203  
A/Molecule type: mRNA  
A/Residues: 1-113 <SMI>  
A/Cross-references: GB:X53643; NID:G50196; PIDN:CAA37694.1; PID:G930142  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:24-39/Region: complementarity-determining 1  
F:35-61/Region: complementarity-determining 2  
F:94-102/Region: complementarity-determining 3  
F:101-113/Region: D region

Query Match 95.4%; Score 566; DB 2; Length 113;  
Best Local Similarity 95.5%; Pred. No. 2.8e-45;  
Matches 107; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 2 IYLTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEMYLQKPGSPKLLTYKSNRRS 61  
Db 2 VVMTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEMYLQKPGSPKLLTYKSNRRS 61  
QY 62 GVPDKFGSGSGGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGPKLEIKR 113  
Db 62 GVPDKFGSGSGGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGPKLEIKR 113  
RESULT 2  
S52028  
Ig kappa chain - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-May-1995 #sequence\_rev150n 21-Jul-1995 #text\_change 21-Jan-2000  
C/Accession: S52028  
R/van Engelen, F.; Schouten, A.; Molitoff, J.W.; Roosen, J.; Dirkse, W.G.; Schu  
submitted to the EMBL Data Library, August 1994  
A/Description: Coordinate expression of antibody subunit genes yields high level  
A/Reference number: S52028  
A/Accession: S52028  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-219 <YAN>  
A/Cross-references: EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PID:G522337  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterodimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 562; DB 2; Length 219;  
Best Local Similarity 95.5%; Pred. No. 1.3e-44;  
Matches 107; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 113  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 113

## RESULT 3

Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C/Accession: PC4203  
R/Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.  
Gene 173, 257-259, 1996  
A/Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mAb  
A/Reference number: PC4202; MUID:97082978; PMID:8964510  
A/Accession: PC4203  
A/Molecule type: mRNA  
A/Residues: 1-219 <KMA>  
A/Cross-references: GB:U29147; NID:G1594225; PIDN:AA52821.1; PID:G1594226  
C/Comment: This protein is specific for human plasma apolipoprotein A-I of high-density  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:112/Domain: V region #status predicted <YRG>  
F:113-219/Domain: C region #status predicted <CRG>

Query Match 94.3%; Score 559; DB 2; Length 219;  
Best Local Similarity 93.8%; Pred. No. 2.5e-44;  
Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 113  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 113

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

## RESULT 4

Ig light chain precursor V-D-J region (6-19) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
C/Accession: B39276  
R/Reininger, L.; Berney, T.; Shibata, T.; Sperl, F.; Merino, R.; Izul, S.  
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990  
A/Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis at  
A/Reference number: A39276; MUID:91088540; PMID:2263605  
A/Accession: B39276  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-131 <RET>  
A/Cross-references: GB:M55313; NID:G198095; PIDN:AA63385.1; PID:G198096  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:35-114/Domain: immunoglobulin homology <IMM>

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 112  
DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 131

## RESULT 5

Ig kappa chain V region (PAc1) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Jul-1989 #sequence\_revision 20-Jul-1989 #text\_change 21-Jan-2000  
C/Accession: A31807  
R/Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.  
J. Biol. Chem. 264, 259-265, 1989  
A/Title: A monoclonal antibody against the platelet fibrinogen receptor contain  
A/Reference number: A31807; MUID:89079661; PMID:2309518  
A/Accession: A31807  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-112 <TAU>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 554; DB 2; Length 112;  
Best Local Similarity 92.8%; Pred. No. 3.5e-44;  
Matches 103; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 112  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 112

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 112  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 112

## RESULT 6

Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26335  
R/Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A/Title: Antibodies that are specific for a single amino acid interchange in a  
A/Reference number: S26309; MUID:91341421; PMID:1908510  
A/Accession: S26335  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-110 <STA>  
A/Cross-references: EMBL:X59183; NID:G52314; PIDN:CAA41893.1; PID:G1334062  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

QY 2 IVLTQSPFLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VMTQTPLSPVSLGDOASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGKLEIKR 110



QY 62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112  
DB 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112

## RESULT 12

ig kappa chain V region (HIC5-4D1) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 21-Jan-2000  
C/Accession: F27887  
R/Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A/Title: Structural and functional implications of a restricted antibody response to a  
A/Reference number: A91043; MUID:86300658; PMID:2427335  
A/Accession: F27887  
A/Molecule type: DNA  
A/Status: preliminary  
A/Experimental source: strain Balb/c  
A/Note: This sequence was determined from the germ-line gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C/Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 542; DB 2; Length 112;  
Best Local Similarity 91.4%; Pred. No. 4,5e-43;  
Matches 102; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
DB 2 VVMTQTPSLPVLSDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
QY 62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112  
DB 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112

## RESULT 13

ig kappa chain precursor V region (3-24) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jan-2000  
C/Accession: C34904; I31485  
R/Bedzlyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A/Title: Active site structure and antigen binding properties of idiotypically cross-re  
A/Reference number: A34903; MUID:90094387; PMID:2104617  
A/Accession: C34904  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-131 <BED>  
R/Bedzlyk, W.D.; Johnson, L.S.; RJordan, G.S.; Voss Jr., E.W.  
J. Biol. Chem. 264, 1565-1569, 1989  
A/Title: Comparison of variable region primary structures within an anti-fluorescein id  
A/Reference number: A31485; MUID:69109167; PMID:2492278  
A/Accession: I31485  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 20-52 <BR2>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 542; DB 2; Length 131;  
Best Local Similarity 90.1%; Pred. No. 5.3e-43;  
Matches 100; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
DB 2 VVMTQTPSLPVLSDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 80

QY 62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112  
DB 61 GVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 131

## RESULT 14

ig kappa chain V region (G2a) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S16112  
R/Vaessen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suerm  
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991  
A/Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 again  
A/Reference number: S16112; MUID:92000313; PMID:1910583  
A/Accession: S16112  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-219 <BIT>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 91.2%; Score 541; DB 2; Length 219;  
Best Local Similarity 89.3%; Pred. No. 1.1e-42;  
Matches 100; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
DB 2 VVMTQTPSLPVLSDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
QY 62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 113  
DB 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 113

## RESULT 15

ig kappa chain V region (H37-60) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 21-Jan-2000  
C/Accession: A27887  
R/Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A/Title: Structural and functional implications of a restricted antibody response  
A/Reference number: A91043; MUID:86300658; PMID:2427335  
A/Accession: A27887  
A/Molecule type: DNA  
A/Residues: 1-112 <CAT>  
A/Experimental source: strain Balb/c  
A/Note: This sequence was determined from the germ-line gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 540; DB 2; Length 112;  
Best Local Similarity 89.2%; Pred. No. 6.9e-43;  
Matches 99; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
DB 2 VVMTQTPSLPVLSDPAISICRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
QY 62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112  
DB 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVMTFGGKLEIK 112

Search completed: November 7, 2003, 07:36:19  
Job time: 14.7342 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 8.14686 Seconds

(Without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_137\_249

Perfect score: 593

Sequence: 1 QIVTQSPISLPVSLGDQAS.....FGSHVPTFGGTYLEIKR 113

## ALIGNMENTS

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	88.5	113	1	KV2G_MOUSE
2	480	80.9	133	1	KV2F_HUMAN
3	457	77.1	117	1	KV2E_HUMAN
4	452	76.2	113	1	KV2D_HUMAN
5	439	74.0	113	1	KV2B_HUMAN
6	435	73.4	113	1	KV2E_MOUSE
7	433.5	73.1	115	1	KV2A_HUMAN
8	429.5	72.4	112	1	KV2C_HUMAN
9	419	70.7	113	1	KV2F_MOUSE
10	416	70.2	112	1	KV2D_MOUSE
11	397.5	67.0	134	1	KV4C_HUMAN
12	385	64.9	133	1	KV4B_HUMAN
13	384	64.8	113	1	KV2C_MOUSE
14	383.5	64.7	114	1	KV4A_HUMAN
15	379.5	64.0	131	1	KV3I_MOUSE
16	376.5	63.5	111	1	KV3H_MOUSE
17	376.5	63.5	111	1	KV3O_MOUSE
18	374.5	63.2	108	1	KV1_CANFA
19	372.5	62.8	111	1	KV2I_MOUSE
20	372	62.7	112	1	KV2A_MOUSE
21	370.5	62.5	111	1	KV3J_MOUSE
22	370.5	62.5	112	1	KV3G_MOUSE
23	370	62.4	110	1	KV3P_MOUSE
24	369.5	62.3	111	1	KV3C_MOUSE
25	369.5	62.3	111	1	KV3Q_MOUSE
26	369.5	62.3	132	1	KV3Z_MOUSE
27	368	62.1	129	1	KV3M_HUMAN
28	365.5	61.8	111	1	KV3A_MOUSE
29	365.5	61.8	111	1	KV3M_MOUSE
30	363.5	61.3	111	1	KV3R_MOUSE
31	361.5	61.0	111	1	KV3N_MOUSE
32	361.5	61.0	136	1	KV5B_MOUSE
33	359	60.5	109	1	KV3B_HUMAN

34	359	60.5	109	1	KV2D_HUMAN	P01622	homo sapien
35	359	60.5	129	1	KV3I_HUMAN	P18135	homo sapien
36	358.5	60.5	111	1	KV3K_MOUSE	P01663	mus musculus
37	356.5	60.1	111	1	KV3S_MOUSE	P01671	mus musculus
38	355.5	59.9	111	1	KV3T_MOUSE	P01657	mus musculus
39	355.5	59.9	111	1	KV3U_MOUSE	P01672	mus musculus
40	355.5	59.9	111	1	KV3V_MOUSE	P01673	mus musculus
41	353.5	59.6	111	1	KV3D_MOUSE	P03977	mus musculus
42	352	59.4	109	1	KV3E_HUMAN	P01623	homo sapien
43	351.5	59.3	149	1	KV5A_MOUSE	P01633	mus musculus
44	351	59.2	108	1	KV2A_HUMAN	P01619	homo sapien
45	349.5	58.9	109	1	KV4D_HUMAN	P83593	homo sapien

## RESULT 1

ID	KV2G_MOUSE	STANDARD	PRT	113 AA
AC	KV2G_MOUSE			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG kappa chain V-II region 26-10.			
OS	mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RY	[1]			
RP	SEQUENCE			
RX	STRAIN-A/T;			
RX	MEDLINE=83178921; PubMed=6404298;			
RA	Novotny J., Margolies M.N.;			
RT	"Amino acid sequence of the light chain variable region from a mouse			
RT	anti-digoxin hybridoma antibody."			
RL	Biochemistry 22:1153-1158(1983).			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA			
CC	PIR; A01914; KWS26.			
CC	PIR; A01914; KWS26.			
DR	HSSP; P80362; IMTL.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KV	Immunoglobulin V region; Monoclonal antibody; Hybridoma.			
FT	DOMAIN	1	23	FRAMWORK-1.
FT	DOMAIN	24	39	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	40	54	FRAMWORK-2.
FT	DOMAIN	55	61	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	62	93	FRAMWORK-3.
FT	DOMAIN	94	102	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	103	112	FRAMWORK-4.
FT	DISULFID	23	93	BY SIMILARITY.
FT	NON_TER	113	113	
SO	SEQUENCE	113 AA;	12273 MW;	F9F39CE949A84C2A CRC64;

Query Match 88.5%; Score 525; DB 1; Length 113;  
Best Local Similarity 88.4%; Pred. No. 5.5e-50;  
Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY	2	IVTQSPISLPVSLGDQASISCRSSQSVHNSNGNTYLEWYLOKRGSPKLLIYVSNRFS	61
DB	2	VWVTQTPSLSPVSLGDQASISCRSSQSVHNSNGNTYLEWYLOKRGSPKLLIYVSNRFS	61
QY	62	GVPDRKSGSGSGDFTLKISRVAEDELGVYCYCGSGVPTFGGTYLEIKR	113
DB	62	GVPRKSGSGSGDFTLKISRVAEDELGVYCYCGSGVPTFGGTYLEIKR	113

RESULT 2

KV2F HUMAN  
ID KV2F HUMAN STANDARD; PRT; 133 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-II region RPMI 6410 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=86041852; PubMed=2997711;  
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and III."  
RL Nucleic Acids Res. 13:6499-6513(1985).  
-----  
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-----  
CC EMBL; Z00020; CAA77315.1; -  
DR PIR; A01890; K2HURP.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; PF00047; IG\_1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR SMART; SM00406; IG\_V.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 60 74 FRAMEWORK-2.  
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 82 113 FRAMEWORK-3.  
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 123 133 FRAMEWORK-4.  
FT NON TER 133 133 BY SIMILARITY.  
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;  
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Query Match 80.9%; Score 480; DB 1; Length 133;  
Best Local Similarity 79.5%; Pred. No. 5e-45;  
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
-----  
QY 2 IVLTQSPVLSPLVSIQDAISCRSSQSIYHSNNTYLEWYLOKQSGSKLLIKYSNRFS 61  
DB 22 VVMTQSPVLSPLVLTGPAISCRSSQSLVSDENLYLWVQRPQSPRRLLIKYKSNRDS 81  
QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVVYCFQSGSHVPMTFGGGTKEIKR 113  
DB 82 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGHMWTGTGQIKVEIKR 133  
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RESULT 3  
KV2E HUMAN  
ID KV2E HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=632927;  
RA Klobbeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain  
RT diversity.";  
RL Nature 309:73-76(1984).  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; Z00009; -, NOT ANNOTATED\_CDS.  
DR PIR; A01889; K2HGM.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; PF00047; IG\_1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR SMART; SM00406; IG\_V.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 1  
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.  
FT DOMAIN 5 27 FRAMEWORK-1.  
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 44 58 FRAMEWORK-2.  
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 66 97 FRAMEWORK-3.  
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 107 116 FRAMEWORK-4.  
FT NON TER 117 117 BY SIMILARITY.  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719B558B1 CRC64;  
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Query Match 77.1%; Score 457; DB 1; Length 117;  
Best Local Similarity 78.6%; Pred. No. 1.3e-42;  
Matches 88; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
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QY 2 IVLTQSPVLSPLVSIQDAISCRSSQSIYHSNNTYLEWYLOKQSGSKLLIKYSNRFS 61  
DB 6 IVMTQSPVLSPLVLTGPAISCRSSQSLVSDENLYLWVQRPQSPRRLLIKYKSNRDS 65  
QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVVYCFQSGSHVPMTFGGGTKEIKR 113  
DB 66 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGHMWTGTGQIKVEIKR 117  
-----  
RESULT 4  
KV2D HUMAN  
ID KV2D HUMAN STANDARD; PRT; 113 AA.  
AC P01617;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-II region TEM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;

[1]  
 RN SEQUENCE (BENCE-JONES PROTEIN TEM).  
 RP MEDLINE=74148480; PubMed=4596149.  
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
 RT "Mucino acid sequence of a kappa Bence Jones protein from a case of  
 RT primary amyloidosis."  
 RL Biochemistry 12:3763-3780(1973).  
 RN [2]  
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEM).  
 RX MEDLINE=73166638; PubMed=4700495;  
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,  
 RA Glenner G.G.;  
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
 RT patient with plasma cell dyscrasia and amyloidosis."  
 RL J. Clin. Invest. 52:1276-1281(1973).  
 CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL  
 CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.  
 CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A  
 CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER  
 CC PIR: A90370; KAHUTW.  
 DR HSSP: P01607; IREI.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGv\_1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Bence-Jones protein; Amyloid.  
 FT DOMAIN 1 23  
 FT 1 23  
 FT 24 39  
 FT 40 54  
 FT 55 61  
 FT 62 93  
 FT 94 102  
 FT 103 112  
 FT 123 93  
 FT 113 113  
 FT NON\_TER  
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;  
 Query Match 76.2%; Score 452; DB 1; Length 113;  
 Best Local Similarity 76.8%; Pred. No. 4, 5e-42;  
 Matches 86; Conservative 12; Mismatches 14; Indels 0; Gaps 0;  
 QY 2 IYLTQSPFLSPVSLDQASISCRSSQSIIVHSNGNTYLEWYLOKPGQSPPLLIYKVSNRFS 61  
 DB 2 IYLTQSPFLSPVSLDQASISCRSSQSIIVHSNGNTYLEWYLOKPGQSPPLLIYKVSNRFS 61  
 QY 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 DB 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 DB 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 RESULT 5  
 KY2B HUMAN STANDARD; PRT; 113 AA.  
 AC P01615;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region FR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76253627; PubMed=821524;  
 RA Riesen W.F., Jaton J.-C.;

RT "Variable region sequence of the light chain from a Waldenstroms IGM  
 RT with specificity for phosphorylcholine."  
 RL Biochemistry 15:3829-3833(1976).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
 CC PIR: A01886; KAHUTR.  
 DR HSSP: P01607; IREI.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGv\_1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT 1 23  
 FT 24 39  
 FT 40 54  
 FT 55 61  
 FT 62 93  
 FT 94 102  
 FT 103 112  
 FT 123 93  
 FT 113 113  
 FT NON\_TER  
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;  
 Query Match 74.0%; Score 439; DB 1; Length 113;  
 Best Local Similarity 72.3%; Pred. No. 1, 1e-40;  
 Matches 81; Conservative 17; Mismatches 14; Indels 0; Gaps 0;  
 QY 2 IYLTQSPFLSPVSLDQASISCRSSQSIIVHSNGNTYLEWYLOKPGQSPPLLIYKVSNRFS 61  
 DB 2 IYLTQSPFLSPVSLDQASISCRSSQSIIVHSNGNTYLEWYLOKPGQSPPLLIYKVSNRFS 61  
 QY 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 DB 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 DB 62 GVPDKFSSGSGSDTFTLKISRVEADLVYICFGQSHVPTFTGGTGKLEIKR 113  
 RESULT 6  
 KY2B MOUSE STANDARD; PRT; 113 AA.  
 AC P03976;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 17529.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=85128968; PubMed=6441768;  
 RA Aederhold R., Herber H., Grutler T., Chang J.Y., Braun D.G.;  
 RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57BL/6  
 RT origin: monoclonal antibodies 17829.1 and 22525.1 specific for the  
 RT group A-streptococcal polysaccharide."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).  
 CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.  
 CC PIR: A01912; KMS17.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IGv\_1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23  
 FT 1 23  
 FT 24 39  
 FT 40 54  
 FT 55 61  
 FT 62 93  
 FT 94 102  
 FT 103 112  
 FT 123 93  
 FT 113 113  
 FT NON\_TER  
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 40 54 FRAMEWORK-2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 73.4%; Score 435; DB 1; Length 113;  
 Best Local Similarity 73.2%; Pred. No. 3.1e-40;  
 Matches 82; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSIIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIKVSNRFS 61  
 DB 2 IVMTQVAFSPNPVITIGTASISCRSSKSLNSNGITTYWTLQRFQSPQLLQMSWLAS 61  
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYVFCFGSHVPTFGGGLTEIKR 113  
 DB 62 GVPDRFSSSGSGTDFTLIRISREVEDGVYVCAHMLELPYFGGGLTEIKR 113

RESULT 7  
 KV2A\_HUMAN STANDARD; PRT; 115 AA.

AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region Cmu.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cmu (kappa-type)";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation";  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR HSP; B91639; K2HUCM.  
 DR HSP; P01607; IREI.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569BC CRC64;

Query Match 73.1%; Score 433.5; DB 1; Length 115;  
 Best Local Similarity 74.3%; Pred. No. 4.6e-40;  
 Matches 84; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

QY 2 IVLTQSPFLSPVSIIGDQASISCRSSQSIYHS-NGNTYLEWYLOKPGQSPKLLIKVSNRFS 60  
 DB 3 IVMTQVAFSPNPVITIGTASISCRSSQSLNLSGDBGNTYLMWYLOKAGQSPQLLITLSTYRA 62

QY 61 SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYVFCFGSHVPTFGGGLTEIKR 113  
 DB 63 SGVDFRFSGSGSGTDFTLKISRVAEDGVYVCMQRLRIFPGGGLTEIKR 115

RESULT 8  
 KV2C\_HUMAN STANDARD; PRT; 112 AA.

AC P01616;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region ML.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA Dreyer W.J.; Gray W.R.; Hood L.E.;  
 RT "The genetic, molecular, and cellular basis of antibody formation:  
 some facts and a unifying hypothesis";  
 RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR HSP; A01887; K2HUCM.  
 DR HSP; P80362; 1MTL.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON TER 112 112  
 SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7AB8481 CRC64;

Query Match 72.4%; Score 429.5; DB 1; Length 112;  
 Best Local Similarity 70.5%; Pred. No. 1.2e-39;  
 Matches 79; Conservative 19; Mismatches 13; Indels 1; Gaps 1;

QY 2 IVLTQSPFLSPVSIIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIKVSNRFS 61  
 DB 2 IVLTQSPFLSPVTPPEPAPISCRSSQNLNLSGCB-YLWYMLEKPEZSLIYLGSNRS 60  
 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYVFCFGSHVPTFGGGLTEIKR 113  
 DB 61 GVPNFRFSGSGSGTFTLKISRVAZAVGVYVCMQRLRIFPGGGLTEIKR 112

RESULT 9

KV2F\_MOUSE STANDARD; PRT; 113 AA.

AC P01630;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 7S3.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE.

```

RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebbersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01913; KWS78.
DR HSSP; P80362; IWTU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR POSITIVE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 70.2%; Score 419; DB 1; Length 113;
Best Local Similarity 70.5%; Pred. No. 1.7e-38;
Matches 79; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 2 IVLTQSPISPVSLGDPQASISCRSSGSIYHSNGNTYLEWYLGKPGSPKLLIYKSNRFS 61
DB 2 IVMTQAPAFNPVTLTGISFSCRSSKSLQSGKITLYLWLPQPGCPOLLITRMSNLAS 61
62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCGSHVPMFTFGGKLEIK 113
62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCGSHVPMFTFGGKLEIK 113
DB 62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCGSHVPMFTFGGKLEIK 113

RESULT 10
KV2D MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83055101; PubMed=7141411;
RA Herbst H., Chang J.-Y., Aebbersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
RT the group A streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KWS81.
DR HSSP; P01607; IREX.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR POSITIVE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
KW

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BDE5F56D789FBC CRC64;

Query Match 70.2%; Score 416; DB 1; Length 112;
Best Local Similarity 72.1%; Pred. No. 3.5e-38;
Matches 80; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 2 IVLTQSPISPVSLGDPQASISCRSSGSIYHSNGNTYLEWYLGKPGSPKLLIYKSNRFS 61
DB 2 IVMTQAPAFNPVTLTGISFSCRSSKSLQSGKITLYLWLPQPGCPOLLITRMSNLAS 61
62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCGSHVPMFTFGGKLEIK 112
62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCANLQELPYTGGGKLEIK 112
DB 62 GVDPKFGSGSGTDFTLTKISRVEADLVGYCYCANLQELPYTGGGKLEIK 112

RESULT 11
KV4C HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCF-1986) to the EMBL/Genbank/DBJ databases.
CC -----
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DR EMBL; X02290; CA26733.1; -.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR POSITIVE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.

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FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 122 133 FRAMEWORK-4.  
 FT NON TER 43 114 BY SIMILARITY.  
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 67.0%; Score 397.5; DB 1; Length 134;  
 Best Local Similarity 69.0%; Pred. No. 4,4e-36;  
 Matches 78; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSQSIYHSNGN-TYLEMYLQKPGQSPKLLIYKVSNEF 60  
 DB 22 IVMTQSPDLSAVSLGERATINCKSSQSIYSSNKNYLAIVYQKPGQSPKLLIYMASTR 81

QY 61 SGVPDPKFGSGSGGTDFTLKISRVEADLVGVYCCFGSHVPTFGGTGLEIKR 113  
 DB 82 SGVPDRFGSGSGGTDFTLTILSSLDQEDVAVYCCQGYTNLFWTGGGTKEIKR 134

## RESULT 12

KV4B\_HUMAN

STANDARD; PRT; 133 AA.

DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-IV region of precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041853; PubMed=2997712;

RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,

Zachau H.G.;

RT "subgroup IV of human immunoglobulin K light chains is encoded by a

single germline gene.";

RL Nucleic Acids Res. 13:6515-6529(1985).

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: Z00022; CA77317.1; -

DR PIR: A01904; KAHU1.

DR HSP: P80362; IWTU.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003623; P:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG\_1.

DR SMART: SM00406; IG\_1.

DR PROSITE: PS50835; IG\_LIKE; 1.

DR Immunoglobulin V region; Signal.

FT CHAIN 1 133 IG KAPPA CHAIN V-IV REGION JT.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 61 75 FRAMEWORK-2.

FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 83 114 FRAMEWORK-3.

FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 123 132 FRAMEWORK-4.

FT BY SIMILARITY.

FT NON TER 133 133  
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 64.9%; Score 385; DB 1; Length 133;  
 Best Local Similarity 68.1%; Pred. No. 9.8e-35;  
 Matches 77; Conservative 16; Mismatches 18; Indels 2; Gaps 2;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSQSIYHSNGN-TYLEMYLQKPGQSPKLLIYKVSNEF 60  
 DB 22 IVMTQSPDLSAVSLGERATINCKSSQSIYSSNKNYLAIVYQKPGQSPKLLIYMASTR 81

QY 61 SGVPDPKFGSGSGGTDFTLKISRVEADLVGVYCCFGSHVPTFGGTGLEIKR 113  
 DB 82 SGVPDRFGSGSGGTDFTLTILSSLDQEDVAVYCCQGYTNLFWTGGGTKEIKR 133

## RESULT 13

KV2C\_MOUSE

STANDARD; PRT; 113 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region MOPC 511.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=81052016; PubMed=6776396;

RA Appella E.;

RT "Amino acid sequence of the light chain variable region of M511, a

phosphorylcholine-binding murine myeloma protein."

RL Mol. Immunol. 17:711-718(1980).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT

BINDS PHOSPHORYLCHOLINE.

DR PIR: A01910; KVM51.

DR HSP: P80362; IWTU.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG\_1.

DR SMART: SM00406; IG\_1.

DR PROSITE: PS50835; IG\_LIKE; 1.

DR Immunoglobulin V region.

FT CHAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 40 54 FRAMEWORK-2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 62 93 FRAMEWORK-3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 103 112 BY SIMILARITY.

FT NON TER 23 93 BY SIMILARITY.

SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 64.8%; Score 384; DB 1; Length 113;  
 Best Local Similarity 66.1%; Pred. No. 1e-34;  
 Matches 74; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSQSIYHSNGN-TYLEMYLQKPGQSPKLLIYKVSNEF 61  
 DB 2 IVITQDELISKVTVSGESVSLSCRSKSLVYDGTYNLFWTGGGTGLEIKR 61

QY 62 GVPDPKFGSGSGGTDFTLKISRVEADLVGVYCCFGSHVPTFGGTGLEIKR 113  
 DB 62 GVPDRFGSGSGGTDFTLTILSSLDQEDVAVYCCQGYTNLFWTGGGTGLEIKR 113

## RESULT 14

KV4A\_HUMAN

STANDARD; PRT; 114 AA.

AC P01625;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-IV region Len.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=76004342; PubMed=50995;  
 RA Schneider M., Hilschmann N.;  
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RN [2]  
 RP REVISION TO 9.  
 RA Salomon A.;  
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PDB; 1EBQ; 01-FEB-01.  
 DR PDB; 1EEU; 03-FEB-01.  
 DR PDB; 1EFQ; 09-FEB-01.  
 DR PDB; 1EK3; 06-MAR-01.  
 DR PDB; 1LVE; 21-JAN-98.  
 DR PDB; 1LVE; 18-MAY-99.  
 DR PDB; 1LVE; 28-MAR-01.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003066; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SMO0406; IG\_1.  
 DR PROSITE; PSS0835; IG\_Like; 1.  
 DR KX Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 41 55 FRAMEWORK-2.  
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 63 94 FRAMEWORK-3.  
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 113 FRAMEWORK-4.  
 FT DISULFID 23 94 BY SIMILARITY.  
 FT NON TER 114 114  
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D1F236485 CRC64;  
 Query Match 64.7%; Score 383.5; DB 1; Length 114;  
 Best Local Similarity 67.3%; Pred. No. 1.2e-34;  
 Matches 76; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
 QY 2 IYLTQSPPLSLPVSLGDQASISCRSSQSIIVH-SNGNTYLENYLQKPGQSPKLLIYKYSNRF 60  
 Db 2 IYLTQSPDLSAVSLGERATINCKSSQSVIYSSNSKNTLYAQKPPQAPKLLIYNASTHE 61  
 QY 61 SGVPPDKFSSGSGSTDTPTLKISRVEADLGYIYFCQSHVPMWTFGGGTXLEIKR 113  
 Db 62 SGVPPDKFSSGSGSTDTPTLTISLQADVAIVYCOQYRSTPYSGGTXLEIKR 114  
 RESULT 15  
 KVAL MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 63 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE=78235887; PubMed=98179;  
 RA Burslein Y., Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 RT the variable and constant regions of immunoglobulin light chain  
 RT precursors: implications on the organization and controlled  
 RT expression of immunoglobulin genes";  
 RL Biochemistry 17:2392-2400(1978).  
 RN [2]  
 RP SEQUENCE OF 21-131.  
 RX MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences";  
 RL Biochemistry 12:760-771(1973).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 DR PIR; B90412; KMSV6.  
 DR HSSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; IG-1Like.  
 DR InterPro; IPR003066; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SMO0406; IG\_1.  
 DR PROSITE; PSS0835; IG\_Like; 1.  
 DR KX Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 59 73 FRAMEWORK-2.  
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 81 112 FRAMEWORK-3.  
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 122 131 FRAMEWORK-4.  
 FT DISULFID 43 131 BY SIMILARITY.  
 FT NON TER 131 131  
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;  
 Query Match 64.0%; Score 379.5; DB 1; Length 131;  
 Best Local Similarity 68.5%; Pred. No. 3.8e-34;  
 Matches 76; Conservative 10; Mismatches 24; Indels 1; Gaps 1;  
 QY 2 IYLTQSPPLSLPVSLGDQASISCRSSQSIIVH-SNGNTYLENYLQKPGQSPKLLIYKYSNRF 61  
 Db 22 IYLTQSPSLAVSLGQRAITSCRASES-VDSYGNFEMWYQKPPQAPKLLIYNASNLES 80  
 QY 62 GVPDPKSSGSGSTDTPTLKISRVEADLGYIYFCQSHVPMWTFGGGTXLEIKR 112  
 Db 81 GVPDPKSSGSGSTDTPTLTIDPVEADAAIYCOQNDNEDPMWTFGGGTXLEIKR 131  
 Search completed: November 7, 2003, 07:28:07  
 Job time : 8.14686 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 37.2644 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992B-84\_COPY\_137\_249

Sequence: 1 QIVLTQSPPLSPVSLGDQAS.....FQGSHPMTFGGGTKLEIKR 113

Scoring cable: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830529

Maximum DB seq Length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTREMBL\_23:\*

Result No.	Score	Query Match	Length	DB	ID	Description
1	564	95.1	238	11	Q9M37	Q9M37 mus muscula
2	536	90.4	238	11	Q8VC6	Q8VC6 mus muscula
3	505	85.2	104	11	Q9J12	Q9J12 mus musculi
4	505	85.2	239	11	Q8VC5	Q8VC5 mus musculi
5	467	78.8	239	4	Q8KCD0	Q8KCD0 mus sapien
6	465.5	78.5	114	4	Q9UL80	Q9UL80 homo sapien
7	456	76.9	239	4	Q8NEK0	Q8NEK0 homo sapien
8	431	72.7	239	11	Q8K0F8	Q8K0F8 mus musculi
9	368.5	62.1	148	11	Q8K122	Q8K122 mus musculi
10	368.5	62.1	111	11	Q920B9	Q920B9 mus musculi
11	368	62.1	109	4	Q9UL78	Q9UL78 homo sapien
12	339.5	57.3	108	4	Q9UL77	Q9UL77 homo sapien
13	338.5	57.1	103	11	Q9UL80	Q9UL80 mus musculi
14	337	56.8	107	4	Q8E9A5	Q8E9A5 homo sapien
15	337	56.8	109	4	Q8E9A5	Q8E9A5 homo sapien
16	335.5	56.6	108	11	Q8VJ10	Q8VJ10 mus musculi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

17	335.5	56.6	214	1	Q8RIAS	mus musculus
18	334.5	56.4	234	4	Q8NEX1	homo sapien
19	333.5	56.1	107	11	Q9REZ9	mus musculus
20	330	55.6	134	11	Q8VDD0	mus musculus
21	329.5	55.6	233	11	Q91WS9	mus musculus
22	328.5	55.4	108	4	Q91WB3	homo sapien
23	326	55.0	109	4	Q91LB5	homo sapien
24	323.5	54.4	99	11	Q9JL74	mus musculus
25	323.5	54.4	108	4	Q9UL70	homo sapien
26	322.5	54.4	108	4	Q9UL79	homo sapien
27	321	54.1	107	4	Q9UL81	homo sapien
28	320	54.0	112	11	Q8K1F2	mus musculus
29	320	54.0	112	11	Q8K1F3	mus musculus
30	317	53.5	114	11	Q8K1F1	mus musculus
31	316.5	53.4	234	11	Q91WF8	mus musculus
32	314.5	53.0	109	11	Q92UB6	mus musculus
33	313	52.8	106	5	Q90410	schistosoma
34	308.5	52.0	234	11	Q8RO62	mus musculus
35	308.5	52.0	234	11	Q8VCP0	mus musculus
36	306.5	51.7	298	11	Q9OYF0	mus musculus
37	304.5	51.3	101	11	Q9JL78	mus musculus
38	295.5	49.8	107	11	Q9JLB4	mus musculus
39	295	49.7	235	11	Q91ML2	mus musculus
40	287.5	48.5	116	4	Q96P6P	homo sapien
41	283.5	47.8	92	11	Q9JL76	mus musculus
42	283	47.7	117	11	Q8K1F0	mus musculus
43	276.5	46.6	127	11	Q92S59	mus musculus
44	262	44.2	241	11	Q921A6	mus musculus
45	260.5	43.9	234	11	Q8RI08	mus musculus

## ALIGNMENTS

## RESULT 1

ID	Q99M37	PRELIMINARY;	PRT;	238 AA
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AC Q99M37; (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 26.3 kDa protein.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 NCBI\_TaxId:10090;

## RESULT 2

Q8VC16

ID

Q8VC16

PRELIMINARY;

PRT; 238 AA.

AC

Q8VC16

PRELIMINARY;

PRT; 238 AA.

DT

01-MAR-2002

(TREMBlrel. 20, Created)

DT

01-MAR-2002

(TREMBlrel. 20, Last sequence update)

DE

Hypothetical 26.2 kDa protein.

OS

Mus musculus (Mouse).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX

NCBI\_TaxID=10090;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Colon;

RA

Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RL

EMBL; BC019760; AAH19760.1; -

DR

InterPro; IPR003006; IG\_MHC.

DR

InterPro; IPR003596; IG\_V.

DR

PIfam; PF00047; IG; 2.

DR

SMART; SM00406; IG; 1.

DR

PROSITE; PS00290; IG\_MHC; 1.

KM

Hypothetical protein.

SQ

SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match

Best Local Similarity

90.4%; Score 536; DB 11; Length 238;

Matches 101; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY

2

IVLTQSLPLPVSLIGDQASISCRSSQSIYHNGNTYLEWYLOKPGQPKLLIYKVSRRFS 61

DB

21

VVMQTPLSLPVSLIGDQASISCRSSQSIYHNGNTYLEWYLOKPGQPKLLIYKVSRRFS 80

QY

62

GVDPKFGSGSGTDFTLKISRVEADLVGYVCFQSGSHVPTFGGTLKLEIKR 113

DB

81

GVDPKFGSGSGTDFTLKISRVEADLVGYVCFQSGSHVPTFGGTLKLEIKR 132

RESULT 3

Q9UL82

PRELIMINARY;

PRT; 104 AA.

AC

Q9UL82

PRELIMINARY;

PRT; 104 AA.

DT

01-OCT-2000

(TREMBlrel. 15, Created)

DT

01-OCT-2000

(TREMBlrel. 15, Last sequence update)

DE

Anti-myosin immunoglobulin light chain variable region

DB

(Fragment).

OS

Mus musculus (Mouse).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX

NCBI\_TaxID=10090;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN=BALB/c;

RX

MEDLINE=20448942; PubMed=10992488;

RA

Malkiel S., Liao L., Cunningham M.W., Diamond B.;

DR InterPro; IPR00306; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 2634 MW; FAGEDCA3B0871D CRC64;

Query Match 78.8%; Score 467; DB 4; Length 239;  
 Best Local Similarity 77.7%; Pred. No. 1.5e-42;  
 Matches 87; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 2 IYLTGSPSLPVLGPGASISCRSSQSIHSGNNTYLEWYLOKPGQSPKLIYKSNRFS 61  
 DB 22 VMTQSPSLPVLGPGASISCRSSQSLVSDGNTYLMFQPGQSPRLIYKSNRDS 81  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCFCGSHVPTFGGSKLEIKR 113  
 DB 82 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMGSHPTFGGSKLEIKR 133

RESULT 6  
 Q9UL80 PRELIMINARY; PRT; 114 AA.

AC G9UL80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berner S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035034; AAD56270.1; -.  
 DR HSSP; P80362; 1WT.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR SMART; SM00407; IG\_2.  
 FT NON\_TER 1  
 FT NON\_TER 114  
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1C01 CRC64;

Query Match 78.5%; Score 465.5; DB 4; Length 114;  
 Best Local Similarity 78.8%; Pred. No. 8.5e-43;  
 Matches 89; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 2 IYLTGSPSLPVLGPGASISCRSSQSIHSGNNTYLEWYLOKPGQSPKLIYKSNRFS 61  
 DB 2 VMTQSPSLPVLGPGASISCRSSQSLVSDGNTYLMFQPGQSPRLIYKSNRDS 61  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCFCGSHVPTFGGSKLEIKR 113  
 DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMGSHPTFGGSKLEIKR 114

RESULT 7  
 Q8NEKO PRELIMINARY; PRT; 239 AA.  
 AC Q8NEKO;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strussberg R.;  
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC030814; AAH30814.1; -.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00407; IG\_1.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 76.9%; Score 456; DB 4; Length 239;  
 Best Local Similarity 76.8%; Pred. No. 2.4e-41;  
 Matches 86; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 2 IYLTGSPSLPVLGPGASISCRSSQSIHSGNNTYLEWYLOKPGQSPKLIYKSNRFS 61  
 DB 22 VMTQSPSLPVLGPGASISCRSSQSLVSDGNTYLMFQPGQSPRLIYKSNRDS 81  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCFCGSHVPTFGGSKLEIKR 113  
 DB 82 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMGSHPTFGGSKLEIKR 133

RESULT 8  
 Q8KOF8 PRELIMINARY; PRT; 239 AA.

AC Q8KOF8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC031498; AAH31498.1; -.  
 DR InterPro; IPR002198; ADH\_Short.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00407; IG\_1.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341FO CRC64;

Query Match 72.7%; Score 431; DB 11; Length 239;  
 Best Local Similarity 72.3%; Pred. No. 1.2e-38;  
 Matches 81; Conservative 14; Mismatches 17; Indels 0; Gaps 0;



DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 OS (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035037; AAD56273.1; -.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Ig\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
 Query Match 57.3%; Score 339.5; DB 4; Length 108;  
 Best Local Similarity 58.9%; Pred. No. 3.7e-29;  
 Matches 66; Conservative 15; Mismatches 26; Indels 5; Gaps 1;  
 QY 2 IVLTQSPFLSPVSLGDPASISCRSSQSIYHSNGNTYLEWTLQKPGQSPKLLIYKVNRFSS 61  
 Db 2 IQMTQSPSSLSASVGRVITTCASQSI-----SSYIMNYQKPKGAPMLLIYAASLSIQS 56  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCQGSHPVTFPGGGLTKLEIKR 113  
 Db 57 GVPDRFSGSGSGTDFTLTISLTQPEDPAFYTCQGSYSTSWTGEGRVETIKR 108  
 RESULT 13  
 Q9UL80 PRELIMINARY; PRT; 103 AA.  
 AC Q9UL80;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-myosin immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BALE/cj  
 RX MEDLINE=20448942; PubMed=1092448;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin";  
 RL Infect. Immun. 68:5803-5808 (2000).  
 DR EMBL; AF206026; AAF69324.1; -.  
 DR HSSP; P80362; LWTL.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Ig\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 103  
 SQ SEQUENCE 103 AA; 103 MW; C06681716C4D16F3 CRC64;

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;  
 Query Match 57.1%; Score 338.5; DB 11; Length 103;  
 Best Local Similarity 63.1%; Pred. No. 4.5e-29;  
 Matches 65; Conservative 15; Mismatches 22; Indels 1; Gaps 1;  
 QY 10 SLPSVSLGDPASISCRSSQSIYHSNGNTYLEWTLQKPGQSPKLLIYKVNRFSGVDPKFSG 69  
 Db 2 SLAVSLGQRATISCRASSVEY-YGSLMGMWYQKPKGAPMLLIYAASVSGVAPRPSG 60  
 QY 70 SSSGTDFTLKISRVEAEDLGVYCQGSHPVTFPGGGLTKLEIKR 112  
 Db 61 SSSGTDFTLTHIPVEDDIAMFYCCQSRKVPVTFPGGGLTKLEIKR 103  
 RESULT 14  
 Q96SA9 PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes";  
 RL J. Immunol. 151:2020-2031 (1998).  
 DR EMBL; U96396; AAB68785.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Ig\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;  
 Query Match 56.8%; Score 337; DB 4; Length 107;  
 Best Local Similarity 60.7%; Pred. No. 6.3e-29;  
 Matches 68; Conservative 16; Mismatches 22; Indels 6; Gaps 2;  
 QY 2 IVLTQSPFLSPVSLGDPASISCRSSQSIYHSNGNTYLEWTLQKPGQSPKLLIYKVNRFSS 61  
 Db 2 IQMTQSPSSLSASVGRVITTCASQSI-----SSYIMNYQKPKGAPMLLIYAASLSIQS 56  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCQGSHPVTFPGGGLTKLEIKR 113  
 Db 57 GVPDRFSGSGSGTDFTLTISLTQPEDPAFYTCQGSYSTSWTGEGRVETIKR 107  
 RESULT 15  
 Q9UL86 PRELIMINARY; PRT; 109 AA.  
 AC Q9UL86;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin kappa chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; Pubmed=9614934;  
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035028; AAD56264.1; -.  
DR HSSP; P80362; 1WT.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1 109 1  
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 56.8%; Score 337; DB 4; Length 109;  
Best Local Similarity 58.4%; Pred. No. 7.1e-29;  
Matches 66; Conservative 21; Mismatches 22; Indels 4; Gaps 1;

QY 1 QIVLTQSPPLSLPVSGLDQASISGRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRF 60  
Db 1 EIVLTQSPPTLSLFPGERATLSGRASQV---SSSYLAWYQOKPQAPRLIYGTSSRA 56  
QY 61 SGVVDKFFSGSGGTDFTLKISRVEADLGVIYCFQGSHPVPTFGGGTKLEIKR 113  
Db 57 TGIPTDRFSSGSGSTDFTLTISRLEPEDFAVIYCOQYGSSTFTFGPTKVIDIKR 109

Search completed: November 7, 2003, 07:34:34  
Job time : 38.3644 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17, Search time 48.7303 Seconds

(Without alignments)  
368.069 Million cell updates/sec

Title: US-09-661-992B-84\_COPY\_137\_249

Sequence: 1 QIVLTGSPSLPVSIGDQAS.....FGSHVPTFGGTLKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

A\_Geneseq\_19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	100.0	249	22 AAB20434	Anti-FTX/FTXa anti
2	570	96.1	249	9 AAB80154	Biochemical anti
3	567	95.6	115	9 AAB81364	Light chain variab
4	567	95.6	115	22 AAB62301	Chimeric Fv (BABS)
5	567	95.6	249	13 AAB21262	pscfvN01 encoding
6	565	94.9	112	23 AAB15704	Mouse monoclonal a
7	563	94.9	149	17 AAM03199	Anti-idiotypic mono
8	563	94.9	149	20 AAY21545	Monoclonal antibod
9	562	94.8	219	21 AAY95258	WOW-1 Fab light ch

10	561	94.6	149	20 AAY49209	Mab 1A7 light chai
11	561	94.6	149	20 AAY28468	Light chain variab
12	558	94.1	263	20 AAY28470	Vh-(Lk)-Y1 of anti
13	556	93.8	109	23 AAB52310	Fv region SC100 an
14	555	93.6	112	20 AAY49217	Light chain variab
15	555	93.6	238	20 AAY17416	Mouse immunoglobul
16	554	93.4	112	20 AAY05239	7absterone bindi
17	552	93.1	112	16 AAB68741	Mab B3 light chain
18	552	93.1	112	17 AAR95217	B3 immunoglobulin
19	552	93.1	219	15 AAR56235	h66-118/h13-65/11-
20	552	93.1	247	14 AAR30091	H and L chain Fv r
21	552	93.1	249	14 AAR30090	H and L chain Fv r
22	552	93.1	249	17 AAR95213	Heavy and light ch
23	551	92.9	113	13 AAR27011	Hypercalcaemia age
24	551	92.9	132	24 AAB74246	Mouse antibody 4D4
25	550	92.7	112	16 AAR82961	Antibody 3S193 11g
26	550	92.7	573	22 AAG64459	Mouse 6D9 catalyti
27	549	92.6	112	16 AAR79248	Light chain variab
28	549	92.6	112	23 ABL010398	Disulphide stabili
29	549	92.6	113	15 AAR56240	VL region of anti-
30	548	92.4	113	17 AAR92995	Humanised antibody
31	548	92.4	113	17 AAR92993	Monoclonal antibod
32	547	92.2	131	15 AAR52772	Marine KC-4 immuno
33	547	92.2	131	15 AAR52790	Variable light cha
34	547	92.2	131	16 AAR70457	Marine IgG monoclo
35	547	92.2	216	19 AAB53598	Fv region SC100 an
36	546	92.1	131	14 AAR32241	Paragut binding a
37	546	92.1	131	14 AAR31587	Mouse monoclonal a
38	545	91.9	122	20 AAY25399	Antibody 4D4
39	545	91.9	140	19 AAB68492	Mouse monoclonal a
40	544	91.7	114	24 AAB57967	Variable light cha
41	543	91.6	109	23 AAB52311	Marine IgG monoclo
42	543	91.6	112	20 AAB52311	Paragut binding a
43	543	91.6	112	23 AAB5713	Mouse monoclonal a
44	543	91.6	113	19 AAB46959	Antibody 4D4
45	543	91.6	238	15 AAR55864	Antibody 4D4

#### ALIGNMENTS

RESULT 1	AA20434	standard; Protein; 249 AA.
ID	AA20434	standard; Protein; 249 AA.
AC	AA20434	
XX	21-JUN-2001	(first entry)
DT	21-JUN-2001	(first entry)
XX	21-JUN-2001	(first entry)
DE	Anti-FTX/FTXa antibody 193/K2 scFv.	
XX	Factor IX; FTX; Factor IXa; FTXa; scFv; antibody; procoagulant;	
KW	Factor VII cofactor; blood coagulation disorder; haemophilia A;	
KW	haemorrhagic diathesis; haemostatic; amydolytic; therapy; mouse.	
OS	Chimeric - Mus musculus.	
XX	Chimeric - Synthetic.	
XX	Chimeric - Synthetic.	
FT	Key	Location/Qualifiers
FT	Protein	1..121
FT	Region	/label= VH
FT	Region	98..110
FT	Region	/label= CDR3
FT	Region	122..135
FT	Region	/label= Linker
FT	Region	136..249
FT	Region	/label= VL
FT	Region	230..238
FT	Region	/label= CDR3
FN	WO200119992-A2.	
XX	22-MAR-2001.	
PD	22-MAR-2001.	

Mab 1A7 light chain  
Light chain variab  
Vh-(Lk)-Y1 of anti  
Fv region SC100 an  
Light chain variab  
Mouse immunoglobul  
7absterone bindi  
Mab B3 light chain  
B3 immunoglobulin  
h66-118/h13-65/11-  
H and L chain Fv r  
H and L chain Fv r  
Heavy and light ch  
Hypercalcaemia age  
Mouse antibody 4D4  
Antibody 3S193 11g  
Mouse 6D9 catalyti  
Light chain variab  
Disulphide stabili  
VL region of anti-  
Humanised antibody  
Monoclonal antibod  
Marine KC-4 immuno  
Variable light cha  
Fv region SC100 an  
Paragut binding a  
Mouse monoclonal a  
Antibody 4D4  
Antibody 4D4

XX 13-SEP-2000; 2000WO-BP08936.  
XX  
XX 14-SEP-1999; 99AT-0001576.  
XX  
XX (BAXT) BAXTER AG.  
XX  
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dornier F;  
XX WPI; 2001-290358/30.  
XX N-PSDB; AAF30724.  
XX  
XX New factor IX/factor IXa antibodies and their derivatives useful for  
XX increasing amidolytic activity of factor IXa, and for treating blood  
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis  
XX  
XX Claim 10; Fig 15; 138pp; English.  
XX  
XX The present sequence is that of a single chain Fv (scFv) derivative  
XX of antibody 193/K2, comprising the heavy (VH) and light (VL) chain  
XX variable regions of 193/K2 joined by an artificial, flexible linker  
XX peptide. The scFv was obtained by PCR amplification of cDNAs for  
XX 193/K2 VH and VL regions and cloning in vector pDA2. 193/K2 is  
XX an example of anti-human factor IX (FIX)/activated factor IX (FIIa)  
XX antibodies of the invention. Anti-FIX/FIIa and their derivatives,  
XX including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor  
XX activity or FIXa activating activity. Administration leads to an  
XX increase in the procoagulant activity of FIXa, even in the presence  
XX of FVIIa inhibitors. This allows for rapid blood coagulation even  
XX in the absence of FVIII or FVIIa, and in the case of FVIII  
XX inhibitor patients. The antibodies and derivatives are used in a  
XX claimed pharmaceutical composition for treating patients with blood  
XX coagulation disorders, especially haemophilia A and haemorrhagic  
XX diathesis.  
XX  
SQ Sequence 249 AA;  
Query Match 100.0%; Score 593; DB 22; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.5e-44;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QIVLTGSPSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIYKYSNRF 60  
DB 137 QIVLTGSPSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIYKYSNRF 196  
QY 61 SGVPDKFSSGSGGTDFTLKISRVEADLGYVYCFQSGSHVPMTFGGGKLEIKR 113  
DB 197 SGVPDKFSSGSGGTDFTLKISRVEADLGYVYCFQSGSHVPMTFGGGKLEIKR 249  
RESULT 2  
AAP80154  
ID AAP80154 standard; protein; 249 AA.  
XX  
XX AAP80154;  
XX  
XX 31-OCT-2002 (updated)  
XX DT 01-JAN-1980 (first entry)  
XX  
XX Biosynthetic antibody binding site.  
XX DE  
XX Biosynthetic antibody binding site; framework region; assay; imaging;  
XX KW multifunctional protein.  
XX  
XX Homo sapiens.  
XX OS Synthetic.  
XX PN WO8809344-A.  
XX PD 01-DEC-1988.  
XX PF 19-MAY-1988; 88WO-US01737.  
XX

PR 21-MAY-1987; 87US-0052800.  
XX  
XX (CREA-) CREATIVE BIOMOLECULES INC.  
XX  
XX Huston JS, Oppermann H;  
XX WPI; 1988-353928/49.  
XX N-PSDB; AAN80180.  
XX  
XX Recombinant multifunctional protein - having antibody binding site and a  
XX sequence for biological activity, ion sequestering or binding to a  
XX solid support.  
XX  
XX Disclosure; Page 7; 15pp; English.  
XX  
XX The biosynthetic antibody binding site forms part of a recombinant  
XX multifunctional protein which also comprises an effector protein, an AA  
XX acid sequence capable of sequestering an ion, or a sequence capable of  
XX binding to a solid support. The BABS comprises the framework region from  
XX murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region  
XX and the complementarity determining region from G-loop-4 heavy chain  
XX variable region and has lysozyme specificity. The effector protein is an  
XX enzyme, toxin, receptor, binding site, growth factor, cytokine  
XX or antimetabolite. The sequence capable of sequestering an ion is  
XX calmodulin or metallothionein. The sequence capable of binding to solid  
XX support is streptavidin or a protein A fragment. The protein may be used  
XX for, eg specific binding assays, affinity purification, bioassays, drug  
XX targeting, imaging and immunological treatment of oncogenic etc.  
XX diseases. The protein offers fewer cleavage sites to circulating  
XX proteolytic enzymes and have improved stability. They reach target organs  
XX rapidly and are cleared quickly from the body. They also have reduced  
XX immunogenicity.  
XX (updated on 31-OCT-2002 to add missing OS field.)  
XX  
SQ Sequence 249 AA;  
Query Match 96.1%; Score 570; DB 9; Length 249;  
Best Local Similarity 94.6%; Pred. No. 1.6e-42;  
Matches 106; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 IVLTGSPSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIYKYSNRF 61  
DB 136 VVMTQTPTSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPKLLIYKYSNRF 195  
QY 62 GVPDKFSSGSGGTDFTLKISRVEADLGYVYCFQSGSHVPMTFGGGKLEIKR 113  
DB 196 GVPDKFSSGSGGTDFTLKISRVEADLGYVYCFQSGSHVPMTFGGGKLEIKR 247  
RESULT 3  
AAP81364  
ID AAP81364 standard; protein; 115 AA.  
XX  
XX AAP81364;  
XX  
XX 31-OCT-2002 (updated)  
XX DT 17-OCT-1990 (first entry)  
XX  
XX Light chain variable domain of biosynthetic antibody binding domain.  
XX DE  
XX Light chain variable domain of biosynthetic antibody binding domain.  
XX KW light chain variable domain; biosynthetic antibody binding domain.  
XX  
XX Homo sapiens.  
XX OS Mus sp.  
XX OS Synthetic.  
XX PN WO8809344-A.  
XX PD 01-DEC-1988.  
XX PF 19-MAY-1988; 88WO-US01737.  
XX 21-MAY-1987; 87US-0052800.  
XX

XX (CREA-) CREATIVE BIOMOLECULES INC.  
 PA Huston JS, Oppermann H;  
 XX MPI; 1989-353928/49.  
 XX N-PSDB; AAN80173.  
 DR  
 DR  
 PT Recombinant multifunctional protein - having antibody binding site and a  
 PT sequence for biological activity, ion sequestering or binding to a solid  
 PT support.  
 XX  
 XX Disclosure; Page ?; 15pp; English.  
 PS  
 CC The light chain variable domain comprises complementarity determining  
 CC regions of g1p4 and framework regions from murine antidioxin monoclonal  
 CC 26-10. The domain forms part of a single chain multi-functional  
 CC biosynthetic protein. The protein also comprises an effector molecule  
 CC with biological activity (eg an enzyme, receptor binding site, growth  
 CC factor, lymphokine, cytokine or antimetabolite), an amino acid sequence  
 CC capable of sequestering an ion (eg calmodulin or metallothionein), or an  
 CC streptavidin or a fragment of protein A). The protein can be used for  
 CC specific binding assays, affinity purification, biocatalysts, drug targeting,  
 CC imaging and immunological treatment of oncogenic and infectious diseases.  
 CC It offers fewer cleavage sites to circulating proteolytic enzymes, and  
 CC improved stability. It reaches target tissues rapidly and is quickly  
 CC cleared from the body. It also has reduced immunogenicity and its design  
 CC facilitates binding to other moieties in drug targeting and imaging  
 CC applications.  
 CC (Updated on 31-OCT-2002 to add missing OS field.)  
 CC  
 CC  
 SQ Sequence 115 AA;  
 XX  
 Query Match 95.6%; Score 567; DB 9; Length 115;  
 Best Local Similarity 93.8%; Pred. No. 1.3e-42;  
 Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 IYLTQSPFLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPRLTIYKSNRRS 61  
 Db 4 VVMTQPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPRLTIYKSNRRS 63  
 QY 62 GVPDRFSSGSGGTDFTLKISRVAEADLGVYYCFQGSHPVMTFGGSKLEIRK 113  
 Db 64 GVPDRFSSGSGGTDFTLKISRVAEADLGVYYCFQGSHPVMTFGGSKLEIRK 115

RESULT 4  
 AAB62301  
 ID AAB62301 standard; Protein; 115 AA.  
 AC  
 XX  
 XX AAB62301;  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Chimeric Fv (BABS) light chain variable domain.  
 XX  
 KW Biosynthetic; antibody binding site; binding assay; drug targeting;  
 KW biocatalysis; imaging; affinity purification; immunological; oncogenic;  
 KW infectious disease; murine; monoclonal 26-10; anti-dioxin; cytostatic;  
 KW antitumoral; monoclonal g1p-4; anti-lysozyme; chimeric.  
 XX  
 OS Mus sp.  
 XX  
 XX US6207804-B1.  
 XX  
 XX PD 27-MAR-2001.  
 XX  
 XX PF 18-DEC-1995; 95US-0575724.  
 XX  
 PR 21-MAY-1987; 87US-0052800.  
 PR 12-MAR-1992; 92US-0850228.  
 PR 19-OCT-1993; 93US-0139901.

PR 30-JUN-1998; 98US-0213671.  
 XX  
 XX (CURA-) CURAS INC.  
 PA Huston JS, Oppermann H;  
 XX MPI; 2001-280767/29.  
 XX N-PSDB; AAF57658.  
 DR  
 DR  
 PT Novel biosynthetic antibody binding site having chimeric polypeptide  
 PT which defines selective antigen binding region and has CDR and  
 PT framework amino acid sequences homologous to different immunoglobulin  
 PT molecules  
 XX  
 XX Disclosure; Fig 4D; 26pp; English.  
 PS  
 CC The invention relates to a biosynthetic antibody binding site that  
 CC comprises disulfide bonded heavy, light variable region (HVR, LVR)  
 CC defining single, complete antigen (Ag1) binding site. HVR, LVR have  
 CC polypeptide domain having sets of complementarity determining regions  
 CC (CDR) and framework (FR) amino acid sequences homologous to first and  
 CC second immunoglobulin, respectively. The biosynthetic antibody binding  
 CC sites are useful in specific binding assays, affinity purification,  
 CC biocatalysis, drug targeting, imaging immunological treatment of various  
 CC oncogenic and infectious diseases. The present sequence represents the  
 CC light chain variable domain of a chimeric Fv (BABS) comprising the CDRs  
 CC of murine monoclonal g1p-4 (anti-lysozyme) and FRs of murine monoclonal  
 CC 26-10 (anti-dioxin).  
 CC  
 CC  
 SQ Sequence 115 AA;  
 XX  
 Query Match 95.6%; Score 567; DB 22; Length 115;  
 Best Local Similarity 93.8%; Pred. No. 1.3e-42;  
 Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 IYLTQSPFLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPRLTIYKSNRRS 61  
 Db 4 VVMTQPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLOKPGQSPRLTIYKSNRRS 63  
 QY 62 GVPDRFSSGSGGTDFTLKISRVAEADLGVYYCFQGSHPVMTFGGSKLEIRK 113  
 Db 64 GVPDRFSSGSGGTDFTLKISRVAEADLGVYYCFQGSHPVMTFGGSKLEIRK 115

RESULT 5  
 AAR21262  
 ID AAR21262 standard; Protein; 249 AA.  
 AC  
 XX  
 XX AAR21262;  
 DT 21-MAY-1992 (first entry)  
 XX  
 DE pscFvNq11 encoding anti-oxazolone antibody.  
 XX  
 KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;  
 KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package;  
 KW immunoglobulin; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key  
 XX Protein 1..118 Location/Qualifiers  
 XX Peptide 119..118 /label = VH  
 XX Protein 139..249 /label = linker  
 XX /label = VL  
 XX W09201047-A.  
 XX 23-JAN-1992.

PF 10-JUL-1991; 91MO-GB01134.  
 PR 15-MAY-1991; 91GB-0010549.  
 PR 10-JUL-1990; 90GB-0015198.  
 PR 19-OCT-1990; 90GB-0022845.  
 PR 12-NOV-1990; 90GB-0024503.  
 PR 06-MAR-1991; 91GB-0004744.  
 XX  
 PA (CAMB-) CAMBRIDGE ANTIBODY.  
 PA (MEDI-) MED RES COUNCIL.  
 XX  
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 PI Jackson RJ, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;  
 PI Winter GP, Bonnett TP;  
 XX  
 XX WPI; 1992-056862/07.  
 DR N-PSDB; AAQ21096.  
 XX  
 PT Producing members of specific binding pairs - by expression in  
 PT recombinant host cells with a secreting replicable genetic  
 PT display package.  
 XX  
 XX Example 9; Fig 13; 209pp; English.  
 CC Oxazalone is a hapten used for studying the immune response and the  
 CC anti-oxazalone antibody. NQ11, has been described by E. Gheradi, R.  
 CC Pannelli, and C. Milstein, (J. Immunol. Method 126 61-68). A plasmid  
 CC contg. the VH and VL genes of NQ11 was converted to the scFv form  
 CC by inserting the BstEII/SacI fragment of scFvD1.3 myc nucleotides  
 CC 432-499 of AAQ21096) between the VH and VL genes to generate  
 CC pscFvNQ11 (protein sequence shown here). This scFv was cloned into  
 CC pGFPs/Xh (see AAQ21095) to generate pAb NQ11. The specific binding  
 CC of pAb NQ11 was confirmed by ELISA.  
 CC See also AAR21260-307, 309-311; AAR2450, 565-581.  
 XX  
 SQ Sequence 249 AA;  
 Query Match 95.6%; Score 567; DB 13; Length 249;  
 Best Local Similarity 96.4%; Pred. No. 2.9e-42;  
 Matches 108; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 IVLTQSPPLSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
 DB 138 IELTQTPLSIPVSLGDQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 197  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMFTFGGGTKLEIKR 113  
 DB 198 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMFTFGGGTKLEIKR 249  
 RESULT 6  
 ID AAE15704 standard; Protein; 112 AA.  
 AC AAE15704;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Mouse monoclonal antibody alpha 340 light chain variable (VK) region.  
 XX  
 KW Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;  
 KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;  
 KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;  
 KW inhibitor.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FH 24..39 /label= CDR1  
 FT /note= "Complementarity determining region 1"  
 FT 55..68 /label= CDR2  
 FT

FT /note= "Complementarity determining region 2"  
 FT 95..102 /label= CDR3  
 FT /note= "Complementarity determining region 3"  
 XX  
 XX WO200188138-A1.  
 XX  
 XX 22-NOV-2001.  
 XX  
 XX 21-MAY-2001; 2001MO-GB02226.  
 XX  
 XX 19-MAY-2000; 2000GB-0011981.  
 XX 24-AUG-2000; 2000GB-0020794.  
 XX  
 XX (\$CAN-) SCANCEL LTD.  
 XX  
 XX Ellis JRM, Durrant LG;  
 XX  
 XX WPI; 2002-062384/08.  
 XX N-PSDB; AAD25247.  
 DR  
 XX  
 PT New humanized form of mouse monoclonal antibody 340 which binds to  
 PT epidermal growth factor receptor and inhibits binding of growth factor,  
 PT useful for treating colorectal, lung, breast, gastric and ovarian  
 PT cancer.  
 XX  
 XX Claim 6; Fig 2; 53pp; English.  
 CC The present invention relates to a humanised form of the antibody 340 (a  
 CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)  
 CC receptor and inhibits binding of BGF), obtainable from the cell line  
 CC deposited with the ECACC under accession number 97021428. The humanised  
 CC form of the antibody 340 is useful in gene therapy, medicine and in the  
 CC manufacture of a medicament for treatment or prophylaxis of cancer. The  
 CC invention is useful for treating colorectal, lung, breast, gastric or  
 CC ovarian cancers or also for preventing the recurrence of cancer after  
 CC initial treatment or surgery. The invention is also useful for enhancing  
 CC a protective immune response against cancer by optimised immunisation  
 CC schedules. The humanised form of the antibody 340 has reduced  
 CC immunogenicity but shows similar binding to cells expressing EGF  
 CC receptor, as the original murine antibody and has increased ability to  
 CC inhibit the growth of EGF receptor expressing cells. The invention is  
 CC used as cell growth and apoptosis inhibitor. The present sequence  
 CC is mouse monoclonal antibody alpha 340 light chain variable (VK) region.  
 XX  
 SQ Sequence 112 AA;  
 Query Match 95.3%; Score 565; DB 23; Length 112;  
 Best Local Similarity 94.5%; Pred. No. 1.9e-42;  
 Matches 104; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IVLTQSPPLSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
 DB 2 VLMQTPSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMFTFGGGTKLEIKR 111  
 DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMFTFGGGTKLEIKR 111  
 RESULT 7  
 ID AAM03199 standard; Protein; 149 AA.  
 AC AAM03199;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 26-FEB-1997 (first entry)  
 XX  
 XX Anti-idiotype monoclonal antibody 1A7 variable light chain.  
 XX  
 KW Murine; mouse; anti-idiotype; monoclonal antibody; Mab; 1A7;  
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;

KM glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;  
 KM malignant melanoma; soft tissue sarcoma; small cell carcinoma;  
 KM vaccine; treatment; palliate; detection; diagnosis;  
 KM recombinant production; purification; probe; primer; assay;  
 KM amplification; gene therapy.  
 OS Mus musculus.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Region 20..42  
 FT /note= "framework region 1"  
 FT Region 43..58  
 FT /note= "complementarity determining region 1"  
 FT Region 59..73  
 FT /note= "framework region 2"  
 FT Region 74..80  
 FT /note= "complementarity determining region 2"  
 FT Region 81..112  
 FT /note= "framework region 3"  
 FT Region 113..121  
 FT /note= "complementarity determining region 3"  
 FT Region 122..131  
 FT /note= "framework region 4"  
 PN MO9622373-A2.  
 XX  
 XX 25-JUL-1996.  
 XX  
 XX 17-JAN-1996; 96MO-US00882.  
 XX  
 PR 17-JAN-1995; 95US-0372676.  
 PR 16-JAN-1996; 96US-0591196.  
 PR 17-JAN-1995; 95US-0372676.  
 PR 16-JAN-1996; 96US-0591196.  
 XX  
 PA (KENT ) UNIV KENTUCKY.  
 XX  
 PI Chatterjee M, Chatterjee SK, Foon KA,  
 XX  
 DR WPI; 1996-354530/35.  
 DR N-PSDB; AAT31332.  
 PT  
 PT Monoclonal antibody 1A7 and related polynucleotide(s) and  
 PT polypeptide(s) - useful to treat or palliate a GD2-associated  
 XX disease, e.g. melanoma and glioma  
 XX  
 PS Claim 8; Fig 1; 141pp; English.  
 XX  
 CC The present sequence is that of the murine anti-idiotypic monoclonal  
 CC antibody (Mab) 1A7 variable light chain. Mab 1A7 was raised against  
 CC the anti-ganglioside 2 (GD2) Mab 14G2a, which binds an unique  
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high  
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,  
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma  
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat  
 CC or palliate such diseases. They can also be used to reduce the  
 CC risk of recurrence of a clinically detectable tumour, and detect an  
 CC anti-GD2 Ab bound to a tumour cell.  
 CC Mab 1A7 overcomes immune tolerance and induces an immune response  
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and  
 CC GD2-specific cells (cellular response). It can be used to purify  
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or  
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or  
 CC anti-GD2 activity.  
 CC The cDNA can be used in expression systems for 1A7 prodn., and in  
 CC the prepn. of probes and primers to respectively assay for 1A7  
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 149 AA;

Query Match 94.9%; Score 563; DB 17; Length 149;  
 Best Local Similarity 93.8%; Pred. No. 3.8e-42;  
 Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 IVLTQSPPLSLPVSLGPDQASISCRSSQSIYHSNGNTYLEWYLRPGQSPKLLIYKASNRRS 61  
 DB 21 VLMQTPTSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLRPGQSPMLLIYFVSNRRS 80  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCCPGQSHVPTFGGTLRIK 113  
 DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCCPGQSHVPTFGGTLRIK 132  
 RESULT 8  
 ID AAY21545  
 AC AAY21545 standard; Protein; 149 AA.  
 XX  
 AC AAY21545;  
 DT 03-AUG-1999 (first entry)  
 XX  
 DE Monoclonal antibody 1A7 light chain variable region.  
 XX  
 KW Psoriasis; immunological response; anti-idiotypic antibody; glutate;  
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;  
 KW monoclonal antibody; 1A7.  
 XX  
 OS Unidentified.  
 XX  
 PN MO9925380-A2.  
 XX  
 PD 27-MAY-1999.  
 XX  
 PF 17-NOV-1998; 98MO-US24607.  
 XX  
 PR 16-NOV-1998; 98US-0192838.  
 PR 17-NOV-1997; 97US-0065774.  
 XX  
 PA (KENT ) UNIV KENTUCKY RES FOUND.  
 XX  
 PI Chatterjee M, Foon KA;  
 XX  
 DR WPI; 1999-347407/29.  
 DR N-PSDB; AAX0629.  
 PT  
 PT Treatment of psoriasis  
 XX  
 PS Disclosure; Fig 2; 48pp; English.  
 XX  
 CC The invention provides a method of treating of psoriasis by administering  
 CC an antigen which has similar immunogenic properties to an antigen  
 CC expressed on cells of psoriatic tissue so that an immunological response  
 CC is elicited in the individual. The antigen stimulates the generation of  
 CC anti-idiotypic antibodies that neutralize the aberrant immune response  
 CC causing the psoriasis. The method is used to treat psoriasis, especially  
 CC chronic plaque, glutate, pustular, plaque-type psoriasis or psoriatic  
 CC arthritis. The compositions allow the individual's own immune system to  
 CC act against psoriatic tissue. The present sequence represents the light  
 CC chain variable region of monoclonal antibody 1A7.  
 XX  
 SQ Sequence 149 AA;  
 Query Match 94.9%; Score 563; DB 20; Length 149;  
 Best Local Similarity 93.8%; Pred. No. 3.8e-42;  
 Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 IVLTQSPPLSLPVSLGPDQASISCRSSQSIYHSNGNTYLEWYLRPGQSPKLLIYKASNRRS 61  
 DB 21 VLMQTPTSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLRPGQSPMLLIYFVSNRRS 80  
 QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCCPGQSHVPTFGGTLRIK 113  
 DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCCPGQSHVPTFGGTLRIK 132

## RESULT 9

AA95258 standard; Protein, 219 AA.

ID AAY95258

AC AAY95258;

DT 12-SEP-2000 (first entry)

DE MOW-1 Fab light chain.

KW MOW-1; Fab; single chain antibody; PAC-1; monoclonal antibody;

KM mouse; integrin; vitronectin receptor alpha-v beta-3;

KN drug delivery; gene therapy; ligand mimetic.

OS Mus musculus.

PN MOW00034780-A2.

PD 15-JUN-2000.

PF 03-DEC-1999; 99MO-EP09460.

PR 04-DEC-1998; 98US-0110950.

PR 23-JUN-1999; 99US-0145458.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PA (SCRI) SCRIPPS RES INST.

PI Shattil SJ, Nemerow GR, Hato T, Stupack DG, Pampori NA;

DR WPI; 2000-442184/38.

DR N-PSDB; AAA27849.

PT Novel monoclonal antibody that selectively binds activated vitronectin

PS receptor in tissue and for delivering therapeutic composition to the

XX Claim 18; Page 15; 42pp; English.

XX The present sequence is that of the light chain of MOW-1 Fab, a

XX novel monovalent ligand-mimetic that selectively binds to activated

XX vitronectin receptor alpha-v beta-3. MOW-1 Fab was created by

XX replacing the 19 amino acid heavy chain complementarity determining

XX region 3 (CDR3) of PAC1 Fab with the 50 amino acid alpha-v

XX integrin-binding domain from adenovirus type 2 penton base protein

XX by splice-overlap PCR (see AAA27850-53). PAC1 is a known monoclonal

XX antibody which immunoreacts with platelet glycoprotein receptor.

XX The modified PAC1 antibody (designated MOW-1) has been expressed as

XX a His-tagged fusion protein in a Drosophila expression system.

XX MOW-1 Fab is used in a claimed method for detecting the presence of

XX activated vitronectin receptor alpha-v beta-3 in a tissue, and in a

XX claimed method for delivery of an agent in a therapeutic composition

XX to such a tissue ex vivo or in vivo, the tissue being selected from

XX neovascular cells, smooth muscle endothelial cells, arterial cells,

XX osteoclasts and tumour cells. The agent in the therapeutic

XX composition is preferably a biologically active compound, especially

XX a gene, antisense nucleic acid or catalytic nucleic acid (claimed).

SQ Sequence 219 AA;

Query Match 94.8%; Score 562; DB 21; Length 219;

Best Local Similarity 93.8%; Pred. No. 7e-42;

Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 IVLTQSPPLSLPVSLGDASTISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61

Db 2 VMTQTPLSLPVSLGDASTISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61

QY 62 GVPDKFSGSGGTFTLKISRVEAEDLGVYYCFQGSHPVMTFGSGTKLEIKR 113

Db 62 GVPDKFSGSGGTFTLKISRVEAEDLGVYYCFQGSHPVMTFGSGTKLEIKR 113

## RESULT 10

AA49209 standard; Protein, 149 AA.

ID AAY49209

AC AAY49209;

DT 07-FEB-2000 (first entry)

DE MAb 1A7 light chain variable region.

KW Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;

KM neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;

KN tumor-associated antigen.

OS Synthetic.

OS Mus sp.

PN US977316-A.

PD 02-NOV-1999.

PF 16-JAN-1996; 96US-0591196.

PR 17-JAN-1995; 95US-0372676.

PA (KENT) UNIV KENTUCKY.

PA Foon KA, Chatterjee SK, Chatterjee M;

DR WPI; 1999-619711/53.

DR N-PSDB; AA231365.

PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological

PS response, useful for the development of products for the detection and

XX treatment of cancers -

XX Claim 1; Fig 1; 74pp; English.

XX The invention provides a monoclonal antibody (MAb) designated 1A7, which

XX elicits an anti-GD2 (tumor-associated antigen) immunological response in

XX humans. MAb 1A7 has defined light and heavy chain variable region

XX sequences. The MAb 1A7 and polypeptides can be used for eliciting an

XX anti-GD2 immune response. The polypeptides can also be used for detecting

XX or purifying anti-GD2 antibody. The products can be used for treating GD2

XX associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue

XX carcinoma, and small cell carcinoma. They can be used for palliating the

XX disease or for reducing the risk of recurrence. The present sequence

XX represents the light chain variable region of MAb 1A7.

SQ Sequence 149 AA;

Query Match 94.8%; Score 561; DB 20; Length 149;

Best Local Similarity 93.8%; Pred. No. 5.8e-42;

Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTQSPPLSLPVSLGDASTISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61

Db 21 VMTQTPLSLPVSLGDASTISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 80

QY 62 GVPDKFSGSGGTFTLKISRVEAEDLGVYYCFQGSHPVMTFGSGTKLEIKR 113

Db 81 GVPDKFSGSGGTFTLKISRVEAEDLGVYYCFQGSHPVMTFGSGTKLEIKR 132

## RESULT 11

AA28468 standard; Protein, 149 AA.

ID AAY28468

AC AAY28468;



RESULT 13  
ABP52310  
ID ABP52310 standard; peptide; 109 AA.  
XX  
AC ABP52310;  
XX  
DT 17-OCT-2002 (first entry)  
XX  
DE Fv region SC100 antibody light chain related amino acid sequence #1.  
XX  
KW Cytotoxic T lymphocyte; CTL; T helper; MAGB3; cytotoxic T cell response;  
KM tumour; immune response; cancer; vaccine; antibody.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
PN WC02058728-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 28-JAN-2002; 2002WC-GB00354.  
XX  
PR 26-JAN-2001; 2001GB-0002145.  
XX  
PA (SCAN-) SCANCEL LTD.  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX  
PI Durrant LG, Parsons T, Robins A;  
XX  
DR WPI; 2002-608418/65.  
XX  
PT Use of polypeptides and nucleic acids encoding the polypeptides, in  
PT manufacturing medicament for stimulating a cytotoxic T cell response  
PT and for preventing or treating cancer, e.g. colorectal, lung, breast or  
PT ovarian cancer -  
XX  
PS Example 11; Page 38; 87pp; English.  
XX  
CC The present invention describes the use of a polypeptide (1) in the  
CC manufacture of a medicament for stimulating a cytotoxic T cell response,  
CC where (1) comprises a first portion comprising the part of human FC that  
CC binds to CD64 and a second portion comprising one or more heterologous  
CC T cell epitopes. Also described is a method of stimulating a cytotoxic  
CC T cell response in a patient such as a mammal, preferably human, by  
CC administering (1) to the patient. (1) has cytostatic activity and can  
CC be used in vaccine production. (1) and the nucleic acid encoding (1) are  
CC useful in the manufacture of a medicament for stimulating cytotoxic T  
CC cell response. The medicament is useful for preventing and/or treating  
CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The  
CC medicament stimulates cytotoxic and helper T cell responses. The  
CC antibodies are useful as vaccines to stimulate helper and cytotoxic T  
CC cell responses. The polypeptides and nucleic acids are useful in  
CC optimising immunisation schedules for enhancing a protective immune  
CC response against cancer. The present sequence represents an Fv region  
CC SC100 antibody light chain related amino acid sequence which is used in  
CC an example from the present invention.  
XX  
SQ Sequence 109 AA;  
XX  
Query Match 93.8%; Score 556; DB 23; Length 109;  
Best Local Similarity 94.4%; Pred. No. 1.1e-41;  
Matches 102; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2 IYLTQSPPLSLPVSLGGDAISCRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61  
DB 2 VLMITQPLSLPVSLGGDAISCRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61  
XX  
QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGGTKL 109  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGGTKL 109  
XX  
RESULT 14

AAV49217  
ID AAV49217 standard; Protein; 112 AA.  
XX  
AC AAV49217;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Light chain variable region consensus sequence.  
XX  
KW Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;  
KM neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;  
XX tumour-associated antigen.  
XX  
OS Synthetic.  
XX  
PN US5977316-A.  
XX  
PD 02-NOV-1999.  
XX  
PF 16-JAN-1996; 96US-0591196.  
XX  
PR 17-JAN-1995; 95US-0372676.  
XX  
PA (KENT) UNIV KENTUCKY.  
XX  
PI Foon KA, Chatterjee SK, Chatterjee M;  
XX  
DR WPI; 1999-619711/53.  
XX  
PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological  
PT response, useful for the development of products for the detection and  
PT treatment of cancers -  
XX  
PS Disclosure; Fig 3C; 74pp; English.  
XX  
CC The invention provides a monoclonal antibody (Mab) designated 1A7, which  
CC elicits an anti-GD2 (tumour-associated antigen) immunological response in  
CC humans. Mab 1A7 has defined light and heavy chain variable region  
CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an  
CC anti-GD2 immune response. The polypeptides can also be used for detecting  
CC or purifying anti-GD2 antibody. The products can be used for treating GD2  
CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue  
CC carcinoma, and small cell carcinoma. They can be used for palliating the  
CC disease or for reducing the risk of recurrence. The present sequence  
CC represents the light chain variable region consensus sequence.  
XX  
SQ Sequence 112 AA;  
XX  
Query Match 93.6%; Score 555; DB 20; Length 112;  
Best Local Similarity 93.7%; Pred. No. 1.4e-41;  
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 2 IYLTQSPPLSLPVSLGGDAISCRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61  
DB 2 VLMITQPLSLPVSLGGDAISCRSSQSIYHSNGNTYLEWYLQKPGQSPKLLIYKSNRFS 61  
XX  
QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGGTKL 112  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSGSHVPMTFGGGTKL 112  
XX  
RESULT 15  
AAV17416  
ID AAV17416 standard; Protein; 238 AA.  
XX  
AC AAV17416;  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE Mouse immunoglobulin E light chain.  
XX  
KM Mouse; immunoglobulin E; IgE; allergy; transgenic animal.  
XX

OS Mus sp.

Key	Location/Qualifiers
EH	1.19
FT	

1.19

FT	Protein	/label= signal
FT	Protein	20..238

```

FT      /label= immunoglobulin_E_light_chain
xy

```

PN EP921189-A1.

PD 09-JUN-1999

PF 13-NOV-1998; 98EP-0309340.

AA 14-NOV-1997; 97JP-0313989.  
PR

XX  
PA (SANY ) SANKYO CO LTD,

PA (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.  
XX

PI Karasuyama H, Matsuoka K, Taya C, Yonemawa H, Yv

DR WPI; 1999-315404/27.

XX

[illegible]

XX  
XX

(STATIN NO; EAGLE NO; DATE; SUGGESTION)

The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IGE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is useful as a model for evaluating the activity and the ability of substances i.e. with anti-allergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IGE) light chain, given in the present invention.

Sequence 238 AA;

Query Match 93.6%; Score 555; DB 20; Length 238;

Matches 104; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 IWTQSP LSPVSLGDQASISCRSSQSI VHSNGNTYLEWYLQKPQSPKLLIYKVSNRRS 61

Db 21 VLMQTPLSPVSLGDQASISCRSSQSI VHSNGNTYL EWTY LQKPQSPKLL YKVSNRFS 80C

QY 62 GVPDKFSGSGSTDTLKISRVEAEDLGVYYCFCGSHVPWTFGGGTKLEIKR 113

db 81 GVPDRFSGSGTDFLTAKISRVEAEDLGYYCFOGSHVPLTFGAGTKLEIKR 132

Search completed: November 7, 2003, 07:27:01  
Job time : 49.7303 secs

Job time : 49.7303 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 7, 2003, 07:30:19 ; Search time 99.1202 Seconds  
(Without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992b-84\_COPY\_137\_249

Sequence: 1 QIVLQSPISLPVSLGDDAS.....FGSHVPTFGGKTLKLR 113

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US10A\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	96.3	112	11 US-09-995-529-10	Sequence 10, Appl
2	563	94.9	149	10 US-09-990-205-2	Sequence 2, Appl
3	561	94.6	149	15 US-10-153-401-2	Sequence 2, Appl
4	558	94.1	263	15 US-10-153-401-66	Sequence 66, Appl
5	555	93.6	112	15 US-10-153-401-15	Sequence 15, Appl
6	551	92.9	132	14 US-10-006-773-15	Sequence 15, Appl
7	541	91.2	114	9 US-09-217-268B-27	Sequence 27, Appl
8	541	91.2	140	9 US-09-341-894-4	Sequence 4, Appl
9	535	90.2	132	9 US-09-736-744-16	Sequence 16, Appl
10	535	90.2	132	12 US-10-231-452-64	Sequence 16, Appl
11	534	90.1	131	12 US-10-010-942B-14	Sequence 14, Appl
12	531	89.5	111	10 US-09-948-049-2	Sequence 2, Appl
13	526	88.7	112	11 US-09-518-737-4	Sequence 4, Appl
14	525	88.5	131	12 US-09-947-839-95	Sequence 95, Appl
15	525	88.5	252	10 US-09-887-853-4	Sequence 4, Appl

16	523	88.2	113	12 US-10-277-471A-6	Sequence 6, Appl
17	523	88.2	262	12 US-10-277-471A-5	Sequence 5, Appl
18	522	88.0	131	15 US-10-138-505-6	Sequence 6, Appl
19	522	88.0	271	15 US-10-138-505-30	Sequence 30, Appl
20	522	88.0	274	15 US-10-138-505-26	Sequence 26, Appl
21	521	87.9	285	9 US-09-883-758-4	Sequence 4, Appl
22	519	87.5	131	15 US-10-138-505-10	Sequence 10, Appl
23	519	87.5	245	15 US-10-138-505-05	Sequence 40, Appl
24	519	87.5	271	15 US-10-138-505-34	Sequence 34, Appl
25	519	87.5	131	12 US-10-138-505-32	Sequence 32, Appl
26	515	87.0	131	12 US-09-947-839-11	Sequence 11, Appl
27	515	86.8	474	15 US-10-270-555-3	Sequence 45, Appl
28	512.5	86.4	127	12 US-09-753-435-45	Sequence 45, Appl
29	512.5	86.4	127	12 US-10-163-942-45	Sequence 45, Appl
30	512	86.3	112	10 US-09-982-992A-4	Sequence 4, Appl
31	512	86.3	131	11 US-09-726-258-35	Sequence 35, Appl
32	512	86.3	242	11 US-09-726-258-42	Sequence 42, Appl
33	508	85.7	112	12 US-10-231-452-8	Sequence 8, Appl
34	508	85.7	298	9 US-09-883-758-2	Sequence 2, Appl
35	507	85.5	112	12 US-10-231-452-12	Sequence 12, Appl
36	505	85.2	112	12 US-10-231-452-13	Sequence 13, Appl
37	504	85.0	112	12 US-10-231-452-14	Sequence 14, Appl
38	503	84.8	100	10 US-09-840-459-28	Sequence 28, Appl
39	502	84.7	116	9 US-09-753-435-66	Sequence 66, Appl
40	502	84.7	116	12 US-10-163-942-66	Sequence 66, Appl
41	500	84.3	100	10 US-09-840-459-26	Sequence 26, Appl
42	500	84.3	111	15 US-10-194-975-119	Sequence 119, Appl
43	494.5	83.4	114	11 US-09-726-258-45	Sequence 45, Appl
44	487	82.1	100	10 US-09-840-459-25	Sequence 25, Appl
45	484	81.6	138	9 US-09-748-960-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-09-995-529-10  
Sequence 10, Application US/09995529  
Publication No. US20030099655A1  
GENERAL INFORMATION:  
APPLICANT: Wackins, Jeffrey D.  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Humanized Collagen Antibodies and  
FILE REFERENCE: P-IX 4976  
CURRENT APPLICATION NUMBER: US/09/995,529  
CURRENT FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-995-529-10

Query Match 96.3%; Score 571; DB 11; Length 112;  
Best Local Similarity 95.5%; Pred. No. 1.9e-49;  
Matches 106; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLQSPISLPVSLGDDASTSCRSSGSIWNSNGTYLEWYLOKFGSPKLIYVSNRFS 61  
DB 2 VLMQYPLSLPLVSLGDDASTSCRSSGSIWNSNGTYLEWYLOKFGSPKLIYVSNRFS 61  
QY 62 GVDPKFGSGSGGTDFTLKISRVEAEDGAVYYCFQSGHVPMTFGGKTLKLR 112  
DB 62 GVDPKFGSGSGGTDFTLKISRVEAEDGAVYYCFQSGHVPMTFGGKTLKLR 112

RESULT 2  
US-09-990-205-2  
Sequence 2, Application US/09990205  
Patent No. US20020150572A1

GENERAL INFORMATION:  
APPLICANT: FOON, Kenneth A.  
TITLE OF INVENTION: CHATTERJEE, Malaya  
FILE REFERENCE: 304142000501  
CURRENT APPLICATION NUMBER: US/09/990,205  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: U.S. 09/192,838  
PRIOR FILING DATE: 1998-11-16  
PRIOR APPLICATION NUMBER: U.S. 60/065,774  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Mus Musculus  
US-09-990-205-2

Query Match 94.6%; Score 563; DB 10; Length 149;  
Best Local Similarity 93.8%; Pred. No. 1,7e-48;  
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYLTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLYEWLQKPGQSPRLITYKSNRFS 61  
DB 21 VMTQTPTSLPVSIGDQASISCRSSQSIYHSNGNTYLYEWLQKPGQSPRLITYKSNRFS 80

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMTFGGKLEIKR 113  
DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMTFGGKLEIKR 132

RESULT 3  
US-10-153-401-2  
Sequence 2, Application US/10153401  
Publication No. US20030114398A1  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/153,401  
FILING DATE: 27-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/293,533  
FILING DATE: 1999-04-15  
APPLICATION NUMBER: US 08/372,676  
FILING DATE: 1995-01-17  
APPLICATION NUMBER: US 08/591,196  
FILING DATE: 1996-01-16  
ATTORNEY/AGENT INFORMATION:  
NAME: Catherine M. Polizzi  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 304142000202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792

TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-153-401-2

Query Match 94.6%; Score 561; DB 15; Length 149;  
Best Local Similarity 93.8%; Pred. No. 2.6e-48;  
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYLTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLYEWLQKPGQSPRLITYKSNRFS 61  
DB 21 VMTQTPTSLPVSIGDQASISCRSSQSIYHSNGNTYLYEWLQKPGQSPRLITYKSNRFS 80

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMTFGGKLEIKR 113  
DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFCGSHVPMTFGGKLEIKR 132

RESULT 4  
US-10-153-401-66  
Sequence 66, Application US/10153401  
Publication No. US20030114398A1  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/153,401  
FILING DATE: 27-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/293,533  
FILING DATE: 1999-04-15  
APPLICATION NUMBER: US 08/372,676  
FILING DATE: 1995-01-17  
APPLICATION NUMBER: US 08/591,196  
FILING DATE: 1996-01-16  
ATTORNEY/AGENT INFORMATION:  
NAME: Catherine M. Polizzi  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 304142000202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-10-153-401-66



DB 62 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 113

## RESULT 8

US-09-341-894-4  
; Sequence 4, Application US/09341894  
; Patent No. US2002016839A1  
; GENERAL INFORMATION:  
; APPLICANT: Piechaczky, Marc  
; APPLICANT: No. US2002016839A11, Daniele  
; TITLE OF INVENTION: Biological material for treating a mammal by antibody gene transfe  
; TITLE OF INVENTION: Pharmaceutical composition containing same  
; FILE REFERENCE: 1994-002  
; CURRENT APPLICATION NUMBER: US/09/341,894  
; CURRENT FILING DATE: 1999-12-15  
; PRIOR APPLICATION NUMBER: FR97/00540  
; PRIOR FILING DATE: 1997-01-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 4  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(420)  
; OTHER INFORMATION: Sequence coding for the variable region of the antibody light ch  
; OTHER INFORMATION: ain  
US-09-341-894-4

Query Match 91.2%; Score 541; DB 10; Length 140;  
Best Local Similarity 90.2%; Pred. No. 2.4e-46;  
Matches 101; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPISLSPVSIAGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 61  
DB 21 VMTQTPLSLPVSLGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 80

QY 62 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 113  
DB 81 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 132

## RESULT 9

US-09-796-744-16  
; Sequence 16, Application US/09796744  
; Patent No. US20020098527A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITTARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: SHOUT, EMI  
; APPLICANT: SAKURADA, MIKIKO  
; APPLICANT: FURUYA, AKIO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: NIWA, RINPEI  
; APPLICANT: SHIBATA, KENJI  
; APPLICANT: YAMASAKI, MOTOO  
; TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
; FILE REFERENCE: 249-170  
; CURRENT APPLICATION NUMBER: US/09/796,744  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: JP 2000-59508  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: JP 2000-401563  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-796-744-16

Query Match 90.2%; Score 535; DB 9; Length 132;  
Best Local Similarity 87.5%; Pred. No. 8.8e-46;  
Matches 98; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPISLSPVSIAGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 61  
DB 21 VMTQTPLSLPVSLGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 80

QY 62 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 113  
DB 81 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 132

## RESULT 10

US-10-231-452-64  
; Sequence 64, Application US/10231452  
; Publication No. US20030175273A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITTARA, KENYA  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: HOSAKA, EMI  
; APPLICANT: TANAKA, AKIO  
; APPLICANT: KOIKE, MASAMICHI  
; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
; FILE REFERENCE: 249-273  
; CURRENT APPLICATION NUMBER: US/10/231,452  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: JP 2001-265144  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 64  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-231-452-64

Query Match 90.2%; Score 535; DB 12; Length 132;  
Best Local Similarity 87.5%; Pred. No. 8.8e-46;  
Matches 98; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPISLSPVSIAGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 61  
DB 21 VMTQTPLSLPVSLGDQASISCRSSQSIYHSNNGNTYLEMYLQKPGQSPKLLIYKSNRFS 80

QY 62 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 113  
DB 81 GVPDRFSGSGGTDFTLKISRVEADLGYYVCFQSHVPTFGGKLEIKR 132

## RESULT 11

US-10-010-942B-14  
; Sequence 14, Application US/10010942B  
; Publication No. US20030165496A1  
; GENERAL INFORMATION:  
; APPLICANT: Bassi, Guriq  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
; FILE REFERENCE: EAM-002  
; CURRENT APPLICATION NUMBER: US/10/010,942B  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL

LOCATION: (1)...(19)  
US-10-010-942B-14

Query Match 90.1%; Score 534; DB 12; Length 131;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
Matches 97; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTPSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 61  
DB 21 VMTQTPLSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 80

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 112  
DB 81 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 131

## RESULT 12

US-09-948-049-2  
Sequence 2, Application US/09948049  
Patent No. US20020156036A1  
GENERAL INFORMATION:

APPLICANT: Nicolau, Yves Claude

TITLE OF INVENTION: Methods and Compositions for Diseases Associated with Amyloidosis

FILE REFERENCE: 14723-0112 49055-261163

CURRENT APPLICATION NUMBER: US/09/948,049

PRIOR FILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: US 60/255,033

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: US 60/230,391

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 111

TYPE: PRT

ORGANISM: Murinae gen. sp.

US-09-948-049-2

Query Match 89.5%; Score 531; DB 10; Length 111;  
Best Local Similarity 89.0%; Pred. No. 1.8e-45;  
Matches 97; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTPSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 61  
DB 3 VMTQTPLSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 62

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 110  
DB 63 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 111

RESULT 13  
US-09-518-737-4  
Sequence 4, Application US/09518737  
Patent No. US2003008321A1  
GENERAL INFORMATION:

APPLICANT: FUKUI, YASUHIKA

APPLICANT: NAGATA, SATOSHI

APPLICANT: SHIRAI, RYUICHI

APPLICANT: SATO, NAOKI

TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING

FILE REFERENCE: 1965/49618

CURRENT APPLICATION NUMBER: US/09/518,737

PRIOR FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: JP 1999-250209

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 112

TYPE: PRT

ORGANISM: Mus musculus

US-09-518-737-4

Query Match 88.7%; Score 526; DB 11; Length 112;  
Best Local Similarity 88.3%; Pred. No. 5.8e-45;  
Matches 98; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTPSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 61  
DB 2 VMTQTPLSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 61

QY 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 112  
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGYVYFCQSHVPTFGGKTLK 112

## RESULT 14

US-09-947-839-95  
Sequence 95, Application US/09947839  
Patent No. US20030138428A1  
GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

Peterson Dr., Roberto L.

Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue peptides with Broad

Carcinoma Specificity, and Kit and

Diagnostic Vaccination and

Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESS: Pretty, Schroeder & Poplawski

STREET: 444 South Flower St., 19th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839

FILING DATE: 06-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/976,288

FILING DATE: <Unknown>

APPLICATION NUMBER: 07/977,696

FILING DATE: No. US20030138428A1ember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P6639938

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 95:

US-09-947-839-95

Query Match 88.5%; Score 525; DB 12; Length 131;  
Best Local Similarity 87.4%; Pred. No. 8.7e-45;  
Matches 97; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTPSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQSPKLLIKYNSRFS 61

Db 21 VMTQTPLSLPVTDFGPASISCRSSQSIHNSNGNTYLEWYLQKFGQSPQULLYKVSIRFS 80  
QY 62 GVDPKFGSGSGTDFTLTKISRVEADLGVYYCFQSGSHVPTFGGKLEIK 112  
81 GVDPKFGSGSGTDFTLTKISRVEADLGVYYCFQSGSHVPTFGGKLEIK 131

RESULT 15  
US-09-887-853-4

; Sequence 4, Application US/09887853  
; Patent No. US20020168375A1

## GENERAL INFORMATION:

APPLICANT: Huston, James S.  
Oppermann, Hermann  
Huston, L. L.  
Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins for  
Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-887-853-4

Query Match 88.5%; Score 525; DB 10; Length 252;

Best Local Similarity 88.4%; Pred. No. 1,8e-44;

Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYLTGSLPLSLPVLGPAASISCRSSQSIHNSNGNTYLEWYLQKFGQSPQULLYKVSIRFS 61  
DB 135 VVMTQTPLSLPVLGPAASISCRSSQSIHNSNGNTYLEWYLQKFGQSPQULLYKVSIRFS 194  
QY 62 GVDPKFGSGSGTDFTLTKISRVEADLGVYYCFQSGSHVPTFGGKLEIK 113  
DB 81 GVDPKFGSGSGTDFTLTKISRVEADLGVYYCFQSGSHVPTFGGKLEIK 131  
QY 195 GVDPKFGSGSGTDFTLTKISRVEADLGVYYCFQSGSHVPTFGGKLEIK 246

Search completed: November 7, 2003, 08:16:52  
Job time: 100.12 secs



SEQ ID NO 2  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Mus Musculus  
US-09-324-191-2

Query Match 94.9%; Score 563; DB 4; Length 149;  
Best Local Similarity 93.8%; Pred. No. 1.1e-47;  
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYLTGSPISLPVSLDQASISCRSSQSIHNSNGTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 21 VLMTQTPISLPVSLDQASISCRSSQSIHNSNGTYLEWYLOKPGQSPKLLIYKVSNRFS 80  
QY 62 GVPDFSGSGSGGTDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTLEIKR 113  
DB 81 GVPDFSGSGSGGTDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTLEIKR 132

## RESULT 3

US-08-331-398A-67  
Sequence 67, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pal, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TIME OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331.398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
OTHER INFORMATION: Light chain region"

US-08-331-398A-67

Query Match 94.8%; Score 562; DB 1; Length 125;  
Best Local Similarity 94.6%; Pred. No. 1.2e-47;  
Matches 106; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYLTGSPISLPVSLDQASISCRSSQSIHNSNGTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
DB 2 VLMTQTPISLPVSLDQASISCRSSQSIHNSNGTYLEWYLOKPGQSPKLLIYKVSNRFS 61  
QY 62 GVPDFSGSGSGGTDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTLEIKR 113  
DB 62 GVPDFSGSGSGGTDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTLEIKR 113

## RESULT 4

US-08-331-397B-67  
Sequence 67, Application US/08331397B  
Patent No. 5981726  
GENERAL INFORMATION:  
APPLICANT: Benhar, Itai  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Use  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331.397B  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126120US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
OTHER INFORMATION: Light chain region"

Query Match 94.8%; Score 562; DB 2; Length 125;  
Best Local Similarity 94.6%; Pred. No. 1.2e-47;  
Matches 106; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSLPVSLISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 61  
DB 2 VLTQTPLSLPVSISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 61  
QY 62 GVPDKFSGSGGTFTLTISRVEAEDGYYICFCGSGSVHPPTFGGKTLKLR 113  
DB 62 GVPDRFSGSGGTFTLTISRVEAEDGYYICFCGSHVPTFGGKTLKLR 113

## RESULT 5

US-08-759-804A-66  
Sequence 66, Application US/08759804A  
Patent No. 5990296  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David J.  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Rai, Lee  
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,804A  
FILING DATE: 03-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,398  
FILING DATE: 28-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-126140US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 FV  
OTHER INFORMATION: Light chain region"  
US-08-759-804A-66

Query Match 94.8%; Score 562; DB 2; Length 125;  
Best Local Similarity 94.8%; Pred. No. 1.2e-47;  
Matches 106; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 IVLTQSPFLSLPVSLISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 61

DB 2 VLTQTPLSLPVSISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 61  
QY 62 GVPDKFSGSGGTFTLTISRVEAEDGYYICFCGSGSVHPPTFGGKTLKLR 113  
DB 62 GVPDRFSGSGGTFTLTISRVEAEDGYYICFCGSHVPTFGGKTLKLR 113

## RESULT 6

US-08-752-844-2  
Sequence 2, Application US/08752844  
Patent No. 5935821  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schilff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-844-2

Query Match 94.8%; Score 561; DB 2; Length 149;  
Best Local Similarity 93.8%; Pred. No. 1.8e-47;  
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSLPVSLISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 61  
DB 21 VLTQTPLSLPVSISGDPASISCRSSQSIIVHSNGNTYLEWTLQKPGQSPKLLIYKSNRFS 80  
QY 62 GVPDKFSGSGGTFTLTISRVEAEDGYYICFCGSGSVHPPTFGGKTLKLR 113  
DB 62 GVPDRFSGSGGTFTLTISRVEAEDGYYICFCGSHVPTFGGKTLKLR 132

## RESULT 7

US-08-591-196-2  
Sequence 2, Application US/08591196  
Patent No. 5973216  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,196  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-196-2

Query Match 94.6%; Score 561; DB 2; Length 149;  
Best Local Similarity 93.8%; Pred. No. 1.8e-47;  
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYLTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLQKPGQSPFLIYKYSNRF 61  
DB 21 VEMTQTPSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLQKPGQSPFLIYFVSNRF 80

QY 62 GVPDKFSSGSGSTDTFTLKISRVEADLGVYVCFQGSHPMTFGGTKEIKR 113  
DB 81 GVPDRFSSGSGSTDTFTLKISRVEADLGVYVCFQGSHPMTFGGTKEIKR 132

RESULT 8  
US-09-293-533-2  
Sequence 2, Application US/09293533  
Patent No. 6509016  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,533  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-293-533-2

Query Match 94.6%; Score 561; DB 4; Length 149;  
Best Local Similarity 93.8%; Pred. No. 1.8e-47;  
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYLTQSPPLSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLQKPGQSPFLIYKYSNRF 61  
DB 21 VEMTQTPSLPVSIGDQASISCRSSQSIYHSNGNTYLEWYLQKPGQSPFLIYFVSNRF 80

QY 62 GVPDKFSSGSGSTDTFTLKISRVEADLGVYVCFQGSHPMTFGGTKEIKR 113  
DB 81 GVPDRFSSGSGSTDTFTLKISRVEADLGVYVCFQGSHPMTFGGTKEIKR 132

RESULT 9  
US-08-752-844-66  
Sequence 66, Application US/08752844  
Patent No. 5935821  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-752-844-66

Query Match 94.1%; Score 558; DB 2; Length 263;  
Best Local Similarity 93.7%; Pred. No. 6.6e-47;  
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 61  
DB 153 VLMTQTFPLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 212  
QY 62 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 112  
DB 213 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 263

## RESULT 10

US-09-293-533-66  
Sequence 66, Application US/09293533  
Patent No. 6509016

GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,533  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-293-533-66

Query Match 94.1%; Score 558; DB 4; Length 263;  
Best Local Similarity 93.7%; Pred. No. 6.6e-47;  
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 61  
DB 153 VLMTQTFPLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 212  
QY 62 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 112  
DB 213 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 263

## RESULT 11

US-08-752-844-15  
Sequence 15, Application US/08752844  
Patent No. 5935821

GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-752-844-15

Query Match 93.6%; Score 555; DB 2; Length 112;  
Best Local Similarity 93.7%; Pred. No. 5e-47;  
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPFLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 61  
DB 2 VLMTQTFPLSPVSLGDDASISCRSSOSIVHNGNTYLEWTLQKPGSPKLLIYVSNRFS 61  
QY 62 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 112  
DB 62 GVPDRFSGSGSGDTFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGLTLK 112

## RESULT 12

US-08-591-196-15

Sequence 15, Application US/08591196  
Patent No. 5977316  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Foon, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,196  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-591-196-15

Query Match 93.6%; Score 555; DB 2; Length 112;  
Best Local Similarity 93.7%; Fred. No. 5e-47; 2; Indels 0; Gaps 0;  
Matches 104; Conservative 5; Mismatches 2;

QY 2 IVLTQSPVLSPLPSVLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 61  
DB 2 VLMQTPLSLPVSLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 61

QY 62 GVPDKFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 112  
DB 62 GVPDRFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 112

RESULT 13  
US-09-293-533-15  
Sequence 15, Application US/09293533  
Patent No. 6509016  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
APPLICANT: Room, Kenneth A.  
APPLICANT: Chatterjee, Sunil K.  
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
NUMBER OF SEQUENCES: 66  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,533  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,844  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Schiff, J. Michael  
REGISTRATION NUMBER: 40,253  
REFERENCE/DOCKET NUMBER: 30414-20002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-293-533-15

Query Match 93.6%; Score 555; DB 4; Length 112;  
Best Local Similarity 93.7%; Fred. No. 5e-47;  
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPVLSPLPSVLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 61  
DB 2 VLMQTPLSLPVSLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 61

QY 62 GVPDKFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 112  
DB 62 GVPDRFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 112

RESULT 14  
US-09-192-545-4  
Sequence 4, Application US/09192545  
Patent No. 6118044  
GENERAL INFORMATION:  
APPLICANT: Karasuyama, Hajime  
APPLICANT: Yonekawa, Hiromichi  
APPLICANT: Taya, Choji  
APPLICANT: Matsuo, Kunie  
TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their U  
FILE REFERENCE: 79979570  
CURRENT APPLICATION NUMBER: US/09/192,545  
CURRENT FILING DATE: 1998-11-13  
EARLIER APPLICATION NUMBER: JP HEI 9-313989  
EARLIER FILING DATE: 1997-11-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES: Description of Artificial Sequence: Designed heavy  
US-09-192-545-4

Query Match 93.6%; Score 555; DB 3; Length 238;  
Best Local Similarity 92.9%; Fred. No. 1.2e-46;  
Matches 104; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVLTQSPVLSPLPSVLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 61  
DB 21 VLMQTPLSLPVSLSGQASISCRSSQSIIVHSNGNTYLEWYLQKRGSPKLLIYKVSNRFS 80

QY 62 GVPDKFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 113  
DB 81 GVPDRFGSGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGTRLEIK 132

RESULT 15  
US-08-331-398A-48  
Sequence 48, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira

```

APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-3600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..112
OTHER INFORMATION: /note="Mouse monoclonal antibody B3"
OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-398A-48

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```

Query Match          93.1%; Score 552; DB 1; Length 112;
Best Local Similarity 93.7%; Pred. No. 9.7e-47;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY 2 IVLTQSPRLSPVSLGQASISCRSSQSIYHSNGNTYLEWYLOKPGQSEPLIYKYSNRFS 61
DB 2 VIMTQSPRLSPVSLGQASISCRSSQSIYHSNGNTYLEWYLOKPGQSEPLIYKYSNRFS 61
QY 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYCGQSHVPMTRGGGKLEIK 112
DB 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYCGQSHVPMTRGGGKLEIK 112

```

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Search completed: November 7, 2003, 07:30:09
Job time : 17.5955 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 15.7997 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_1\_122

Perfect score: 644  
Sequence: 1 EVQLQESGGGLVQPGSSKL.....FTVMWTFDVGAGTLVTS 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539.5	83.8	122	2	E27888
2	518	80.4	112	2	S26327
3	517.5	80.4	117	2	PI0249
4	516	80.1	119	2	F27888
5	514.5	79.9	120	2	S55536
6	514.5	79.9	120	2	S55537
7	514.5	79.9	138	2	S09258
8	514	79.8	121	2	I27887
9	510.5	79.3	117	2	PI0252
10	509	79.0	119	2	D27889
11	508.5	79.0	120	2	S55539
12	508	78.9	121	2	H27888
13	501.5	77.9	120	2	S55538
14	500.5	77.7	119	2	PH0098
15	500.5	77.7	124	2	C27888
16	500	77.6	118	2	B27889
17	498	77.3	119	2	PH0097
18	498	77.3	548	2	S38864
19	497	77.2	118	2	PH0096
20	496	77.0	254	2	B31780
21	493	76.6	121	2	A27888
22	493	76.6	128	2	S26780
23	493	76.6	139	2	S38808
24	492.5	76.5	138	2	S31666
25	489	75.9	121	2	H27887
26	487	75.6	108	2	PH1010
27	486	75.5	123	2	S33557
28	485.5	75.4	152	2	B6471
29	484.5	75.2	119	2	S31107

30	484	75.2	121	2	B27888	Ig heavy chain V r
31	483.5	75.1	111	2	PH1007	Ig heavy chain V r
32	483	75.0	121	2	D27888	Ig heavy chain V r
33	482.5	74.9	118	2	S20641	Ig heavy chain V r
34	482	74.8	121	2	S55540	Ig heavy chain V r
35	480.5	74.6	108	2	PH1006	Ig heavy chain V r
36	480.5	74.6	124	2	I27888	Ig heavy chain V r
37	480	74.5	123	2	G27888	Ig heavy chain V r
38	477.5	74.1	119	2	B34353	anti-peptide Fab'
39	477.5	74.1	142	2	C34903	Ig heavy chain pre
40	477	74.1	108	2	PI0248	Ig heavy chain V r
41	477	74.1	112	2	A27889	Ig heavy chain V r
42	475	73.8	147	2	I37780	Ig variable region
43	473	73.4	106	2	PH1008	Ig heavy chain V r
44	472.5	73.4	111	2	S40090	Ig heavy chain - m
45	472.5	73.4	119	2	C36005	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

E27888

Ig heavy chain V region (H35-C6) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C/Accession: E27888

R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody respon

A/Reference number: A91043; PMID:86300658; PMID:2427335

A/Accession: E27888

A/Molecule type: DNA

A/Residues: 1-122 <CAT>

A/Experimental source: strain Balb/c

A/Note: this sequence was determined from the germline gene

C/Comment: This chain was isolated from a hybridoma protein that binds influenza

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.8% Score 539.5; DB 2; Length 122;

Best Local Similarity 86.1%; Pred. No. 6.5e-41;

Matches 105; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVQPGSSKLSCASGFTSSYTMWVQTPERLRBMVATISSGSSITYY 60

DB 1 DVQLVSGGGLVQPGSSKLSCASGFTSSYTMWVQTPERLRBMVATISSGSSITYY 60

QY 61 PDVYKGRFTISRDNAKNTLYLQNSLRSEDTANYCTREGGGFTVMWY-PDVWGAGTLVT 119

DB 61 PDVYKGRFTISRDNAKNTLYLQNSLRSEDTANYCTREGGGFTVMWY-PDVWGAGTLVT 120

QY 120 VS 121

DB 121 VS 122

## RESULT 2

S26327

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 21-Jan-2000

C/Accession: S26327

R/Starik, S.B.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a

A/Reference number: S26309; PMID:91341421; PMID:1508510

A/Accession: S26327

A/Molecule type: mRNA

A/Residues: 1-112 <STA>

A/Cross-references: EMBL:X59192

C/Superfamily: immunoglobulin V region; immunoglobulin homology

**C;Keywords:** heterotetramer; immunoglobulin F;9-91/Domain: immunoglobulin homology <IMM>

Query Match	80.4%;	Score 518;	DB 2;	Length 112;
Best Local Similarity	87.1%;	Pred. No. 4.7e-39;		
Matches 101; Conservative	4;	Mismatches 7;	Indels 4;	Gaps 2;

Qy 7 SGGGLVMPGSGLKIKSCAASGFTSSSYMSVWRQTPKRLKLEWATISSGGSITYPDSVG 66  
Db 1 SGGGLVMPGSGLKIKSCAASGFTSSSYMSVWRQTPKRLKLEWATISSGC-STYPPDSVG 59

### RESULT 3

Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C/Accession: F10249  
R/Shomchik: M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisecky, D.; Marshak-Rochstein, J.  
J. Exp. Med. 171, 265-297, 1990  
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A/Reference number: P10231; PMID:2104919  
A/Accession: F10249  
A/Molecule type: mRNA  
A/Residues: 1-117 <SHL>  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/1-30/Region: framework 1  
F/15-98/Domain: immunoglobulin homology <IMM>  
F/31-35/Region: complementarity-determining 1  
F/36-49/Region: framework 2  
F/50-66/Region: complementarity-determining 2  
F/67-98/Region: framework 3  
F/99-108/Region: complementarity-determining 3  
F/109-117/Region: framework 4

	Query Match	Similarity	%	Score	DB 2.5	DB 2.5	Length
	Best Local	Similarity	83.3%	Score	No. 5.5e-39	Mismatches	12
	Matches	100	Conservative	5	Indels	3	Gaps
QY	1	EVQLOESGGGGLVPPGSGSLKLSGCAAGPFTSSATYMSWVRPEPKRLPHEVATISSGGSSTFY	60				
DB	1	EKLVESGGGGLVPPGSGSLKLSGCAAGPFTSSATYMSWVRPEPKRLPHEVATISSGGSSTFY	60				
QY	61	PDVYGRFTISDNNANNTLYLQMSLRSEDTYMYCTREGGCFYVNVYDVGAGATLVY	120				
DB	61	PDVYGRFTISDNNANNTLYLQMSLRSEDTYMYCTREGGCFYVNVYDVGAGATLVY	117				

## RESULT 4

Ig heavy chain V region (H158-89H4) - mouse  
 C|Species: Mus musculus (house mouse)  
 C|Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C|Accession: F27888  
 R|Caton, A.J.; Brownlee, G.G.; Stauff, L.M.; Gerhard, W.  
 E|MO J. 5, 1577-1587, 1986  
 A|Title: Structural and functional implications of a restricted antibody response to a c  
 A|Reference number: A91043; PMID:8650658; PMID:2427335  
 A|Accession: F27888  
 A|Molecule type: DNA  
 A|Residues: 1-119 <CAT>  
 A|Experimental source: strain Balb/c  
 A|Note: This sequence was determined from the germine gene  
 C|Comment: This chain was isolated from a hybridoma protein that binds influenza virus l  
 C|Superfamily: immunoglobulin V region; immunoglobulin homology  
 C|Keywords: heterotrimer; immunoglobulin  
 F|15-98|Domain: immunoglobulin homology <IM4>

Query Match	80.1%	Score 516;	DB 2;	Length 119;
Best Local Similarity	84.3%	Pred. No. 7.6e-39;		
Matches 102;	Conservative	5;	Mismatches 12;	Indels 2;
				Gaps 1.

```

QY      1  EVQLQSSGGGGLVPRGSGSLTSCAASGFTFSSTYSWVRQTEKLEWVAITISGGSSTYY 60
      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  DVLTAVESGGGLVPRGSGSLTSCAASGFTFSSTYSWVRQTEKLEWVAITISGGSSTYY 60
QY      61  PDSVKGRFTISRDKAKNTLYLQMSLRSEDTAMYCTREGGFTVMYFDVWGAGILVTY 120
      71  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  PDSVKGRFTISRDKAKNTLYLQMSLRSEDTAMTYCPR--GETYYDAMDIMGGSITVY 118
QY      121  S 121
      121  S 121
Db      119  S 119

```

## RESULT

ig heavy chain V region pe20 - mouse (fragment)  
C|Species: Mus musculus (house mouse)  
C|Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #extc\_change 23-Jul-1999  
C|Accession: S55536  
R|Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 392-346, 1995  
A|Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies in the variable region genes.  
A|Reference number: S55528; MUID:952929763; PMID:7536650  
A|Accession: S55536  
A|Status: preliminary  
A|Molecule type: mRNA  
A|Residues: 1-120 <BOB>  
A|Cross-references: EMBL:X85589; NID:g854304; PIDN:CA57925.1; PID:g854305  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: heterotetramer; immunoglobulin  
F|14-97|Domain: immunoglobulin homology <IM>

[illegible]

## RESULT

Ig heavy chain V region pe21 - mouse (Fragment)  
 C|Species: Mus musculus (house mouse)  
 C|Date: 27-Oct-1995 #sequence\_revastion 03-Nov-1995 #ext\_change 23-Jul-1999  
 C|Accession: S55537  
 R|Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
 J. Mol. Biol. 247, 932-946, 1995  
 A|Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies  
 uctions in the variable region genes.  
 A|Reference number: S55528; MUID:95239763; PMID:7536850  
 A|Accession: S55537  
 A|Status: preliminary  
 A|Molecule type: mRNA  
 A|Residues: 1-120 <BOB>  
 A|Cross-references: EMBL:X82590; NID:G854306; PIDD:CA57926.1; PID:G854307  
 C|Superfamily: immunoglobulin V region; immunoglobulin homology  
 C|Keywords: heterotetramer; immunoglobulin  
 F|14-97|Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 514.5; DB 2; Length 120;  
 Best Local Similarity 85.1%; Pred. No. 1e-38;  
 Matches 103; Conservative 3; Mismatches 14; Indels 1; Gaps 1;

QY 2 VOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 61  
 1 VOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 DB 1 VOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 QY 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 121  
 61 DSVKGRFTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 119  
 DB 61 DSVKGRFTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 119  
 QY 122 A 122  
 120 S 120  
 DB 120 S 120

## RESULT 7

S09258  
 Ig heavy chain V region precursor - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999  
 C/Accession: S09258  
 R/Hamada, H.; Maizawa, K.; Tsuruo, T.  
 Nucleic Acids Res. 18, 1900, 1990  
 A/Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK  
 A/Reference number: S09258; MUID:90245594; PMID:2110659  
 A/Accession: S09258  
 A/Molecule type: DNA  
 A/Residues: 1-138 <HAM>  
 A/Cross-references: EMBL:X51719; NID:953207; PIDD:CAA36012.1; PID:9297545  
 C/Genetics:  
 A/Introns: 16/1  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterodimer; immunoglobulin  
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 514.5; DB 2; Length 138;  
 Best Local Similarity 83.6%; Pred. No. 1.2e-38;  
 Matches 102; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 20 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 79  
 DB 20 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 79  
 QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 120  
 60 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 136  
 DB 60 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 136  
 QY 121 SA 122  
 137 SA 138  
 DB 137 SA 138

## RESULT 8

I27897  
 Ig heavy chain V region (H37-45) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C/Accession: I27897  
 R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMBO J. 5, 1577-1587, 1986  
 A/Title: Structural and functional implications of a restricted antibody response to a  
 A/Reference number: A91043; MUID:86300658; PMID:2427335  
 A/Accession: I27897  
 A/Molecule type: DNA  
 A/Residues: 1-121 <CAT>  
 A/Experimental source: strain Balb/c  
 A/Note: this sequence was determined from the germ-line gene  
 C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin

F/15-96/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 514; DB 2; Length 121;  
 Best Local Similarity 83.5%; Pred. No. 1.2e-38;  
 Matches 101; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 1 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 DB 1 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 120  
 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 120  
 DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 120  
 QY 121 S 121  
 121 S 121  
 DB 121 S 121

## RESULT 9

PL0252  
 Ig heavy chain V region (anti-DNA, clones 2B3VH, 6B8VH, and 3G9VH) - mouse (frag  
 C/Species: Mus musculus (house mouse)  
 C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C/Accession: PL0252; PL0251  
 R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pietsky, D.; Marshak-Roth  
 J. Exp. Med. 171, 265-297, 1990  
 A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and  
 A/Reference number: PL0231; MUID:9011618; PMID:2104919  
 A/Accession: PL0252  
 A/Molecule type: mRNA  
 A/Residues: 1-117 <SHL>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/1-30/Region: framework 1  
 F/15-96/Domain: immunoglobulin homology <IMM>  
 F/31-35/Region: complementarity-determining 1  
 F/36-49/Region: framework 2  
 F/50-66/Region: complementarity-determining 2  
 F/67-98/Region: framework 3  
 F/99-108/Region: complementarity-determining 3  
 F/109-117/Region: framework 4

Query Match 79.3%; Score 510.5; DB 2; Length 117;  
 Best Local Similarity 82.5%; Pred. No. 2.3e-38;  
 Matches 99; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLQSSGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 1 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 DB 1 EVILVESGGGLVKGPGSLKLSGCAAGFTSSSYTMSWVROTPKRLKLEWVATISSGGSSTYY 60  
 QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 120  
 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 117  
 DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGGFTVMVYFDVWAGTLVTV 117

## RESULT 10

D27889  
 Ig heavy chain V region (H36-2) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C/Accession: D27889  
 R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMBO J. 5, 1577-1587, 1986  
 A/Title: Structural and functional implications of a restricted antibody response  
 A/Reference number: A91043; MUID:86300658; PMID:2427335  
 A/Accession: D27889  
 A/Molecule type: DNA  
 A/Residues: 1-119 <CAT>  
 A/Experimental source: strain Balb/c  
 A/Note: this sequence was determined from the germ-line gene  
 C/Comment: This chain was isolated from a hybridoma protein that binds influenza  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 509; DB 2; Length 119;  
Best Local Similarity 81.8%; Pred. No. 3.1e-38;  
Matches 99; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
DB 1 EVQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 120  
DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 118  
QY 121 \$ 121  
DB 119 \$ 119

## RESULT 11

S55539

Ig heavy chain V region pe24 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S55539

R.Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A&gt;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55539

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 &lt;BOB&gt;

A/Cross-references: EMBL:X82593; NID:g854312; PIDD:CA57929.1; PID:g854313

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 79.0%; Score 508.5; DB 2; Length 120;  
Best Local Similarity 83.5%; Pred. No. 3.5e-38;  
Matches 101; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

QY 2 VQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 61  
DB 1 VQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
QY 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 121  
DB 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 119  
QY 122 A 122  
DB 120 \$ 120

## RESULT 12

H27888

Ig heavy chain V region (H27-40) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C/Accession: H27888

R.Catton, A.J.; Brownlee, G.G.; Straud, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A&gt;Title: Structural and functional implications of a restricted antibody response to a

A/Reference number: A91043; MUID:86300658; PMID:2427335

A/Accession: H27888

A/Molecule type: DNA

A/Residues: 1-121 &lt;CAT&gt;

A/Experimental source: strain Balb/c

A/Note: this sequence was determined from the germline gene

C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.9%; Score 508; DB 2; Length 121;  
Best Local Similarity 81.8%; Pred. No. 3.9e-38;  
Matches 99; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
DB 1 EVQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 120  
DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 120  
QY 121 \$ 121  
DB 121 \$ 121

## RESULT 13

S55538

Ig heavy chain V region pe22 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S55538

R.Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A&gt;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55538

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 &lt;BOB&gt;

A/Cross-references: EMBL:X82591; NID:g854308; PIDD:CA57927.1; PID:g854309

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 77.9%; Score 501.5; DB 2; Length 120;  
Best Local Similarity 81.8%; Pred. No. 1.5e-37;  
Matches 99; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 2 VQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 61  
DB 1 VQLDSGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVAITSSGSSSTYY 60  
QY 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 121  
DB 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYCTREGGFTVMWYFDVWGAGTLVTV 119  
QY 122 A 122  
DB 120 \$ 120

## RESULT 14

PH0098

Ig heavy chain V region (anti-cyclosporin G) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996

C/Accession: PH0098

R.Schmiltner, D.; Pech, O.; Zeder, G.; Heinrich, G.F.; Koehner, H.P.; Queniaux, V.

Mol. Immunol. 27, 1025-1038, 1990

A&gt;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporin

A/Reference number: PH0087; MUID:91042649; PMID:2122240

A/Accession: PH0098

A/Molecule type: mRNA

A/Residues: 1-119 &lt;SCH&gt;

A/Note: the authors translated the codon GTG for residue 104 as Gly

C/Superfamily: immunoglobulin V region; immunoglobulin homology



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OM protein - protein search, using SW model

Run on: November 7, 2003, 07:21:18 / Search time 8.79573 Seconds

(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_1\_122

Sequence: 1 EVQLQESGGGLVPGGSLKL.....FTVMNYFDVWGAGTLVTVSA 122

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	469	72.8	117 1 HV55_MOUSE	P18526 mus musculus
2	464	72.0	117 1 HV54_MOUSE	P18525 mus musculus
3	462	71.7	98 1 HV57_MOUSE	P18527 mus musculus
4	460.5	71.5	97 1 HV56_MOUSE	P18527 mus musculus
5	453	70.3	117 1 HV58_MOUSE	P18529 mus musculus
6	441	68.5	136 1 HV16_MOUSE	P01783 mus musculus
7	433	67.2	117 1 HV53_MOUSE	P18524 mus musculus
8	426	66.1	117 1 HV59_MOUSE	P18530 mus musculus
9	419	65.1	117 1 HV3C_HUMAN	P01764 homo sapien
10	417	64.8	122 1 HV38_HUMAN	P01768 homo sapien
11	416	64.6	119 1 HV38_MOUSE	P01808 mus musculus
12	413	64.1	114 1 HV3B_HUMAN	P01763 homo sapien
13	411	63.8	122 1 HV20_MOUSE	P01789 mus musculus
14	409.5	63.6	121 1 HV3J_HUMAN	P01771 homo sapien
15	404.5	62.8	115 1 HV32_MOUSE	P01801 mus musculus
16	404	62.7	116 1 HV3T_HUMAN	P01781 homo sapien
17	402.5	62.5	123 1 HV18_MOUSE	P01787 mus musculus
18	402	62.4	122 1 HV21_MOUSE	P01790 mus musculus
19	402	62.4	126 1 HV3K_HUMAN	P01792 homo sapien
20	401.5	62.3	123 1 HV19_MOUSE	P01788 mus musculus
21	401.5	62.3	142 1 HV01_MOUSE	P01805 rattus norv
22	400.5	62.2	117 1 HV02_MOUSE	P01785 canis fami
23	400.5	62.2	123 1 HV22_MOUSE	P01781 mus musculus
24	399.5	62.0	115 1 HV3D_HUMAN	P01765 homo sapien
25	398.5	61.9	120 1 HV3E_HUMAN	P01766 homo sapien
26	398	61.8	119 1 HV3M_HUMAN	P01774 homo sapien
27	397.5	61.7	123 1 HV23_MOUSE	P01792 mus musculus
28	397.5	61.7	123 1 HV24_MOUSE	P01793 mus musculus
29	397.5	61.7	144 1 HV26_MOUSE	P01795 mus musculus
30	397	61.6	122 1 HV3A_HUMAN	P01762 homo sapien
31	396.5	61.6	115 1 HV33_MOUSE	P01802 mus musculus
32	396.5	61.6	116 1 HV05_CARAU	P19181 carassius a
33	394.5	61.3	113 1 HV27_MOUSE	P01796 mus musculus

34	394.5	61.3	113 1 HV30_MOUSE	P01799 mus musculus
35	393	61.0	119 1 HV37_MOUSE	P01807 mus musculus
36	391.5	60.8	115 1 HV3F_HUMAN	P01767 homo sapien
37	390.5	60.6	113 1 HV3I_MOUSE	P01800 mus musculus
38	390	60.6	111 1 HV35_MOUSE	P01804 mus musculus
39	390	60.6	119 1 HV3N_HUMAN	P01775 homo sapien
40	389.5	60.5	119 1 HV3I_HUMAN	P01770 homo sapien
41	389	60.4	122 1 HV3H_HUMAN	P01769 homo sapien
42	388.5	60.3	113 1 HV28_MOUSE	P01797 mus musculus
43	388	60.2	120 1 HV3U_HUMAN	P01782 homo sapien
44	386	59.9	114 1 HV01_CANPA	P01784 canis fami
45	385.5	59.9	123 1 HV25_MOUSE	P01794 mus musculus

## ALIGNMENTS

## RESULT 1

ID	HV55_MOUSE	STANDARD	PRT	117 AA.
AC	P18526;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG heavy chain V region 345 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BAIB/CT;			
RX	MEDLINE=89279149; PubMed=2499654;			
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;			
RT	"Early Onset of Somatic Mutation in Immunoglobulin VH genes during			
RT	the primary immune response."			
RT	J. Exp. Med. 169:2007-2019(1989).			
CC	1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.			
DR	PIR; J05052; HVMS34.			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro; IPR007110; IG-11ke.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IgV_1.			
DR	SMART; SM00406; IgV_1.			
DR	PROSITE; PS50835; IG_LINK; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	19	IG HEAVY CHAIN V REGION 345.
FT	CHAIN	20	117	FRAMEWORK-1.
FT	DOMAIN	20	49	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	50	54	FRAMEWORK-2.
FT	DOMAIN	55	68	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	69	85	FRAMEWORK-3.
FT	DOMAIN	86	117	BY SIMILARITY.
FT	DISULFID	41	115	
FT	NON_TER	117	117	
SQ	SEQUENCE	117 AA;	12902 MW;	49380E4627ACA39A CRC64;

Query Match 72.8%; Score 469; DB 1; Length 117;  
Best Local Similarity 91.8%; Pred. No. 1.1e-40;  
Matches 90; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY	1	EVQLQESGGGLVPGGSLKSCAAGFTSSVTMSVNRQTPERKLEWNTISSGGSSTY	60
DB	20	EVQLVSSGGGLVPGGSLKSCAAGFTSSVTMSVNRQTPERKLEWNTISSGGSSTY	79
QY	61	PDVSKGRFTISRDNAKNTLYIQGSSSLRSFDTAMYYCTR	98
DB	80	PDVYKGRFTISRDNAKNTLYIQGSSSLRSFDTAMYYCAR	117
RESULT 2			
		HV54_MOUSE	

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ID HV54 MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT STGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CE6A469861 CRC64;

Query Match 72.0%; Score 464; DB 1; Length 117;
Best Local Similarity 89.8%; Pred. No. 3,7e-40;
Matches 89; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 60
DB 20 EVKLVSQGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 79
QY 61 PDSVKGRTISRDNANKNTLYLQMSLSRSEDTAMYCTR 98
DB 80 PDIYKGRFTISRDNANKNTLYLQMSLSRSEDTAMYCAR 117

RESULT 3
HV57 MOUSE STANDARD; PRT; 98 AA.
ID HV57 MOUSE STANDARD; PRT; 98 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 6-96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

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CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; JTO501; HVMS96.
DR HSSP; P01772; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 IG-LIKE.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7E92BF95B CRC64;

Query Match 71.7%; Score 462; DB 1; Length 98;
Best Local Similarity 90.8%; Pred. No. 4,8e-40;
Matches 89; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 60
DB 1 EVKLVSQGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 60
QY 61 PDSVKGRTISRDNANKNTLYLQMSLSRSEDTAMYCTR 98
DB 61 PDSVKGRTISRDNANKNTLYLQMSLSRSEDTAMYCAR 98

RESULT 4
HV56 MOUSE STANDARD; PRT; 97 AA.
ID HV56 MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; JTO504; HVMS91.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 IG-LIKE.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33F55DA893 CRC64;

Query Match 71.5%; Score 460.5; DB 1; Length 97;
Best Local Similarity 91.8%; Pred. No. 6,7e-40;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 60
DB 1 EVKLVSQGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLKLEWVATISGGSSTYY 59
QY 61 PDSVKGRTISRDNANKNTLYLQMSLSRSEDTAMYCTR 98
DB 60 PDSVKGRTISRDNANKNTLYLQMSLSRSEDTAMYCAR 97

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RESULT 5
HVS8 MOUSE STANDARD; PRT; 117 AA.
ID HV53 MOUSE
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RC MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019 (1989).
CL -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J05056; HVMS57.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 70.3%; Score 453; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 4.8e-39;
Matches 87; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTMNWRTPEKRLIEWATISSGSSSTYY 60
DB 20 EYHLYVESGGGLVPGGSLKSCVYSGFTFNKYMWSWRQPEKRLIEWATISSGGLYTY 79
QY 61 PDSYKGRFTISRDNAKNTLYLQMSSLRSSEDTAMYCTR 98
DB 80 PDSYKGRFTISRDNAKNTLYLQMSSLRSSEDTAMYCAR 117

RESULT 6
HVS6 MOUSE STANDARD; PRT; 136 AA.
ID HV16 MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Botnelli A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

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RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637 (1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adeugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RT Nature 265:299-304 (1977).
CC -----
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CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> M (IN REF. 2).
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 68.5%; Score 441; DB 1; Length 136;
Best Local Similarity 72.4%; Pred. No. 9.3e-38;
Matches 89; Conservative 10; Mismatches 20; Indels 4; Gaps 2;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTMNWRTPEKRLIEWATISSGSSSTYY 60
DB 17 DQVLVESGGGLVPGGSLKSCAASGFTFSYSGMHWRCAPKGLIEWATISSGSLHY 76
QY 61 PDSYKGRFTISRDNAKNTLYLQMSSLRSSEDTAMYCTRGGGFTNMY-FDYWGAGTLYT 119
DB 77 ADYVGRFTISRDNPNTLYLQMTLSRSEDTAMYYCARWG--NTPYAMDYWGQSTSVT 133
QY 120 VSA 122
DB 134 VSS 136

RESULT 7
HVS3 MOUSE STANDARD; PRT; 117 AA.
ID HV53 MOUSE
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;

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RX MEDLINE=69279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR HSP; J0503; HVMSRF.
DR HSP; P01810; 2PBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 67.2%; Score 433; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 5e-37;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTSSITMSWVRQTPKRLIEWATISGGSSTTY 60
D 20 DVKLVESGGGLVPGGSLKSCAASGFTSSITMSWVRQTPKRLIEWATISGGSSTTY 79
QY 61 PDVSKGRFTISRDNAKNTLYLQMSLSRSEDTAMYCTR 98
D 80 PDVSKGRFTISRDNAKNTLYLQMSLSRSEDTALYYCAR 117

RESULT 8
HV59 MOUSE STANDARD; PRT; 117 AA.
ID HV59_MOUSE
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=69279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR HSP; J0507; HVMS39.
DR HSP; P01810; 2PBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 66.1%; Score 426; DB 1; Length 117;
Best Local Similarity 83.7%; Pred. No. 2.6e-36;
Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTSSITMSWVRQTPKRLIEWATISGGSSTTY 60
D 20 EVKLVESGGGLVPGGSLKSCAASGFTSSITMSWVRQTPKRLIEWATISGGSSTTY 79
QY 61 PDVSKGRFTISRDNAKNTLYLQMSLSRSEDTAMYCTR 98
D 80 PDVSKGRFTISRDNAKNTLYLQMSLSRSEDTALYYCAR 117

RESULT 9
HV3C HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G, Rabbits T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- Similarity: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: U00236; AAA83516.1; -
DR EMBL: M55415; AAA58735.1; -.
DR PIR: A02047; H3H026.
DR PDB: 1HOU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV@.
DR GO: GO:0005726; P:antigen binding activity; NAS.
DR GO: GO:0005935; P:immune response; NAS.
DR GO: GO:0069583; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 65.1%; Score 419; DB 1; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.3e-35;
Matches 79; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

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QY 1 EVQLDSGGGLVPRGSLKSCAASGFTFSSTYSWVRQTPKRLKLEWNTATISSGGSSTYY 60  
 DB 20 EVQLDSGGGLVPRGSLKSCAASGFTFSSTYSWVRQTPKRLKLEWNTATISSGGSSTYY 79  
 QY 61 PDVYKGRFTISRDNKNTLYLQWSSLRSEPTAMVYCR 98  
 DB 80 GDSVYKGRFTISRDNKNTLYLQWSSLRSEPTAMVYCR 117

## RESULT 10

HV3G HUMAN STANDARD; PRT; 122 AA.  
 AC P01768;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region CAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=81013853; PubMed=6774332;  
 RA Lehman D.W., Putnam F.W.,  
 RT "Amino acid sequence of the variable region of a human mu chain:  
 RT location of a possible JH segment."  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).  
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  
 CC PATIENT WITH MACROGLOBULINEMIA.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02051; M3HUM.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Pyroglutamate carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE  
 FT MOD\_RES 1 1 PYROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252FLC2 CRC64;

Query Match 64.8%; Score 417; DB 1; Length 122;  
 Best Local Similarity 64.8%; Pred. No. 2.2e-35;  
 Matches 79; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVQLDSGGGLVPRGSLKSCAASGFTFSSTYSWVRQTPKRLKLEWNTATISSGGSSTYY 60  
 DB 1 QVELVESGGGVVZVGRSLRSCAASGFTFSNYAMWVRQPGKGLKLEWNTATISSGGSSTYY 60  
 QY 61 PDVYKGRFTISRDNKNTLYLQWSSLRSEPTAMVYCRREGGCTVMVYFVWGAAGLTVY 120  
 DB 61 ABSYKGRFTISRDNKNTLYLQWSSLRSEPTAMVYCARDRPLVGYRAFMVWGCGTLTVY 120

QY 121 SA 122  
 DB 121 SS 122

RESULT 11  
 HV38 MOUSE STANDARD; PRT; 119 AA.  
 AC P01808;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region T601.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX MEDLINE=79223895; PubMed=111245;  
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.,  
 RT "Structural evidence for independent joining region gene in  
 RT immunoglobulin heavy chains from anti-galactan myeloma proteins and  
 RT its potential role in generating diversity in  
 RT complementarity-determining regions."  
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN  
 CC THAT BINDS GALACTAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02078; AVM8T6.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13169 MW; BC38CC84B6EA00E8 CRC64;

Query Match 64.6%; Score 416; DB 1; Length 119;  
 Best Local Similarity 68.0%; Pred. No. 2.7e-35;  
 Matches 83; Conservative 10; Mismatches 25; Indels 4; Gaps 1;

QY 1 EVQLDSGGGLVPRGSLKSCAASGFTFSSTYSWVRQTPKRLKLEWNTATISSGGSSTYY 60  
 DB 1 EVQLDSGGGLVPRGSLKSCAASGFTFSSTYSWVRQTPKRLKLEWNTATISSGGSSTYY 60  
 QY 61 PDVYKGRFTISRDNKNTLYLQWSSLRSEPTAMVYCRREGGCTVMVYFVWGAAGLTVY 120  
 DB 61 TPELNKFTISRDNKNTLYLQWSSKVSSTDTALVYCARIG---YGYEDVWGAAGTTLTVY 116  
 QY 121 SA 122  
 DB 117 SS 118

## RESULT 12

HV3B HUMAN STANDARD; PRT; 114 AA.  
 AC P01763;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region WE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=83273707; PubMed=6410398;  
 RA Goni F., Frangione B.,  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 RT (protein WE) with antibody activity against 3,4-pyruvylated  
 RT galactose in Klebsiella polysaccharides K30 and K33."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
 CC WALDENSTROM'S MACROGLOBULINEMIA.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02046; M3HWE.  
 DR HSSP; P01772; 2FB4.

DR GO; GO:000576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig-MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Pyroglutamate carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD RES 1 114  
 FT NON TER 114 AA; 12256 MW; D88294FB418A0787 CRC64;  
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A0787 CRC64;  
 Query Match 64.1%; Score 413; DB 1; Length 114;  
 Best Local Similarity 65.6%; Pred. No. 5.1e-35;  
 Matches 80; Conservative 19; Mismatches 15; Indels 8; Gaps 2;

QY 1 EVQLQESGGGLVPRGGSILKLSCAASGFTSSSYMSWRQTPERKLEWANTISGSGSTYY 60  
 DB 1 QVQLVDSGGGLVPRGGSILKLSCAASGFTSSSYMSWRQTPERKLEWANTISGSGSTYY 60  
 QY 61 PDVSKGRFTISRDNKNTLYLQMSLSRSEPTAMYYCTREGGFTVMNYPDVWGAGTLTV 120  
 DB 61 ADVSKGRFTISRDNKNTLYLQMSLSRSEPTAMYYCTREGGFTVMNYPDVWGAGTLTV 112  
 QY 121 SA 122  
 DB 113 SS 114

RESULT 13  
 HV20 MOUSE STANDARD; PRT; 122 AA.  
 AC P01789;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region M603.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80199926; PubMed=679593;  
 RA Early P., Huang H., Davis M., Calame K., Hood L.;  
 RT "An immunoglobulin heavy chain variable region gene is generated from  
 RT three segments of DNA: VH, D and JH.";  
 RL Cell 19:381-392(1980).  
 RN [2]  
 RP SEQUENCE OF 1-120.  
 RX MEDLINE=75017346; PubMed=4213527;  
 RA Rudikoff S., Potter M.;  
 RT "Variable region sequence of the heavy chain from a phosphorylcholine  
 RT binding myeloma protein.";  
 RL Biochemistry 13:4033-4038(1974).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.  
 RX MEDLINE=75065510; PubMed=4530984;  
 RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,  
 RA Davies D.R.;  
 RT "The three-dimensional structure of a phosphorylcholine-binding mouse  
 RT immunoglobulin Fab and the nature of the antigen binding site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:4296-4302(1974).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B0795; AYMS63.  
 DR PDB; 1MCP; 15-JUL-92.  
 DR PDB; 2MCP; 15-JUL-92.  
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure.  
 FT DOMAIN 1 121  
 FT SITE 33 33  
 FT SITE 33 33  
 FT SITE 52 52  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 17 25  
 FT TURN 30 31  
 FT STRAND 33 39  
 FT TURN 41 42  
 FT STRAND 46 50  
 FT TURN 54 55  
 FT STRAND 61 61  
 FT TURN 64 69  
 FT STRAND 70 75  
 FT TURN 76 79  
 FT STRAND 80 86  
 FT HELIX 90 92  
 FT STRAND 94 103  
 FT STRAND 107 112  
 FT STRAND 116 120  
 FT NON TER 122 122  
 SQ SEQUENCE 122 AA; 13626 MW; BA2C86443B64F0F CRC64;  
 Query Match 63.8%; Score 411; DB 1; Length 122;  
 Best Local Similarity 64.5%; Pred. No. 8.8e-35;  
 Matches 80; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 EVQLQESGGGLVPRGGSILKLSCAASGFTSSSYMSWRQTPERKLEWANTISGSGS--ST 58  
 DB 1 EVQLVDSGGGLVPRGGSILKLSCAASGFTSSSYMSWRQTPERKLEWANTISGSGS--ST 60  
 QY 59 YPDVSKGRFTISRDNKNTLYLQMSLSRSEPTAMYYCTREGGFTVMNYPDVWGAGTLTV 118  
 DB 61 EYASVSKGRFTISRDNKNTLYLQMSLSRSEPTAMYYCTREGGFTVMNYPDVWGAGTLTV 118  
 QY 119 TVSA 122  
 DB 119 TVGS 122

RESULT 14  
 HV30 HUMAN STANDARD; PRT; 121 AA.  
 AC P01771;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region H11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=79124695; PubMed=420800;  
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;  
 RT "Amino acid sequence of the VH region of human myeloma  
 RT cryoimmunoglobulin IgG H11.";  
 RL Biochemistry 18:553-560(1979).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02054; G1H0H.  
 DR HSSP; P01772; 2FB4.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrolydione carboxylic acid.  
FT DOMAIN 1 112 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 13566 MW; 480FC35610BF5DAB CRC64;

Query Match 63.6%; Score 409.5; DB 1; Length 121;  
Best Local Similarity 64.8%; Pred. No. 1.2e-34;  
Matches 79; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWRQTPPKRLIEWATISSGSSITY 60  
DB 1 QVQLVQAGGGLVQPGGSLRLSCAASGFTFSNYGMHWROAPKGLGWAVIWNYSRTYY 60  
QY 61 PSDVKGRFTISRDNANNTLYIQMSISRSBDTAMYYCTREGGFTVMYFDVWGAGTLVTV 120  
DB 61 GDSVKGRFTISRDNANNTLYIQMSISRSBDTAMYYCTREGGFTVMYFDVWGAGTLVTV 119  
QY 121 SA 122  
DB 120 SS 121

RESULT 15  
HV32\_MOUSE  
ID HV32\_MOUSE STANDARD; PRT; 115 AA.  
AC P01801;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region J606.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slinkard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-  
binding proteins.";  
RT J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS INULIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; C92811; AYMS06.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 114 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 62.8%; Score 404.5; DB 1; Length 115;  
Best Local Similarity 63.7%; Pred. No. 3.8e-34;  
Matches 79; Conservative 19; Mismatches 15; Indels 11; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWRQTPPKRLIEWATI--SSGSSST 58

DB 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSNYGMHWROAPKGLGWAVIWNYSRTYY 60  
QY 59 YPDSVKGRFTISRDNANNTLYIQMSISRSBDTAMYYCTREGGFTVMYFDVWGAGTLV 118  
DB 61 HYAESVKGRFTISRDNANNTLYIQMSISRSBDTAMYYCTREGGFTVMYFDVWGAGTLV 111  
QY 119 TVSA 122  
DB 112 TVSA 115

Search completed: November 7, 2003, 07:28:08  
Job time : 8.79573 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18, Search time 40.2323 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_1\_122

Sequence: 1 EVQLQESGGGLVQPGGSLKL.....FTVMYFDWMAAGILVTVSA 122

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteria:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	80.9	487	11 Q99XA4	Q99XA4 mus musculus
2	515.5	80.0	119	11 Q920E7	Q920E7 mus musculus
3	493.5	76.6	479	11 Q91WP5	Q91WP5 mus musculus
4	487	74.9	471	11 Q8TC77	Q8TC77 homo sapien
5	482.5	74.9	480	11 Q91X81	Q91X81 mus musculus
6	466.5	72.4	486	11 Q91Z07	Q91Z07 mus musculus
7	455.5	70.7	597	4 Q96B89	Q96B89 homo sapien
8	453	70.3	473	11 Q91Z05	Q91Z05 mus musculus
9	450	69.9	437	11 Q91A14	Q91A14 mus musculus
10	443.5	68.9	121	4 Q9UL71	Q9UL71 homo sapien
11	442	68.6	118	4 Q9UL91	Q9UL91 homo sapien
12	441	68.5	613	4 Q8WUK1	Q8WUK1 homo sapien
13	439.5	68.2	116	4 Q9UL93	Q9UL93 homo sapien
14	438	68.0	573	4 Q8WU38	Q8WU38 homo sapien
15	437.5	67.9	499	4 Q8WUK4	Q8WUK4 homo sapien
16	436	67.7	494	4 Q96K68	Q96K68 homo sapien

17	434.5	67.5	113	4 Q9UL90	Q9UL90 homo sapien
18	432	67.1	147	4 Q9Y509	Q9Y509 homo sapien
19	430	66.8	122	4 Q9UL84	Q9UL84 homo sapien
20	426	66.1	118	4 Q9UL72	Q9UL72 homo sapien
21	417	64.8	112	4 Q9HCC1	Q9HCC1 homo sapien
22	410.5	63.7	493	4 Q8NCI6	Q8NCI6 homo sapien
23	405	62.9	95	4 Q9UL86	Q9UL86 homo sapien
24	390.5	60.6	131	4 Q9UL68	Q9UL68 homo sapien
25	382	59.3	469	11 Q8RV99	Q8RV99 mus musculus
26	381	59.2	298	11 Q9QXF0	Q9QXF0 mus musculus
27	380.5	59.1	521	4 Q8N4Y9	Q8N4Y9 homo sapien
28	369	57.3	484	11 Q8VER0	Q8VER0 mus musculus
29	363	56.4	613	11 Q8VCX7	Q8VCX7 mus musculus
30	353.5	54.9	168	11 Q8VDC9	Q8VDC9 mus musculus
31	350	54.3	145	11 Q924R3	Q924R3 mus musculus
32	344.5	53.5	473	11 Q9DBL4	Q9DBL4 mus musculus
33	343.5	53.3	144	11 Q924P5	Q924P5 mus musculus
34	342	53.1	124	4 Q9UL92	Q9UL92 homo sapien
35	341.5	53.0	104	4 Q9UL87	Q9UL87 homo sapien
36	339	52.6	124	6 Q9N0W6	Q9N0W6 homo sapien
37	337	52.3	124	6 Q9N0W4	Q9N0W4 oxyctolagus
38	336	52.2	143	11 Q91V67	Q91V67 mus musculus
39	336	52.2	278	11 Q921K1	Q921K1 mus musculus
40	335.5	52.1	112	4 Q9UG83	Q9UG83 homo sapien
41	334	51.9	159	4 Q96Q80	Q96Q80 homo sapien
42	331.5	51.5	125	4 Q9UL95	Q9UL95 homo sapien
43	327	50.8	143	11 Q924Q5	Q924Q5 mus musculus
44	326.5	50.7	117	11 Q9QXF0	Q9QXF0 mus musculus
45	326.5	50.7	147	11 Q925S3	Q925S3 mus musculus

## ALIGNMENTS

## RESULT 1

ID	Q99XA4	PRELIMINARY:	PRT:	487 AA.
AC	Q99XA4	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical 52.6 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCSI_TextID=10090;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strasbourg R.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC004786; AA04786.1; ..			
DR	HSSP; P01820; 2FEJ.			
DR	InterPro; IPR007110; IG_1ike.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; Ig_4.			
DR	SMART; SM00406; IgV_1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; 2.			
KW	Hypothetical protein.			
SQ	SEQUENCE 487 AA; 52554 MW; 7DC8B96DB33077B CRC64;			

Query Match	80.9%;	Score 521;	DB 11;	Length 487;
Best local similarity	81.5%;	Pred. No. 6.2e-45;		
Matches 101;	Conservative	5;	Mismatches 16;	Indels 2;
Gaps				1;
QY	1	EVQLQESGGGLVQPGGSLKLSKASAGFTFSYTWYRQPEKLEWYATISGSGSYTY	60	
DB	20	EVQLVDSGGGLVQPGGSLKLSKASAGFTFSYTWYRQPEKLEWYATISGSGSYTY	79	
QY	61	PDSYKARFTISRDAKATLTLYIQMWSLRSEDTAMYYCTREGGGFYVNNY--PDVWAGTLV	118	
DB	80	PDVWAGFTISRDAKATLTLYIQMWSLRSEDTAMYYCTREGGGFYVNNY--PDVWAGTLV	139	

QY 119 TVSA 122  
DB 140 TVSS 143

## RESULT 2

Q920E7 PRELIMINARY; PRT; 119 AA.

ID Q920E7

AC Q920E7

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Pterin-mimicking anti-idiotope heavy chain variable region (fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RM [1]

RP SEQUENCE FROM N.A.

RA Aikin J.D., Iape A., Jennings I.G., Horvath O., Cotton R.G.H.;

RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed

in Mammalian Cells";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307937; AL09421.1; -

DR InterPro; IPR007110; IG\_1ike.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_Like; 1.

FT NON TER

FT 119 119

SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match

Best Local Similarity 80.0%; Score 515.5; DB 11; Length 119;

Matches 104; Conservative 3; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLQESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 60  
DB 1 EVOLVESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 60  
QY 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCTREGGGFTVNMVFDVWGAGTAVTV 120  
DB 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCARH-GDYDVG--FAVWGAGTAVTV 117  
QY 121 SA 122  
DB 119 SA 119

## RESULT 3

Q91WPS

Q91WPS PRELIMINARY; PRT; 479 AA.

AC Q91WPS

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical 51.6 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RA Strussberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013656; AF013656.1; -

DR InterPro; IPR007110; IG\_1ike.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IGV; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_Like; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
DR Hypothetical protein.  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match

Best Local Similarity 76.6%; Score 493.5; DB 11; Length 479;

Matches 95; Conservative 9; Mismatches 11; Indels 7; Gaps 1;

QY 1 EVOLQESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 60  
DB 20 EVOLVESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 79  
QY 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCTREGGGFTVNMVFDVWGAGTAVTV 120  
DB 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCTREGGGFTVNMVFDVWGAGTAVTV 132  
QY 121 SA 122  
DB 133 SS 134

## RESULT 4

Q9TC77 PRELIMINARY; PRT; 471 AA.

ID Q9TC77

AC Q9TC77

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI\_TaxID=9606;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Strussberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024289; AA024289.1; -

DR InterPro; IPR007110; IG\_1like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF00047; IGV; 4.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_Like; 4.

DR PROSITE; PS00290; IG\_MHC; 2.

KW Hypothetical protein.

SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match

Best Local Similarity 75.6%; Score 487; DB 4; Length 471;

Matches 92; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLQESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 60  
DB 20 EVOLVESGGGLVPRGSLKLSCAAGFTFSYTSWVROTPEKRLKLEWYATISSGSSSTYY 79  
QY 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCTREGGGFTVNMVFDVWGAGTAVTV 120  
DB 61 PDSVKGRTTISRDNAKNTLYIQMSSLRSEDTAMYYCTREGGGFTVNMVFDVWGAGTAVTV 139  
QY 121 SA 122  
DB 140 SS 141

## RESULT 5

Q91XE1

Q91XE1 PRELIMINARY; PRT; 480 AA.

AC 091207; 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Unknown (Protein for IMAGE:4224494) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010798; AAH10798.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_4.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
FT NON TER 1  
SQ SEQUENCE 480 AA; 51936 MW; 20B9234BEP2B41ED CRC64;

Query Match 74.9%; Score 482.5; DB 11; Length 480;  
Best Local Similarity 76.2%; Pred. No. 5.3e-41;  
Matches 93; Conservative 14; Mismatches 10; Indels 5; Gaps 2;

QY 1 EVOLDSGGGLVPGGSLKLSCAASGFTSSYTWVWQTPERKLEWVATISSGGSSTYY 60  
DB 19 DYLVSSGGGLVPGGSLRLSCAASGFTSSYTWVWQTPERKLEWVATISSGGSSTYY 78  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPAAMYCTREGGGFTVMYF--DVGAGTL 120  
DB 79 PDSMKGRFTISRDNKNTLYLQMSLSRSEDPAVYCYTR--GDY---WYFDVWGA GTTVV 133  
QY 121 SA 122  
DB 134 SS 135

RESULT 6  
Q91207 PRELIMINARY; PRT; 486 AA.  
ID 091207;  
AC 091207; 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 52.7 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Strausberg R.;  
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010324; AAH10324.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_4.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 72.4%; Score 466.5; DB 11; Length 486;  
Best Local Similarity 71.3%; Pred. No. 2.3e-39;  
Matches 92; Conservative 10; Mismatches 14; Indels 13; Gaps 3;

QY 1 EVOLDSGGGLVPGGSLKLSCAASGFTSSYTWVWQTPERKLEWVATISSGGSSTYY 60  
DB 20 EYLVSSGGGLVPGGSLRLSCVSGFSTYSYTWVWQTPERKLEWVATISSGGSSTYY 78  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPAAMYCTREGGGFTVMYF--DVGAGTL 113  
DB 79 PDSVKGRTISRDNKNTLYLQMSLSRSEDPAAMYCVRPEIPITYSGS----YFDSWG 133  
QY 114 AGTVTVSA 122  
DB 134 QGTITTVSS 142

RESULT 7  
Q96BB9 PRELIMINARY; PRT; 597 AA.  
ID 096BB9;  
AC 096BB9; 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015760; AAH15760.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_5.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 70.7%; Score 455.5; DB 4; Length 597;  
Best Local Similarity 68.8%; Pred. No. 4e-38;  
Matches 86; Conservative 18; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVOLDSGGGLVPGGSLKLSCAASGFTSSYTWVWQTPERKLEWVATISSGGSSTYY 60  
DB 20 EVOLDSGGGLVPGGSLRLSCAASGFTSSYTWVWQTPERKLEWVATISSGGSSTYY 79  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPAAMYCTREGGGFTVMYF--DVGAGTL 117  
DB 80 ADSVKGRTISRDNKNTLYLQMSLSRSEDPAVYCAADPRGYSASGNYTREDYWGQTL 139  
QY 118 VTVSA 122  
DB 140 VTVSS 144

RESULT 8  
Q91205 PRELIMINARY; PRT; 473 AA.  
ID 091205;  
AC 091205; 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 51.9 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010327; AA010327.1; -  
DR MGI: 2144967; A0044919;  
DR InterPro: IPR000345; CytC\_heme\_bind.  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig\_3.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS00130; CYTOCHROME\_C; 1.  
DR PROSITE: PS00835; Ig\_Like; 4.  
DR PROSITE: PS00290; Ig\_MHC; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 70.3%; Score 453; DB 11; Length 473;  
Best Local Similarity 72.6%; Pred. No. 5,4e-38;  
Matches 90; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 1 EVQLQESGGGLVPGGSLRLSCAASGFTSSYTMHWROTPPEKRLIEWATISSGGSSTYY 60  
DB 20 EVQLVESGGGLVPGGSRRLSCAASGFTSDYGMHWVQAPEKGLIEWATISSGGSSTYY 79  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNY-EDVWGAGTLV 118  
DB 80 ADVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYYCAR------LMLFRIDYWGAGTLV 133  
QY 119 TVSA 122  
DB 134 TVSS 137

## RESULT 9

Q9RLA4 PRELIMINARY; PRT; 437 AA.  
ID Q9RLA4;  
AC Q9RLA4-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)  
DE Gamma1 heavy chain of Mab7 (Fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blifter rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF152372; AAD40243.1; -  
DR HSSP: P01842; 7FAB.  
DR MGI: MGI:96446; Igh-4.  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_4.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS00835; Ig\_Like; 4.  
DR PROSITE: PS00290; Ig\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 69.9%; Score 450; DB 11; Length 437;  
Best Local Similarity 76.9%; Pred. No. 1e-37;  
Matches 93; Conservative 3; Mismatches 17; Indels 8; Gaps 2;

QY 2 VQLQESGGGLVPGGSLRLSCAASGFTSSYTMHWROTPPEKRLIEWATISSGGSSTYY 61  
DB 60 ADVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYYCAR------LMLFRIDYWGAGTLV 118

DB 1 VQLQESGGGLVPGGSLRLSCAASGFTSSYTMHWROTPPEKRLIEWATISSGGSSTYY 59  
QY 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYEDVWGAGTLVTVS 121  
DB 60 DSVKGRFTIYDKORNIISLQMSLSRSEDPTAMYYCAR------YSAYWGPGTLVTVS 112  
QY 122 A 122  
DB 113 A 113

## RESULT 10

Q9UL71 PRELIMINARY; PRT; 121 AA.  
ID Q9UL71;  
AC Q9UL71;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96277139; PubMed=9614934;  
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035043; AAD56279.1; -  
DR HSSP: P01772; 2F84.  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS00835; Ig\_Like; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFPA5D50736 CRC64;

Query Match 68.9%; Score 443.5; DB 4; Length 121;  
Best Local Similarity 69.7%; Pred. No. 9,4e-38;  
Matches 85; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVPGGSLRLSCAASGFTSSYTMHWROTPPEKRLIEWATISSGGSSTYY 60  
DB 1 EVQLVESGGGLVPGGSRRLSCAASGFTSDYGMHWVQAPEKGLIEWATISSGGSSTYY 79  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYEDVWGAGTLVTV 120  
DB 61 ADVKGRFTISRDNKNTLYLQMSLSRSEDPTAMYYCAR-GRYTTIYDFRDMGGSTMTV 119  
QY 121 SA 122  
DB 120 SS 121

## RESULT 11

Q9UL91 PRELIMINARY; PRT; 118 AA.  
ID Q9UL91;  
AC Q9UL91;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

OX  NCB1_Taxid=9606;
RN  [1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035023; AAD56259.1; -.
DR  HSSP; P01772; 2FB4.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER
FT  NON_TER
SQ  SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match
Best Local Similarity 68.6%; Score 442; DB 4; Length 118;
Matches 87; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

QY  1 EVQLDSGGGLVKGPGSLKLSGASGFTFSSYTMGWRQTEPEKRELEWATISSGGSSTYY 60
DB  1 EVQLVESGGGLVQPGSLKLSGASGFTFSISMWVRQAFKGLHWAVISYDSNKTY 60
QY  61 PDVKGRTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 120
DB  61 ADVKGRFTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 116

QY  121 S 121
DB  117 S 117

RESULT 12
ID  Q8WTK1 PRELIMINARY; PRT; 613 AA.
AC  Q8WTK1;
DT  01-MAR-2002 (TREMBlrel. 20, Created)
DT  01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX  NCB1_Taxid=9606;
RN  [1]
RN  SEQUENCE FROM N.A.
RA  Strusberg R.;
RA  Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR  EMBL; BC020240; AAH20240.1; -.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 5.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; 3.
KW  Hypothetical protein.
SQ  SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match
Best Local Similarity 68.5%; Score 441; DB 4; Length 613;
Matches 86; Conservative 14; Mismatches 15; Indels 12; Gaps 2;

QY  1 EVQLDSGGGLVKGPGSLKLSGASGFTFSSYTMGWRQTEPEKRELEWATISSGGSSTYY 60
DB  20 QVQLVESGGGLVQPGSLKLSGASGFTFSISMWVRQAFKGLHWAVISYDSNKTY 79

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QY  61 PDVKGRTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 115
DB  80 ADVKGRFTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 132
QY  116 TLNVTYSA 122
DB  133 TMTVTYSS 139

RESULT 13
ID  Q9UL93 PRELIMINARY; PRT; 116 AA.
AC  Q9UL93;
DT  01-MAY-2000 (TREMBlrel. 13, Created)
DT  01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE  Myosin-reactive immunoglobulin heavy chain variable region
DE  (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX  NCB1_Taxid=9606;
RN  [1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035021; AAD56257.1; -.
DR  HSSP; P01772; 2FB4.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER
FT  NON_TER
SQ  SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match
Best Local Similarity 68.2%; Score 439.5; DB 4; Length 116;
Matches 88; Conservative 10; Mismatches 18; Indels 5; Gaps 2;

QY  2 VQLDSGGGLVKGPGSLKLSGASGFTFSSYTMGWRQTEPEKRELEWATISSGGSSTYY 61
DB  1 VQLVESGGGLVQPGSLKLSGASGFTFSISMWVRQAFKGLHWAVISYDSNKTY 60
QY  62 DSVKGRFTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 121
DB  61 DSVKGRFTISRDNKNTLYIQMSLSRSEDYAMYYCTREGGFTVNMVFDWGAGTLVTV 115

QY  122 A 122
DB  116 S 116

RESULT 14
ID  Q8WU38 PRELIMINARY; PRT; 573 AA.
AC  Q8WU38;
DT  01-MAR-2002 (TREMBlrel. 20, Created)
DT  01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX  NCB1_Taxid=9606;
RN  [1]

```

RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RA Strausberg R.;  
 RI Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC021276; AAH21276.1; -  
 DR InterPro: IPR007110; IG\_1ike.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG; 4.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; 2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 68.0%; Score 438; DB 4; Length 573;  
 Best Local Similarity 68.5%; Pred. No. 2,4e-36;

Matches 85; Conservative 12; Mismatches 25; Indels 2; Gaps 1;

QY 1 EVQLVDSGGGLVPGGSLKLSCAASGFTFSSTMSVVRQTPKRLKLVATISGGSSITY 60  
 DB 20 EVQLVDSGGGLVPGGSLKLSCAASGFTFDYAMHWVRQAPGKLEWVSGISWNSGSIY 79

QY 61 PDSVKGRFTISRDNKNTLYLQNSLRSEDTAMVYCTREGGGFTVNWYF--DYGAGELY 118  
 DB 80 ADSVKGRFTISRDNKNSLYLQNSLRADPTALYCAKSGSGSYIGYGMDFWGQGITV 139

QY 119 TVSA 122  
 DB 140 TVSS 143

RESULT 15

Q8NSK4 PRELIMINARY; PRT; 499 AA.

ID Q8NSK4

AC Q8NSK4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxId=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Strausberg R.;

RI Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC032249; AAH32249.1; -

DR InterPro: IPR003599; IG.

DR InterPro: IPR007110; IG\_1ike.

DR InterPro: IPR003597; IG\_GL.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; IG; 4.

DR SMART: SM00409; IG; 4.

DR SMART: SM00407; IGV; 2.

DR PROSITE: PS00835; IG\_LIKE; 4.

DR PROSITE: PS00290; IG\_MHC; 1.

KM Hypothetical protein.

SQ SEQUENCE 499 AA; 53376 MW; 93A5C99582054F32 CRC64;

Query Match 67.9%; Score 437.5; DB 4; Length 499;

Best Local Similarity 66.9%; Pred. No. 2,2e-36;

Matches 85; Conservative 13; Mismatches 24; Indels 5; Gaps 1;

QY 1 EVQLVDSGGGLVPGGSLKLSCAASGFTFSSTMSVVRQTPKRLKLVATISGGSSITY 60  
 DB 20 EVQLVDSGGGLVPGGSLKLSCAASGFTFDYAMHWVRQAPGKLEWVSGISWNSGSIY 79

QY 61 PDSVKGRFTISRDNKNTLYLQNSLRSEDTAMVYCTRE----GGGFTVNWYFDWGAG 115

DB 80 ADSVKGRFTISRDNKNSLYLQNSLRVEDPTALYCAADPTKCSGSGSLGYMDWNGKG 139  
 QY 116 TVTVSA 122  
 DB 140 TVTVSS 146

Search completed: November 7, 2003, 07:34:35  
 Job time : 40.323 secs



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XX PF 13-SEP-2000; 2000MO-EP08936.
XX PR 14-SEP-1999; 99AT-0001576.
XX PA (BAXT ) BAXTER AG.
XX PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX DR WPI; 2001-290358/30.
XX DR N-PSDB; AAF30725.
XX PT New factor IX/factor IXa antibodies and their derivatives useful for
XX PT increasing amidolytic activity of factor IXa, and for treating blood
XX PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX PS Claim 12; Fig 16; 138pp; English.

CC The present sequence is that of a single chain Fv (scFv) derivative
CC of antibody 198/AB2, comprising the heavy (VH) and light (VL) chain
CC variable regions of 198/AB2 joined by an artificial, flexible linker
CC peptide. The scFv was obtained by PCR amplification of cDNAs from
CC 198/AB2 VH and VL regions and cloning in vector pDAP2. 198/AB2 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIIa)
CC antibodies of the invention. Anti-FIX/FIIa and their derivatives,
CC including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of FVIIa inhibitors. This allows for rapid blood coagulation even
CC in the absence of FVIII or FVIIa, and in the case of FVIII
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis.
XX SQ Sequence 249 AA;

Query Match 100.0%; Score 644; DB 22; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-54;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPRGSGIKLSCAASGFTSSYTMWVROTPERKLEWVAITISGGSSTYY 60
DB 1 EVQLQESGGGLVPRGSGIKLSCAASGFTSSYTMWVROTPERKLEWVAITISGGSSTYY 60

QY 61 PDYKGRFTISRDNKNTLYLQMSLSRSEPTAMYCTRESGGFTVMYEDVWGAGTLVTV 120
DB 61 PDYKGRFTISRDNKNTLYLQMSLSRSEPTAMYCTRESGGFTVMYEDVWGAGTLVTV 120

QY 121 SA 122
DB 121 SA 122

RESULT 2
AAB20442
ID AAB20442 standard; Protein; 294 AA.
XX
XX AAB20442;
XX
XX 21-JUN-2001 (first entry)
XX
XX Anti-FIX/FIIa antibody 198/BI-myc-tag fusion.
XX
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX myc-tag.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Synthetic.
XX Chimeric - Escherichia coli.

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FH Key Location/Qualifiers
FH Peptide 1..22
FH Protein /label= Signal_peptide
FH Protein /label= Mature_protein
FH Protein /label= scFv
FH Region 23..144
FH Region /label= VH
FH Misc-difference 76
FH Peptide /note= "encoded by GGN"
FH Peptide 145..159
FH Peptide /label= Linker
FH Region 160..271
FH Peptide /label= VL
FH Peptide 272..274
FH Protein /label= Spacer
FH Peptide 275..286
FH Peptide /label= Myc_tag
FH Peptide 287..288
FH Peptide /label= Spacer
FH Peptide 289..294
FH Peptide /label= His_tag

XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX WPI; 2001-290358/30.
XX DR N-PSDB; AAF30732.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX Example 18; Fig 34; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a Pelb
XX leader; a single chain Fv (scFv) derivative of antibody 198/BI
XX comprising the heavy (VH) and light (VL) chain variable regions of
XX 198/BI joined by an artificial, flexible linker peptide; a spacer;
XX a myc-tag peptide; a spacer; and a C-terminal 6His affinity tag.
XX 198/BI is an example of anti-human Factor IX (FIX)/activated Factor
XX IX (FIIa) antibodies of the invention. Anti-FIX/FIIa cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FVIIa inhibitors. This allows for rapid blood coagulation even
XX in the absence of FVIII or FVIIa, and in the case of FVIII inhibitor
XX patients. The antibodies and derivatives are used in a claimed
XX pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis. The scFv-myc-tag fusion was expressed in E. coli. It
XX exhibited FVIII-like activity.
XX
XX SQ Sequence 294 AA;

Query Match 96.9%; Score 624; DB 22; Length 294;
Best Local Similarity 96.7%; Pred. No. 1.5e-52;
Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPRGSGIKLSCAASGFTSSYTMWVROTPERKLEWVAITISGGSSTYY 60
DB 23 EVQLVESGGGLVPRGSGIKLSCAASGFTSSYTMWVROTPERKLEWVAITISGGSSTYY 82

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QY      61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGGFTVNWYEDVWAGTLVTV 120
      |||
Db      83 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGGFTVNWYEDVWAGTISVTV 142
QY      121 SA 122
      ||
Db      143 SS 144

RESULT 3
AAB20438
ID      AAB20438 standard; Protein; 325 AA.
XX
AC      AAB20438;
XX
DT      21-JUN-2001 (first entry)
XX
DE      Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
XX
KM      Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
KW      Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW      haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW      bivalent antibody; plasmid pZiP-198AB2#102.
XX
OS      Chimeric - Mus musculus.
OS      Chimeric - Synthetic.
OS      Chimeric - Escherichia coli.
XX
FH      Key
      location/Qualifiers
FT      Peptide
      1..22
      /label= Signal_peptide
      /note= "PelB leader"
FT      Protein
      23..325
      /label= Mature_Protein
FT      Region
      23..144
      /label= scFv
      /label= VH
FT      Misc-difference
      76
      /note= "encoded by GGN"
FT      Peptide
      145..159
      /label= linker
FT      Region
      160..271
      /label= VL
FT      Misc-difference
      166
      /note= "encoded by TNT"
FT      Misc-difference
      181
      /note= "encoded by TCN"
FT      Peptide
      272..274
      /label= Spacer
FT      Protein
      275..284
      /label= Hinge
FT      Protein
      285..319
      /label= Helix
FT      Peptide
      320..325
      /label= His_tag
XX
PN      WO200119992-A2.
XX
PD      22-MAR-2001.
XX
PF      13-SEP-2000; 2000MO-EP08936.
XX
PR      14-SEP-1999; 99AT-0001576.
XX
PA      (BAXT ) BAXTER AG.
XX
PI      Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
DR      WPI; 2001-290358/30.
XX
DR      N-PSDB; AAF30728.
XX
PT      New factor IX/factor IXa antibodies and their derivatives useful for

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PT      Increasing amidolytic activity of factor IXa, and for treating blood
PT      coagulation disorders such as haemophilia A and haemorrhagic diathesis
PS      Example 16; Fig 28; 138pp; English.
XX
CC      The present sequence is that of a bivalent miniantibody comprising
CC      a PelB leader peptide, the single chain Fv (scFv) fragment of
CC      antibody 198/B1 (subclone AB2), an amphipathic helical structure
CC      and a C-terminal 6His tag. The protein was expressed in
CC      Escherichia coli from plasmid pZiP198AB2#102 (see AAF30728).
CC      Antibody 198/B1 is an example of anti-human Factor IX
CC      (FIX)/activated Factor IX (FIXa) antibodies of the invention.
CC      Anti-FIX/FIXa antibodies and their derivatives have FVIIIa cofactor
CC      activity or FIXa activating activity. Administration leads to an
CC      increase in the procoagulant activity of FIXa, even in the presence
CC      of FVIIIa inhibitors. This allows for rapid blood coagulation even
CC      in the absence of FVIII or FVIIIa, and in the case of FVIII
CC      inhibitor patients. The antibodies and derivatives are used in a
CC      claimed pharmaceutical composition for treating patients with blood
CC      coagulation disorders, especially haemophilia A and haemorrhagic
CC      diathesis. The bivalent miniantibody exhibited FVIII-like
CC      activity.
XX
SQ      Sequence 325 AA;
XX
Query Match          96.9%; Score 624; DB 22; Length 325;
Best Local Similarity 96.7%; Pred. No. 1.6e-52;
Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY      1 EVYLOESGGGLVPGGSLKLSCAAGFTFSSYTNMSVROTPEKRLIEWATISSGGSSTY 60
      |||
Db      23 EVKLVESGGGLVPGGSLKLSCAAGFTFSSYTNMSVROTPEKRLIEWATISSGGSSTY 82
QY      61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGGFTVNWYEDVWAGTLVTV 120
      |||
Db      83 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGGFTVNWYEDVWAGTISVTV 142
QY      121 SA 122
      ||
Db      143 SS 144

RESULT 4
AAB20437
ID      AAB20437 standard; Protein; 732 AA.
XX
AC      AAB20437;
XX
DT      21-JUN-2001 (first entry)
XX
DE      Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
XX
KM      Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW      Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW      haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW      alkaline phosphatase.
XX
OS      Chimeric - Mus musculus.
OS      Chimeric - Synthetic.
OS      Chimeric - Escherichia coli.
XX
FH      Key
      location/Qualifiers
FT      Peptide
      1..22
      /label= Signal_peptide
FT      Protein
      23..732
      /label= Mature_protein
FT      Protein
      23..271
      /label= scFv
FT      Region
      23..144
      /label= VH
FT      Misc-difference
      76
      /note= "encoded by GGN"
FT      Peptide
      145..159

```

```

FT      Region /label= Linker
FT      160..271
FT      /label= VL
FT      Peptide 272..275
FT      /label= Spacer
FT      Protein 276..725
FT      /label= Alkaline_phosphatase
FT      Peptide 726..732
FT      /label= Hts_tag
XX
XX      MO200119992-A2.
XX
XX      22-MAR-2001.
XX
XX      13-SEP-2000; 2000MO-EP08936.
XX
XX      14-SEP-1999; 99AT-0001576.
XX
XX      (BAXT ) BAXTER AG.
XX
XX      Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX      WPI; 2001-290358/30.
XX      N-PSDB; AAB30727.
XX
XX      New factor IX/factor IXa antibodies and their derivatives useful for
XX      increasing amidolytic activity of factor IXa, and for treating blood
XX      coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX      Example 16; Fig 26; 138pp; English.
XX
XX      The present sequence is that of a fusion protein comprising: a pelb
XX      leader; a single chain Fv (scfv) derivative of antibody 198/B1
XX      comprising the heavy (VH) and light (VL) chain variable regions of
XX      198/B1 joined by an artificial, flexible linker peptide; a spacer;
XX      Escherichia coli alkaline phosphatase; and a C-terminal 6His
XX      affinity tag. 198/B1 is an example of anti-human Factor IX
XX      (FIX)/activated Factor IX (FIXa) antibodies of the invention.
XX      Anti-FIX/FIXa antibodies and their derivatives, including scfv
XX      fragments, have FvIIIa cofactor activity or FIXa activating
XX      activity. Administration leads to an increase in the procoagulant
XX      activity of FIXa, even in the presence of FvIIIa inhibitors. This
XX      allows for rapid blood coagulation even in the absence of FvIII or
XX      FvIIIa, and in the case of FvIII inhibitor patients. The
XX      antibodies and derivatives are used in a claimed pharmaceutical
XX      composition for treating patients with blood coagulation disorders,
XX      especially haemophilia A and haemorrhagic diathesis. The
XX      scfv-alkaline phosphatase was expressed in E. coli. It exhibited
XX      FvIII-like activity.
XX
XX      Sequence 732 AA;
XX
XX      Query Match 96.9%; Score 624; DB 22; Length 732;
XX      Best Local Similarity 96.7%; Pred. No. 4,2e-52;
XX      Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX      1 EVOLQSGGGVGRGSLKSCAASGFTSSYMSWYRPERLEWVAVTSSGSSSTY 60
XX      |||
XX      23 EVKIVSGGGVGRGSLKSCAASGFTSSYMSWYRPERLEWVAVTSSGSSSTY 82
XX
XX      61 PDVYKGRFTISRDAKOTLYLQWSSLRSEDTAMYYCTREGSGFTVMVFPDVGAGTLVTV 120
XX      83 PDVYKGRFTISRDAKOTLYLQWSSLRSEDTAMYYCTREGSGFTVMVFPDVGAGTSVTV 142
XX
XX      QY 121 SA 122
XX      Db 143 SS 144
XX
XX      RESULT 5
XX      AAB20436
XX      ID AAB20436 standard; Protein: 249 AA.

```

```

AC      AAB20436;
XX
XX      21-JUN-2001 (first entry)
XX
XX      Anti-FIX/FIXa antibody 198/A1 scfv.
XX
XX      Factor IX; FIX; Factor IXa; FIXa; scfv; antibody; procoagulant;
XX      Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX      haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
XX
XX      Chimeric - Mus musculus.
XX      Chimeric - Synthetic.
XX
XX      Key Location/Qualifiers
XX      FH 1..122
XX      FT /label= VH
XX      FT 99..111
XX      FT /label= CDR3
XX      FT 123..136
XX      FT /label= Linker
XX      FT 137..249
XX      FT /label= VL
XX      FT 230..238
XX      FT /label= CDR3
XX      FT Misc-difference 142
XX      FT /note= "encoded by ACN"
XX      FT Misc-difference 224
XX      FT /note= "encoded by GCN"
XX
XX      MO200119992-A2.
XX
XX      22-MAR-2001.
XX
XX      13-SEP-2000; 2000MO-EP08936.
XX
XX      14-SEP-1999; 99AT-0001576.
XX
XX      (BAXT ) BAXTER AG.
XX
XX      Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX      WPI; 2001-290358/30.
XX      N-PSDB; AAB30726.
XX
XX      New factor IX/factor IXa antibodies and their derivatives useful for
XX      increasing amidolytic activity of factor IXa, and for treating blood
XX      coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX      Example 10; Fig 17; 138pp; English.
XX
XX      The present sequence is that of a single chain Fv (scfv) derivative
XX      of antibody 198/A1, comprising the heavy (VH) and light (VL) chain
XX      variable regions of 198/A1 joined by an artificial, flexible linker
XX      peptide. The scfv was obtained by PCR amplification of cDNAs for
XX      198/A1 VH and VL regions and cloning in vector pDAR2. 198/A1 is
XX      an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
XX      antibodies of the invention. Anti-FIX/FIXa and their derivatives,
XX      including scfv and CDR3 fragments, have Factor VIIIa (FvIIIa) cofactor
XX      activity or FIXa activating activity. Administration leads to an
XX      increase in the procoagulant activity of FIXa, even in the presence
XX      of FvIIIa inhibitors. This allows for rapid blood coagulation even
XX      in the absence of FvIII or FvIIIa, and in the case of FvIII
XX      inhibitor patients. The antibodies and derivatives are used in a
XX      claimed pharmaceutical composition for treating patients with blood
XX      coagulation disorders, especially haemophilia A and haemorrhagic
XX      diathesis.
XX
XX      Sequence 249 AA;
XX
XX      Query Match 94.6%; Score 609; DB 22; Length 249;
XX      Best Local Similarity 93.4%; Pred. No. 3.4e-51;
XX      Matches 114; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLLEWATISGGGSSTYY 60  
 DB 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLLEWATISGGGSSTYY 60  
 QY 61 PDSVKGRTISRDNAKNTLYLQMSLSRSEPTAMYYCTREGGFTVNWPDVWAGTILTV 120  
 DB 61 PDSVKGRTISRDNAKNTLYLQMSLSRSEPTAMYYCTREGGFTVNWPDVWAGTILTV 120  
 QY 121 SA 122  
 DB 121 SS 122

RESULT 6  
 ABPe0555  
 ID ABPe0555 standard; protein; 134 AA.  
 XX  
 AC ABPe0555;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Murine antibody 14F3 heavy chain variable region.  
 XX  
 DE Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;  
 KM antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;  
 KM neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;  
 KM bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;  
 KM insulin-dependent diabetes; inflammatory bowel disease;  
 KM multiple sclerosis; heavy chain variable region;  
 KM complementary determining region; CDR.  
 XX  
 OS Mus musculus.  
 XX

Key Location/Qualifiers  
 FH Region 31..35  
 FT /label= CDR1  
 FT 50..66  
 FT /label= CDR2  
 FT 99..110  
 FT /label= CDR3  
 FT  
 PN WO200295012-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 03-MAY-2002; 2002WO-US14246.  
 XX  
 PR 18-MAY-2001; 2001US-292031P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Sweet RW, Tornetta MA, Wattam TA;  
 XX  
 PI Sweet RW, Tornetta MA, Wattam TA;  
 XX  
 DR WPI; 2003-156758/15.  
 DR N-PSDB; ABV99887.  
 XX  
 PT New monoclonal antibody having the characteristics of a monoclonal  
 PT antibody 14F3, useful for treating or preventing osteopathic diseases,  
 PT e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.  
 PT psoriasis, or diabetes  
 XX  
 PS Disclosure; Page 8; 51pp; English.  
 XX

CC The invention relates to a novel monoclonal antibody having the  
 CC identifying characteristics of, or that is a monoclonal antibody 14F3.  
 CC An antibody of the invention has osteopathic, antirheumatic,  
 CC antiarthritic, antiinflammatory, cytostatic, antipsoriatic, antidiabetic,  
 CC and neuroprotective activity. The polynucleotides encoding the antibodies  
 CC of the invention may have a use in gene therapy. The antibodies and  
 CC polypeptides are useful for treating or preventing osteopathic diseases,  
 CC such as rheumatoid arthritis, osteoporosis, metastatic and primary bone  
 CC cancer, wear debris induced osteolysis or osteoarthritis, and immune

CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory  
 CC bowel disease or multiple sclerosis. The present sequence represents the  
 CC heavy chain variable region of the murine monoclonal antibody 14F3 of the  
 CC invention. The sequence contains three complementary determining regions  
 CC (CDR's).  
 SQ Sequence 134 AA;

Query Match 83.6%; Score 538.5; DB 24; Length 134;  
 Best Local Similarity 85.2%; Pred. No. 1.2e-44;  
 Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLLEWATISGGGSSTYY 60  
 DB 1 EVQLVSGGGLVQPGGSLKLSCAASGFTFSRYGMSWVRQTPKRLLEWATISGGGSSTYY 60  
 QY 61 PDSVKGRTISRDNAKNTLYLQMSLSRSEPTAMYYCTREGGFTVNWPDVWAGTILTV 120  
 DB 61 PDSVKGRTISRDNAKNTLYLQMSLSRSEPTAMYYCTREGGFTVNWPDVWAGTILTV 119  
 QY 121 SA 122  
 DB 120 SS 121

RESULT 7  
 AAB20434  
 ID AAB20434 standard; Protein; 249 AA.  
 XX  
 AC AAB20434;  
 XX  
 DT 21-JUN-2001 (first entry)  
 XX  
 DE Anti-Flx/FixA antibody 193/K2 scFv.  
 XX

Key Location/Qualifiers  
 FH Protein 1..121  
 FT /label= VH  
 FT 98..110  
 FT /label= CDR3  
 FT 122..135  
 FT /label= Linker  
 FT Protein 136..249  
 FT /label= VL  
 FT 230..238  
 FT /label= CDR3  
 FT  
 PN WO200119992-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 13-SEP-2000; 2000WO-EP08936.  
 XX  
 PR 14-SEP-1999; 99AT-0001576.  
 XX  
 PA (BAXT ) BAXTER AG.  
 PA  
 PI Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 XX  
 PI WPI; 2001-290358/30.  
 DR N-PSDB; AAF30724.  
 XX  
 PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing antolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX

PS Claim 10; Fig 15; 138pp; English.

XX  
CC The present sequence is that of a single chain Fv (scFv) derivative  
CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain  
CC variable regions of 193/K2 joined by an artificial, flexible linker  
CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
CC 193/K2 VH and VL regions and cloning in vector pDAP2. 193/K2 is  
CC an example of anti-human Factor IX (FIX)/activated Factor IX (Fika)  
CC antibodies of the invention. Anti-FIX/Fika and their derivatives,  
CC including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor  
CC activity or FIXa activating activity. Administration leads to an  
CC increase in the procoagulant activity of FIXa, even in the presence  
CC of FVIIa inhibitors. This allows for rapid blood coagulation even  
CC in the absence of FVIII or FVIIa, and in the case of FVIII  
CC inhibitor patients. The antibodies and derivatives are used in a  
CC claimed pharmaceutical composition for treating patients with blood  
CC coagulation disorders, especially haemophilia A and haemorrhagic  
CC diathesis.

SQ Sequence 249 AA;

Query Match 83.5%; Score 537.5; DB 22; Length 249;  
Best Local Similarity 85.4%; Pred. No. 3e-44;  
Matches 105; Conservative 8; Mismatches 7; Indels 3; Gaps 2;

QY 1 EVOLQESGGGLVKGSGSLKSCAAGFTFSSTYMSWVRQTPKRLKLEWATISSGSSSTYY 60  
DB 1 EVOLVESGGGLVKGSGSLKSCAAGFTFSSTYMSWVRQTPKRLKLEWATISSGSSSTYY 60

QY 61 PDSVKGRTISRDNKATLYLQMSLSSEDTAMYYCTRBGGG-GFTVNMVFDVWAGTLVTV 119  
DB 61 PDSVKGRTISRDNKATLYLQMSLSSEDTAMYYCTRBGGG-GFTVNMVFDVWAGTLVTV 119

QY 120 VSA 122  
DB 119 VSA 121

RESULT 8  
AAE16426 AAE16426 standard; Protein; 121 AA.

AC AAE16426;  
XX  
DT 09-APR-2002 (first entry)

DE Mouse antibody 2A4 heavy chain variable region.

XX  
XX Mouse; antibody 2A4; heavy chain variable region; osteopathic; psoriasis;  
XX cytostatic; antiinflammatory; osteoporosis; bone cancer; immune disease;  
XX inflammatory bowel disease; multiple sclerosis; osteopenic disease;  
XX rheumatoid arthritis; diabetes.

OS Mus sp.

XX  
XX Key Location/Qualifiers

FT Region 30..35

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region 50..66

FT /label= CDR

FT /note= "Complementarity determining region"

FT /label= CDR

FT /note= "Complementarity determining region"

XX  
XX MO200191793-A1.

XX  
XX 06-DEC-2001.

XX  
XX 24-MAY-2001; 2001WO-US16865.

XX  
XX 26-MAY-2000; 2000US-207628P.

XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Blake SM, Sweet RM, Taylor AH, Wattam TA;

DR WPI; 2002-122040/16.

DR N-PEDB; AAD26948.

PT New anti-RANK ligand monoclonal antibodies, useful for treating or  
PT preventing osteopenic diseases (e.g. arthritis, osteoporosis or bone  
PT cancer) or immune disease (e.g. psoriasis, inflammatory bowel disease  
PT or multiple sclerosis)

PS Claim 6; Page 9; 50pp; English.

CC The invention relates to anti-RANK monoclonal antibodies which has the  
CC identifying characteristics of monoclonal antibody 2A4. The antibody or  
CC polypeptide is useful for treating or preventing osteopenic diseases  
CC (e.g., rheumatoid arthritis, osteoporosis, metastatic and primary bone  
CC cancer, wear debris induced osteolysis or osteoarthritis) or immune  
CC diseases (e.g., psoriasis, insulin dependent, diabetes, inflammatory  
CC bowel disease or multiple sclerosis). The antibody is also useful for  
CC treating and diagnosing conditions mediated by the RANK ligand. The  
CC present sequence is mouse antibody 2A4 heavy chain variable region.

SQ Sequence 121 AA;

Query Match 82.7%; Score 532.5; DB 23; Length 121;  
Best Local Similarity 84.4%; Pred. No. 4e-44;  
Matches 103; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVOLQESGGGLVKGSGSLKSCAAGFTFSSTYMSWVRQTPKRLKLEWATISSGSSSTYY 60  
DB 1 EVOLVESGGGLVKGSGSLKSCAAGFTFSSTYMSWVRQTPKRLKLEWATISSGSSSTYY 60

QY 61 PDSVKGRTISRDNKATLYLQMSLSSEDTAMYYCTRBGGG-GFTVNMVFDVWAGTLVTV 120  
DB 61 PDSVKGRTISRDNKATLYLQMSLSSEDTAMYYCTRBGGG-GFTVNMVFDVWAGTLVTV 119

QY 121 SA 122  
DB 120 SS 121

RESULT 9  
ABG74241 ABG74241 standard; Protein; 140 AA.

AC ABG74241;

DT 22-APR-2003 (first entry)

DE Mouse antibody MB3.6 heavy chain variable region.

XX  
XX T-cell receptor; cytostatic; dermatological; neuroprotective;  
XX immunostimulant; GDS; ganglioside antigen; MB3.6; PSNA; tumour; 308; 404;  
XX 3E11; prostate-specific membrane antigen; zeta signalling chain;  
XX CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
XX small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

XX  
XX US2002132983-A1.

XX  
XX 19-SEP-2002.

XX  
XX 10-DEC-2001; 2001US-0006773.

XX  
XX 30-NOV-2000; 2000US-250087P.

XX  
XX 30-NOV-2000; 2000US-250089P.

XX  
XX (JUNG/) JUNGHANS R P.

XX Junghans RP;  
PI  
XX  
PR WPI; 2003-208946/20.  
DR  
XX N-PSDB; ABX16566.  
DR  
XX  
PT New chimeric molecule useful in treating patients with disorders, such  
PT as melanoma, neuroendocrine disorders, prostate and small cell lung  
PT cancer comprises GD3 and/or PSMA binding domains of antibody -  
XX  
XX  
PS Disclosure; Page 9, 35pp; English.  
XX  
XX The invention relates to a chimeric molecule comprising the GD3  
CC (ganglioside antigen) binding domain of antibody M3.6, with any of 3  
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
CC binding domain of antibody 3D8, 4D4 and 3B11, with variable gene  
CC sequences, the zeta signaling chain of the T cell receptor and an  
CC intervening Cdelta alpha hinge in which cysteine residues have been mutated.  
CC The chimeric molecules expressed in T cells or NK cells or other  
CC effector cells are useful in treating patients with cancers expressing  
CC the GD3 (M3.6 derivatives) or PSMA antigen (3D8, 4D4, 3B11  
CC derivatives), and/or together with each other or with heterologous  
CC constructs to engage additional stimulatory and functional properties  
CC of the effector cells to enhance the antitumour therapeutic efficacy  
CC (claimed). They are particularly useful in disorders including  
CC melanoma, neuroendocrine tumours and prostate and small cell lung  
CC cancer. The present sequence represents the mouse antibody M3.6 heavy  
CC chain variable region.  
SQ Sequence 140 AA;  
Query Match 81.9%; Score 527.5; DB 24; Length 140;  
Best Local Similarity 82.4%; Pred. No. 1.4e-43;  
Matches 103; Conservative 5; Mismatches 10; Indels 7; Gaps 2;  
QY 1 EVQLQESGGGLVQPGGSLKSCAASGTFSSYTMNWQTPERKLEWVAITISGGSSITY 60  
DB 20 EVVAVESGGGFGVPGGSLKSCAAGFTFSRYAMSWVRQTPERKLEWVAITISGGSHITY 79  
QY 61 PDSVKGRTISRDNAAKNTLYIQMSLSRSEPTAMYYCTRG---GGFTVMWYDVGAGTLV 117  
DB 80 PDSVKGRTISRDNAAKNTLYIQMSLSRSEPTAIYICARPGYDGA---WFDVWAGAGTT 135  
QY 118 VTUSA 122  
DB 136 VTVSS 140  
RESULT 10  
AAU72814 standard; Protein; 119 AA.  
ID AAU72814;  
XX  
AC AAU72814;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DB Humanised mouse TRA-8 anti-human DR5 antibody #4.  
XX  
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;  
KW TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;  
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;  
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;  
KW myaethenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.  
OS Synthetic.  
XX  
XX WO200183560-A1.  
XX  
XX 08-MCV-2001.  
XX

PF 02-MAY-2001; 2001WO-US14151.  
XX  
XX  
XX 02-MAY-2000; 2000US-201344P.  
PR  
XX  
XX (UABR-) UAB RES FOUND.  
PA  
XX  
XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;  
PI  
XX WPI; 2002-049338/06.  
DR  
XX  
XX  
PT Novel antibody specific for tumour necrosis factor-related  
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in  
PT cancer -  
XX  
XX  
PS Example 26; Page 212-213; 229pp; English.  
XX  
XX The invention describes a novel antibody which recognizes a tumour  
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
CC activity to a cell expressing DR5 in vivo. It is also useful for  
CC preparing a therapeutic for selective apoptosis of abnormal or  
CC dysregulated cells, and for inhibiting cell proliferation in a cell,  
CC preferably a human breast, ovary, colon, hematopoietic, prostate,  
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may  
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The  
CC antibody is used to treat an autoimmune disease, systemic lupus  
CC erythematosus, Hashimoto's disease, rheumatoid arthritis,  
CC graft-versus-host disease, Sjogren's syndrome, Chron's disease,  
CC pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,  
CC autoimmune haemolytic anaemia, sterility, myaethenia gravis, multiple  
CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,  
CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerular nephritis, hypoplastic anaemia, rejection after organ  
CC transplantation, and numerous malignancies of lung, prostate, liver,  
CC ovary, lymphatic or breast tissue. This sequence shows one of the  
CC humanised anti-DR5 antibodies described in the method of the invention.  
SQ Sequence 119 AA;  
Query Match 80.7%; Score 519.5; DB 23; Length 119;  
Best Local Similarity 83.6%; Pred. No. 7.1e-43;  
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;  
QY 1 EVQLQESGGGLVQPGGSLKSCAASGTFSSYTMWQTPERKLEWVAITISGGSSITY 60  
DB 1 EVMLVBSGGGLVQKGGSLKSCAASGTFSSYTMWQTPERKLEWVAITISGGSSITY 60  
QY 61 PDSVKGRTISRDNAAKNTLYIQMSLSRSEPTAMYYCTRGEGGFTVMWYDVGAGTLV 120  
DB 61 PDSVKGRTISRDNAAKNTLYIQMSLSRSEPTAMYYCARRDSMTT---DYGQGITLV 117  
QY 121 SA 122  
DB 118 SS 119  
RESULT 11  
AAU72801 standard; Protein; 464 AA.  
ID AAU72801;  
XX  
AC AAU72801;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DB TRA-8 heavy chain.  
XX  
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;  
KW TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;  
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;  
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;  
KW myaethenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW

KM glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.  
XX Mus musculus.  
XX  
XX NO200183560-A1.  
PN  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001MO-US14151.  
XX  
PR 02-MAY-2000; 2000US-201344P.  
XX  
PA (UABR-) UAB RES FOUND.  
XX  
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;  
XX  
DR WPI; 2002-049338/06.  
DR N-PSDB; AAS97062.  
XX  
PT Novel antibody specific for tumour necrosis factor-related  
XX apoptosis-inducing ligand, useful for inhibiting cell proliferation in  
XX cancer -  
PS Claim 26; Page 198-199; 229pp; English.  
XX  
XX The invention describes a novel antibody which recognises a tumour  
XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
XX DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
XX activity to a cell expressing DR5 in vivo. It is also useful for  
XX preparing a therapeutic for selective apoptosis of abnormal or  
XX dysregulated cells, and for inhibiting cell proliferation in a cell,  
XX preferably a human breast, ovary, colon, haematopoietic, prostate,  
XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may  
XX also be administered e.g. paclitaxel, taxol or cycloheximide. The  
XX antibody is used to treat an autoimmune disease, systemic lupus  
XX erythematosus, Hashimoto's disease, rheumatoid arthritis,  
XX graft-versus-host disease, Sjogren's syndrome, Chron's disease,  
XX pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,  
XX autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple  
XX sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,  
XX allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
XX glomerular nephritis, hypoplastic anaemia, rejection after organ  
XX transplantation, and numerous malignancies of lung, prostate, liver,  
XX ovary, lymphatic or breast tissue. Peptides used to design primers for  
XX isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and  
XX AAU72802), TRA-8 are shown in AAU72799 and AAU72800.  
SQ Sequence 464 AA;  
Query Match 80.7%; Score 519.5; DB 23; Length 464;  
Best Local Similarity 83.6%; Pred. No. 3; Se-42; Mismatches 15; Indels 3; Gaps 1;  
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Db 1 EVQLQESGGGLVPRGSLKSCAAGFTFSYTMVWROTPKRLKRWATISSGSSSTYY 60  
20 EFWLVESGGGLVPRGSLKSCAAGFTFSYTMVWROTPKRLKRWATISSGSSSTYY 79  
QY 61 PDSVKGKFTISRDNKNTLYLQMSLSRSEDPTAMYYCTRBGGGFTVNMVYFDVWGAGTLVTV 120  
Db 80 PDSVKGKFTISRDNKNTLYLQMSLSRSEDPTAMYYCTRBGGGFTVNMVYFDVWGAGTLVTV 136  
QY 121 SA 122  
Db 137 SS 138  
RESULT 12  
AAW57576  
ID AAW57576 standard; protein; 118 AA.  
XX  
AC AAW57576;  
XX  
DT 03-SEP-1998 (first entry)

XX  
DB Chimeric H chain SEQ ID NO:46 for an antibody against hPTRP.  
XX  
XX Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;  
XX L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CR;  
XX hypophosphataemia; pathogen; vitamin D resistance; V region; C region;  
XX humanised.  
XX  
XX Synthetic.  
XX OS Chimeric - Mus sp.  
XX OS Chimeric - Homo sapiens.  
XX  
XX WO9813388-A1.  
XX  
XX 02-APR-1998.  
XX  
XX 24-SEP-1997; 97WO-JP03382.  
XX  
XX 24-JUL-1997; 97JP-0214168.  
XX PR 26-SEP-1996; 96JP-0255196.  
XX  
XX (CHUS) CHUGAI SEIYAKU KK.  
XX  
XX Sato K, Wakahara Y, Yabuta N;  
XX  
XX WPI; 1998-230640/20.  
XX  
XX New chimeric antibodies against human parathormone related  
XX peptide(s) - useful for e.g. treatment of hypercalcaemia and other  
XX disorders caused by malignant neoplasm(s)  
XX  
XX Claim 5; Page 111-112; 182pp; Japanese.  
XX  
XX New antibodies have been developed which are specific for human  
XX parathormone related peptides (hPTRP). The antibodies comprise chimeric  
XX L and/or H chains, where the C region is of human and L region of mouse  
XX origin. The present sequence represents a specifically claimed region of  
XX an antibody of the invention. Host cells, transformed with vectors  
XX containing DNA encoding antibodies of the invention, can be used to  
XX produce the antibodies. The antibodies may be used to treat  
XX hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
XX pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
XX breast, kidney, bladder, womb or prostate or malignant lymphoma. They  
XX may also be used for treatment of hypophosphataemia such as that due to  
XX pathogens or to vitamin D resistance.  
SQ Sequence 118 AA;  
Query Match 80.6%; Score 519; DB 19; Length 118;  
Best Local Similarity 83.6%; Pred. No. 7; Se-43; Mismatches 11; Indels 4; Gaps 1;  
Matches 102; Conservative 5;  
Db 1 EVQLQESGGGLVPRGSLKSCAAGFTFSYTMVWROTPKRLKRWATISSGSSSTYY 60  
1 EFWLVESGGGLVPRGSLKSCAAGFTFSYTMVWROTPKRLKRWATISSGSSSTYY 60  
QY 61 PDSVKGKFTISRDNKNTLYLQMSLSRSEDPTAMYYCTRBGGGFTVNMVYFDVWGAGTLVTV 120  
Db 61 PDSVKGKFTISRDNKNTLYLQMSLSRSEDPTAMFYCARQ---TMTYFAVWGAGTLVTV 116  
QY 121 SA 122  
Db 117 SA 118  
RESULT 13  
AAW89627  
ID AAW89627 standard; Protein; 118 AA.  
XX  
AC AAW89627;  
XX  
DT 14-APR-1999 (first entry)

DE Mouse humanised antibody #23-57-137-1 heavy chain mature protein.  
 XX  
 XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;  
 KM inhibitor; humanised.  
 XX  
 XX Mus sp.  
 OS Synthetic.  
 XX  
 XX WO9851329-A1.  
 PN  
 XX  
 PD 19-NOV-1998.  
 XX  
 XX 13-MAY-1998; 98WO-JP02116.  
 PF  
 XX 18-JUL-1997; 97JP-0194445.  
 PR 15-MAY-1997; 97JP-0125505.  
 XX  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX  
 PI Ishii K, Sato K, Tsunenari T;  
 DR WPI; 1999-070101/06.  
 XX  
 XX Inhibitors of binding of parathyroid hormone related peptide to its  
 PT receptor - useful for, e.g. treatment of cachexia arising from  
 PT cancer or other diseases  
 XX  
 PS Example 2; Page 72-73; 125pp; Japanese.  
 XX  
 XX The present invention describes compositions for the treatment of  
 CC cachexia containing a substance which inhibits the binding of a  
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an  
 CC active component. This substance may be an antagonist to the receptor,  
 CC or an antibody (preferably monoclonal) or antibody fragment.  
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.  
 CC The present invention also describes a humanised antibody prepared  
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for  
 CC the treatment of cachexia arising in connection with diseases such as  
 CC cancer, thereby improving the quality of life of the patient. The  
 CC present sequence represents mouse humanised antibody heavy chain from  
 CC #23-57-137-1 from the present invention.  
 CC  
 XX  
 SQ Sequence 118 AA;  
 Query Match 80.6%; Score 519; DB 20; Length 118;  
 Best Local Similarity 83.6%; Pred. No. 7.9e-43;  
 Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;  
 QY 1 EVQLQESGGGLVPRGSGIKLSCAASGFTFSYTMWVQTPERKLEWVAITSSGGSSTYY 60  
 DB 1 EVQLVESGGDLVPRGSGIKLSCAASGFTFSYGMWIRQTDRKLEWVAITSSGGSSTYY 60  
 QY 61 PDSTVKGRTISRDNAAKNTLYLQMSLSRSEDTANYYCTREGGSGFTVMYFDVWAGTLVTV 120  
 DB 61 PDSTVKGRTISRDNAAKNTLYLQMSLSRSEDTANYYCTREGGSGFTVMYFDVWAGTLVTV 116  
 QY 121 SA 122  
 DB 117 SA 118  
 RESULT 14  
 AA77502  
 ID AA77502 standard; Protein; 118 AA.  
 XX  
 XX AA77502;  
 AC  
 XX 26-APR-2000 (first entry)  
 DT  
 XX Peptide seq ID No: 46.  
 DE  
 XX Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.  
 KM  
 XX

OS Mus musculue.  
 XX  
 XX WO200000219-A1.  
 PN  
 XX  
 XX 06-JAN-2000.  
 PD  
 XX  
 XX 25-JUN-1999; 99WO-JP03433.  
 PF  
 XX 26-JUN-1998; 98JP-0180143.  
 PR  
 XX  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX  
 PI Sato K, Tsunenari T;  
 DR WPI; 2000-117115/10.  
 XX  
 XX Treatment of hypercalcemic crisis with a substance inhibiting binding  
 PT of parathyroid hormone related peptide to its receptor -  
 PT  
 XX  
 PS Example 2; Page 87-88; 120pp; Japanese.  
 XX  
 XX The invention relates to a method of treatment of hypercalcemic crisis.  
 CC A composition for the treatment of hypercalcemic crisis contains as  
 CC active component a substance which inhibits the binding of parathyroid  
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used  
 CC for the treatment of hypercalcemic crisis, such as that associated with  
 CC a malignant tumour.  
 CC  
 XX  
 SQ Sequence 118 AA;  
 Query Match 80.6%; Score 519; DB 21; Length 118;  
 Best Local Similarity 83.6%; Pred. No. 7.9e-43;  
 Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;  
 QY 1 EVQLQESGGGLVPRGSGIKLSCAASGFTFSYTMWVQTPERKLEWVAITSSGGSSTYY 60  
 DB 1 EVQLVESGGDLVPRGSGIKLSCAASGFTFSYGMWIRQTDRKLEWVAITSSGGSSTYY 60  
 QY 61 PDSTVKGRTISRDNAAKNTLYLQMSLSRSEDTANYYCTREGGSGFTVMYFDVWAGTLVTV 120  
 DB 61 PDSTVKGRTISRDNAAKNTLYLQMSLSRSEDTANYYCTREGGSGFTVMYFDVWAGTLVTV 116  
 QY 121 SA 122  
 DB 117 SA 118  
 RESULT 15  
 AA63382  
 ID AA63382 standard; Protein; 118 AA.  
 XX  
 XX AA63382;  
 AC  
 XX 15-OCT-2001 (first entry)  
 DT  
 XX Amino acid sequence of a murine polypeptide.  
 DE  
 XX Parathyroid hormone-associated peptide; PTHrP; dental disease.  
 KM  
 XX Mus musculue.  
 OS  
 XX WO200154725-A1.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 14-DEC-2000; 2000WO-JP08875.  
 PF  
 XX 25-JAN-2000; 2000JP-0083034.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Kato A, Suzuki M, Sugimoto T;  
 PI

DR WPI, 2001-465459/50.  
XX Parathyroid hormone-associated peptide binding inhibitors useful for  
PT treating dental disease -  
XX  
XX  
PS Disclosure, Page 102-103, 140pp, Japanese.  
XX  
XX The specification describes a treatment for dental diseases. The  
CC treatment comprises a substance that inhibits binding between  
CC parathyroid hormone-associated peptide and its receptor. The  
CC present sequence represents a murine protein, which is used in the  
CC course of the invention.  
XX

SQ Sequence 118 AA;

Query Match 80.6%; Score 519; DB 22; Length 118;

Best Local Similarity 83.6%; Pred. No. 7.9e-43;

Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVQLVDSGGGLVYPGGSLKLSCAAGFTFSSYTMWVWROTPKRLKLVATISSGGSSTYY 60

Db 1 EVQLVDSGGDLVYPGGSLKLSCAAGFTFSSYGMWVIRQTPDKRLKLVATISSGGSSTYY 60

QY 61 PDSVKGRFTISRDAKNTLYLQMSSLRSDPTAMVYCTPRGSGFTVMVFPDVWGAGTLYTV 120

Db 61 PDSVKGRFTISRDAKNTLYLQMSSLRSDPTAMVYCTPRGSGFTVMVFPDVWGAGTLYTV 116

QY 121 SA 122

Db 117 SA 118

Search completed: November 7, 2003, 07:27:02  
Job time : 52.6115 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 107.015 Seconds  
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195,799 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_1\_122

Perfect score: 644  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUB\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529.5	82.2	123	US-09-144-886-60	Sequence 60, Appl
2	527.5	81.9	140	US-10-006-773-4	Sequence 4, Appl
3	519.5	80.7	119	US-10-281-479A-61	Sequence 61, Appl
4	519.5	80.7	119	US-10-275-132A-61	Sequence 61, Appl
5	519.5	80.7	119	US-10-286-132A-61	Sequence 61, Appl
6	519.5	80.7	119	US-10-281-479A-61	Sequence 61, Appl
7	519.5	80.7	119	US-10-286-132A-61	Sequence 61, Appl
8	519.5	80.7	119	US-10-286-132A-61	Sequence 61, Appl
9	519.5	80.7	119	US-10-286-132A-61	Sequence 61, Appl
10	519.5	80.6	118	US-10-337-981-46	Sequence 46, Appl
11	519.5	80.6	118	US-10-337-981-46	Sequence 46, Appl
12	519.5	80.6	118	US-10-337-981-46	Sequence 46, Appl
13	519.5	80.6	118	US-10-337-981-46	Sequence 46, Appl
14	519.5	80.6	118	US-10-337-981-46	Sequence 46, Appl
15	517.5	80.4	144	US-09-881-823-12	Sequence 12, Appl

16	517.5	80.4	155	US-10-077-624-7	Sequence 7, Appl
17	517.5	80.4	155	US-10-077-624-7	Sequence 7, Appl
18	515.5	80.0	140	US-09-286-240-4	Sequence 4, Appl
19	514.5	79.9	123	US-09-144-886-61	Sequence 61, Appl
20	513.5	79.7	119	US-10-281-479A-60	Sequence 60, Appl
21	513.5	79.7	119	US-10-275-180A-60	Sequence 60, Appl
22	513.5	79.7	119	US-10-286-132A-60	Sequence 60, Appl
23	510	79.2	124	US-09-518-737-2	Sequence 2, Appl
24	504	78.3	116	US-10-169-351-37	Sequence 43, Appl
25	502	78.0	116	US-10-169-351-37	Sequence 43, Appl
26	500	77.6	118	US-09-144-886-63	Sequence 63, Appl
27	496.5	77.1	119	US-10-281-479A-56	Sequence 56, Appl
28	496.5	77.1	119	US-10-275-180A-56	Sequence 56, Appl
29	496.5	77.1	119	US-10-286-132A-56	Sequence 56, Appl
30	496	77.0	118	US-09-144-886-62	Sequence 62, Appl
31	495	76.9	116	US-10-169-351-45	Sequence 45, Appl
32	494.5	76.8	117	US-10-078-757B-56	Sequence 56, Appl
33	494.5	76.8	119	US-10-281-479A-59	Sequence 59, Appl
34	494.5	76.8	119	US-10-275-180A-59	Sequence 59, Appl
35	494.5	76.8	119	US-10-286-132A-59	Sequence 59, Appl
36	493	76.6	116	US-10-169-351-39	Sequence 39, Appl
37	493	76.6	116	US-10-169-351-47	Sequence 47, Appl
38	492	76.4	116	US-10-169-351-35	Sequence 35, Appl
39	491.5	76.3	119	US-10-281-479A-31	Sequence 31, Appl
40	491.5	76.3	119	US-10-275-180A-31	Sequence 31, Appl
41	491.5	76.3	119	US-10-286-132A-31	Sequence 31, Appl
42	490	76.1	125	US-09-917-410-4	Sequence 4, Appl
43	489.5	76.0	125	US-10-169-351-31	Sequence 31, Appl
44	489.5	76.0	125	US-10-169-351-102	Sequence 102, Appl
45	489.5	76.0	252	US-10-169-351-49	Sequence 49, Appl

#### ALIGNMENTS

RESULT 1  
US-09-144-886-60  
; Sequence 60, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-60

Query Match	82.2%	Score 529.5	DB 10;	Length 123;
Best local Similarity	80.5%	Pred. No. 4,66-42;		
Matches	99;	Conservative	10;	Mismatches 13;
				Indels 1;
				Gaps 1;
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QY	61	PDVSGRFTISRDNAKNTLYIQMSSLRSEDTMYTCRGGFTVNNYFDWGAGITVT	119	
DB	61	PDVSGRFTISRDNAKNTLYIQMSSLRSEDTMYTCRGGFTVNNYFDWGAGITVT	120	
QY	120	VSA 122		
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RESULT 2
US-10-006-773-4
; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti-
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

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Best Local Similarity 82.4%; Pred. No. 8,1e-42;
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QY      1 EVOLQESGGGLVYKPGGSLKLSCAASGFTSSYTMWVROTPEKRLKLEWVATISSGGSSTYY 60
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QY      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREG--GGFTVWVYFDVWGAGTL 117
      80 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREG--GGFTVWVYFDVWGAGTL 135
DB      118 VTYSA 122
      136 VTYSS 140

RESULT 3
US-10-281-479A-61
; Sequence 61, Application US/10281479A
; Publication No. US2003013392A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: /No. US2003013392A1e = Sync
US-10-281-479A-61

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DB      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVWVYFDVWGAGTLV 120
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QY      121 SA 122
      118 SS 119

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; Sequence 61, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPT
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030190687A1e =
US-10-275-180A-61

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Best Local Similarity 83.6%; Pred. No. 3.8e-41;
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

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      1 EVAVVESGGGFLYKPGGSLKLSCAAGFTSRVMSVWROTPEKRLKLEWATISSGGSSTYY 60
DB      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVWVYFDVWGAGTLV 120
      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVWVYFDVWGAGTLV 117
QY      121 SA 122
      118 SS 119

RESULT 5
US-10-286-132A-61
; Sequence 61, Application US/10286132A
; Publication No. US20030196637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.

```

```

; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; FILE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286.132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 119
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-61

Query Match
Best Local Similarity 80.7%; Score 519.5; DB 12; Length 119;
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 60
DB 1 EVMALVESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 60
QY 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120
DB 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 117

QY 121 SA 122
DB 118 SS 119

RESULT 6
US-10-281-479A-23
; Sequence 23, Application US/10281479A
; Publication No. US2003013932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US2003013932A1e = Synthe
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US-10-281-479A-23

Query Match
Best Local Similarity 80.7%; Score 519.5; DB 12; Length 462;
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 60
DB 20 EVMALVESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 79
QY 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120
DB 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 136

QY 121 SA 122
DB 137 SS 138

RESULT 7
US-10-286-132A-23
; Sequence 23, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lobuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-23

Query Match
Best Local Similarity 80.7%; Score 519.5; DB 12; Length 462;
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 60
DB 20 EVMALVESGGGLYKPGGSLKLSCAASGFTFSSTYSWVRQTPERKLEWVAITISGGSSITY 79
QY 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120
DB 80 PDSVKGRTTISRDNKNTLYLQMSLSRSEDPTAMYYCTREGGFTVNNYFDVWGAGTLVTV 136

QY 121 SA 122
DB 137 SS 138

RESULT 8
US-10-275-180A-23
; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
```

APPLICANT: Zhou, Tong  
APPLICANT: Ichikawa, Kimihisa  
APPLICANT: Kimbely, Robert P.  
APPLICANT: Koopman, William J.  
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS  
FILE REFERENCE: 21085.002905  
CURRENT APPLICATION NUMBER: US/10/275,180A  
CURRENT FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 23  
LENGTH: 464  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: /No. US20030190687A1e =  
US-10-275-180A-23

Query Match 80.7%; Score 519.5; DB 12; Length 464;  
Best Local Similarity 83.6%; Pred. No. 1,6e-40;  
Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLQSSGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 60  
DB 20 EVLVESGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 79  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120  
DB 80 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYYCARQDMMIT---DYGQGTTLTV 136  
QY 121 SA 122  
DB 137 SS 138

RESULT 9  
US-09-423-800-46  
Sequence 46, Application US/09423800  
Patent No. US20020165363A1  
GENERAL INFORMATION:  
APPLICANT: SATO, KOH  
APPLICANT: TSUNENARI, TOSHIAKI  
APPLICANT: ISHII, KIMIE  
TITLE OF INVENTION: CACHEXIA REMEDY  
FILE REFERENCE: 04853-0036  
CURRENT APPLICATION NUMBER: US/09/423,800  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: PCT/JP98/02116  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: JP 125505/1997  
PRIOR FILING DATE: 1997-05-15  
PRIOR APPLICATION NUMBER: JP 194445/1997  
PRIOR FILING DATE: 1997-07-18  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 46  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-423-800-46

Query Match 80.6%; Score 519; DB 10; Length 118;  
Best Local Similarity 83.6%; Pred. No. 4.1e-41;  
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLQSSGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 60  
DB 1 EVLVESGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 60  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120

DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMFYCARQ---TTMTYFAVWGAGTLVTV 116  
QY 121 SA 122  
DB 117 SA 118

RESULT 10  
US-10-337-981-46  
Sequence 46, Application US/10337981  
Publication No. US20030138424A1  
GENERAL INFORMATION:  
APPLICANT: SATO, KOH  
APPLICANT: TSUNENARI, TOSHIAKI  
APPLICANT: ISHII, KIMIE  
TITLE OF INVENTION: CACHEXIA REMEDY  
FILE REFERENCE: 04853-0036  
CURRENT APPLICATION NUMBER: US/10/337,981  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: PCT/JP98/02116  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: JP 125505/1997  
PRIOR FILING DATE: 1997-05-15  
PRIOR APPLICATION NUMBER: JP 194445/1997  
PRIOR FILING DATE: 1997-07-18  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 46  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-337-981-46

Query Match 80.6%; Score 519; DB 12; Length 118;  
Best Local Similarity 83.6%; Pred. No. 4.1e-41;  
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLQSSGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 60  
DB 1 EVLVESGGGLVYKPGGSLKLSGASGFTSSYTMWVROTPEKRLWVATISSGGSSTYY 60  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYYCTREGGFTVNNYFDVWGAGTLVTV 120  
DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMFYCARQ---TTMTYFAVWGAGTLVTV 116  
QY 121 SA 122  
DB 117 SA 118

RESULT 11  
US-10-182-018-46  
Sequence 46, Application US/10182018  
Publication No. US20030049211A1  
GENERAL INFORMATION:  
APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES  
FILE REFERENCE: PH-1092-PCT  
CURRENT APPLICATION NUMBER: US/10/182,018  
CURRENT FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: JP 2000-83034  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-182-018-46

Query Match 80.6%; Score 519; DB 15; Length 118;  
Best Local Similarity 83.6%; Pred. No. 4.1e-41;  
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

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QY 1 EVOLDSGGGLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 1 EVOLVESGGDLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
QY 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMYYCTRBGGGFTVNNYFDVWGAGTLVTV 120
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMFYCARQ-----TTMTYFAYWGQGLTVTV 116
QY 121 SA 122
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 117 SA 118

RESULT 12
US-10-169-003-46
; Sequence 46, Application US/10169003
; Publication No. US20030124119A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation for
; FILE REFERENCE: PH-1093-PCT
; CURRENT APPLICATION NUMBER: US/10/169,003
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 11-375203
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-169-003-46

Query Match 80.6%; Score 519; DB 15; Length 118;
Best Local Similarity 83.6%; Pred. No. 4,1e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLDSGGGLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
; TYPE: PRT
; ORGANISM: Mus musculus
Db 1 EVOLVESGGDLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
QY 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMYYCTRBGGGFTVNNYFDVWGAGTLVTV 120
; TYPE: PRT
; ORGANISM: Mus musculus
Db 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMFYCARQ-----TTMTYFAYWGQGLTVTV 116
QY 121 SA 122
; TYPE: PRT
; ORGANISM: Mus musculus
Db 117 SA 118

RESULT 13
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 14445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 76
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; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76

Query Match 80.6%; Score 519; DB 10; Length 137;
Best Local Similarity 83.6%; Pred. No. 4,9e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLDSGGGLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 20 EVOLVESGGDLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 79
QY 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMYYCTRBGGGFTVNNYFDVWGAGTLVTV 120
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 80 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMFYCARQ-----TTMTYFAYWGQGLTVTV 135
QY 121 SA 122
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 136 SA 137

RESULT 14
US-10-337-981-76
; Sequence 76, Application US/10337981
; Publication No. US20030138424A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/10/337,981
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-76

Query Match 80.6%; Score 519; DB 12; Length 137;
Best Local Similarity 83.6%; Pred. No. 4,9e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

QY 1 EVOLDSGGGLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 60
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 20 EVOLVESGGDLVYKPGGSLKLSGASGFTFSSTYTWKVRQTPKRLKLEWVATISSGGSSTYY 79
QY 61 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMYYCTRBGGGFTVNNYFDVWGAGTLVTV 120
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 80 PDSVKGRTISRDNKNTLYLQWSSLRSSEDTAMFYCARQ-----TTMTYFAYWGQGLTVTV 135
QY 121 SA 122
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 136 SA 137

RESULT 15
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
```

```

; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/681,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Murine
; US-09-881-823-12

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Query Match      80.4%; Score 517.5; DB 9; Length 144;
Best Local Similarity 80.5%; Pred. No. 7.1e-41;
Matches 99; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY      1 EVQLVESGGGLVPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLKLEWATISGGSSITY 60
      20 DVKLVESSGGGLVMPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLKLEWATISGGSSITY 79
QY      61 PDSEVKGRTISRDNKNTLYLQWSSLRSDFTAMYCTREGGFTVWNY-FDYWGAGTLVT 119
      80 PDSEVKGRTISRDNKNTLYLQWSSLRSDFTAMYCTREGGFTVWNY-FDYWGAGTLVT 139
QY      120 VSA 122
      140 VSS 142
Db

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Search completed: November 7, 2003, 08:16:53  
 Job time : 107.015 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 17.9172 Seconds  
(without alignments)  
286.098 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_1\_122

Perfect score: 644

Sequence: 1 EVQIQESGGGLVXPGSLK.....FTVMYDPVWAGATLVYSA 122

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents, AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	511.5	79.4	247 5	PCT-US94-07659-2 Sequence 2, Appl
2	505.5	78.5	119 4	US-08-875-674A-1 Sequence 1, Appl
3	502	78.0	135 3	US-08-579-378A-16 Sequence 16, Appl
4	501.5	77.9	119 4	US-08-875-674A-3 Sequence 3, Appl
5	500.5	77.7	119 2	US-08-475-000-16 Sequence 16, Appl
6	500.5	77.7	119 2	US-08-483-199-16 Sequence 16, Appl
7	500.5	77.7	119 2	US-08-484-508-16 Sequence 16, Appl
8	494	76.7	118 1	US-08-326-362-2 Sequence 2, Appl
9	490	76.1	135 3	US-08-579-378A-20 Sequence 20, Appl
10	490	76.0	443 5	PCT-US96-13152-4 Sequence 4, Appl
11	489.5	76.0	239 2	US-08-553-497A-18 Sequence 18, Appl
12	488	75.8	123 1	US-08-356-272-3 Sequence 3, Appl
13	486	75.5	120 2	US-07-934-373C-4 Sequence 4, Appl
14	486	75.5	120 3	US-08-437-642B-4 Sequence 4, Appl
15	486	75.5	120 3	US-08-146-206C-4 Sequence 4, Appl
16	485.5	75.4	121 1	US-08-339-582-2 Sequence 2, Appl
17	485.5	75.4	123 4	US-09-344-587-13 Sequence 13, Appl
18	485	75.3	109 2	US-08-793-490-6 Sequence 6, Appl
19	483.5	75.1	117 3	US-08-752-633A-3 Sequence 3, Appl
20	483.5	75.1	136 4	US-08-976-183A-31 Sequence 31, Appl
21	483.5	75.1	136 4	US-08-976-183A-32 Sequence 32, Appl
22	483.5	75.1	136 4	US-08-976-183A-33 Sequence 33, Appl
23	483.5	75.0	136 4	US-08-976-183A-34 Sequence 34, Appl
24	483.5	75.0	116 2	US-08-888-366-10 Sequence 10, Appl
25	482.5	74.9	125 1	US-08-331-398A-65 Sequence 65, Appl
26	482.5	74.9	125 1	US-08-331-397B-65 Sequence 65, Appl
27	482.5	74.9	125 2	US-08-759-804A-64 Sequence 64, Appl

28	481.5	74.8	113 1	US-07-789-344A-10 Sequence 10, Appl
29	481	74.7	122 2	US-07-934-373C-21 Sequence 21, Appl
30	481	74.7	122 3	US-08-437-642B-21 Sequence 21, Appl
31	481	74.7	122 4	US-08-146-206C-21 Sequence 21, Appl
32	481	74.7	122 5	PCT-US93-07832-21 Sequence 21, Appl
33	479.5	74.5	117 4	US-09-339-922A-6 Sequence 6, Appl
34	479.5	74.5	237 2	US-08-224-591-16 Sequence 16, Appl
35	479.5	74.5	237 2	US-08-926-789-16 Sequence 16, Appl
36	479.5	74.5	241 2	US-08-224-591-18 Sequence 18, Appl
37	479.5	74.5	241 2	US-08-926-789-18 Sequence 18, Appl
38	479.5	74.5	245 4	US-09-069-821-5 Sequence 5, Appl
39	479.5	74.5	265 4	US-09-420-592A-5 Sequence 5, Appl
40	478.5	74.3	136 1	US-08-253-877C-57 Sequence 57, Appl
41	478.5	74.3	136 2	US-08-452-164A-57 Sequence 57, Appl
42	478.5	74.3	239 2	US-07-956-399-4 Sequence 4, Appl
43	478	74.2	116 2	US-08-888-366-12 Sequence 12, Appl
44	477	74.1	140 3	US-08-983-607-32 Sequence 32, Appl
45	476	73.9	120 4	US-09-025-769B-38 Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
PCT-US94-07659-2  
Sequence 2, Application PC/TUS9407659  
GENERAL INFORMATION:  
APPLICANT: Young, Peter  
APPLICANT: Gross, Mitchell  
APPLICANT: Jonak, Zdenka L.  
APPLICANT: Theisen, Timothy  
APPLICANT: Hurlie, Mark  
APPLICANT: Jackson, Jeffrey R.  
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
TITLE OF INVENTION: Disorders in Man  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SmithKline Beecham Corporation - Corp.  
ADDRESSER: Intellectual Property  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07659-2  
Query Match 79.4%; Score 511.5; DB 5; Length 247;

Best Local Similarity 82.0%; Pred. No. 8e-47;  
Matches 100; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

QY 1 EVOLQSGGGLVPRGSGSLKSCAAGFTFSYTMWVROTPKRLKLEWVATISSGGSSTYY 60  
DB 20 EVHLVSSGGGLVPRGSGSLKSCAAGFTFSYTMWVROTPKRLKLEWVATISSGGSSTYY 79  
QY 61 PDSVKGFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGGFTVNWYFDVWAGATLVTV 120  
DB 80 PDSVKGFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGGFTVNWYFDVWAGATLVTV 136  
QY 121 SA 122  
DB 137 SS 138

## RESULT 2

US-08-875-674A-1  
Sequence 1, Application US/08875674A

Patent No. 6572857  
GENERAL INFORMATION:

APPLICANT: MONTERO CASIMIRO, J. E.  
APPLICANT: LOMBARDO VALADARES, J.

APPLICANT: P. REZ RODR GUEZ, R.  
APPLICANT: SIERRA BU ZQUEZ, P.

APPLICANT: TOMO BRAVO, B. R.  
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lackenhach Siegel Marzullo Aronson & Greenspan, P. C.

STREET: One Chase Road  
CITY: Scarsdale

STATE: New York  
COUNTRY: U.S.A.

ZIP: 10583

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).  
OPERATING SYSTEM: Windows 95.

SOFTWARE: Word Perfect 5.0 for Windows 95.  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,674A  
FILING DATE: 17-July-1997

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00004  
FILING DATE: 18-NOV-1996

ATTORNEY/AGENT INFORMATION:  
NAME: HENRY A. MARZULLO, JR.

REGISTRATION NUMBER: 20,910  
REFERENCE/DOCKET NUMBER: P-12

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 723-4300

TELEFAX: (914) 723-4301  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 Amino acid residues.

TYPE: Amino acid.  
STRANDEDNESS: Unknown.

TOPOLOGY: Unknown.  
MOLECULE TYPE: Protein

HYPOTHETICAL: NO  
ANTI-SENSE: NO

FRAGMENT TYPE: -N Terminal fragment.  
ORIGINAL SOURCE:

ORGANISM: Mice Balb/C  
INDIVIDUAL ISOLATE: for CIA

TISSUE TYPE: Murine hybridoma  
IMMEDIATE SOURCE:

CLONE: Sub-clone for CIA  
FEATURE:

IDENTIFICATION METHOD: Experimental.  
OTHER INFORMATION: Sequence corresponding to the variable region

Patent No. 6572857  
OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing h  
OTHER INFORMATION: designated as sub-clone for CIA.  
US-08-875-674A-1

Query Match 78.5%; Score 505.5; DB 4; Length 119;  
Best Local Similarity 82.0%; Pred. No. 1.4e-46;

Matches 100; Conservative 2; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVOLQSGGGLVPRGSGSLKSCAAGFTFSYTMWVROTPKRLKLEWVATISSGGSSTYY 60  
DB 1 EVHLVSSGGGLVPRGSGSLKSCAAGFTFSYTMWVROTPKRLKLEWVATISSGGSSTYY 60  
QY 61 PDSVKGFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGGFTVNWYFDVWAGATLVTV 120  
DB 61 PDSVKGFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGGFTVNWYFDVWAGATLVTV 117  
QY 121 SA 122  
DB 118 SS 119

## RESULT 3

US-08-579-378A-16  
Sequence 16, Application US/08579378A

Patent No. 6210671  
GENERAL INFORMATION:

APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent'n Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8

FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8

FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Liebeschuetz, Joe O.  
REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-579-378A-16

Query Match	78.0%;	Score 502;	DB 3;	Length 135;
Best Local Similarity	80.3%;	Pred. No. 3.8e-46;		
Matches 98;	Conservative 9;	Mismatches 9;	Indels 6;	Gaps 2

OY 1 EVOLIOEGGGLVPPGGSLKLKSCAASGFRTSSATVMNVOPEKRLEMAWATSIGGSSTYY 60  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 20 EVKLVSEGGLVPFGSLLKACAAAGFTISTYAMSWAQTPERKLEMVAISITSG -styy 78

OY . PDSVGKGFTSRDINAKNTLYLQMSLSRSBDTAMYCTREGGGETVMNFEDVWGALTYV 120  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 79 PDsvkgRfTSrDNAnILYLqMssLRSDtAmYCAdIdo-----yEdImgQtIAtv 133

OY 121 GA 122  
| : |  
Db 134 SS 135

RESULT 4  
US-08-87

; Sequence 3, Application US/08875674A  
; Patent No. 6572857

1 APPLICANT: MONTERO CASIMIRO, J. E.  
 2 APPLICANT: LOMBARDERO VALLADARES, J.  
 3 APPLICANT: P REZ RODR GUEZ, R.  
 4 APPLICANT: SIERRA BL ZQUEZ, P.  
 5 APPLICANT: TORMO BRAVO, B. R.  
 6 TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses  
 7 NUMBER OF SEQUENCES: 4  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSER: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.  
 10 STREET: One Chase Road  
 11 City: Scarsdale  
 12 STATE: New York  
 13 COUNTRY: U.S.A.

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
; COMPUTER: Compatible PC IBM (80486, 8 M Ram)

```

```

?
?   OPERATING SYSTEM:  Windows 95.
?
?   SOFTWARE:  Word Perfect 5.0 for Win
?
?   CURRENT APPLICATION DATA:
?
?   APPLICATION NUMBER:  US/08/875,674A
?   FILING DATE:  17-July-1997
?
?   C:\PROG\WORDPERF\
?

```

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/000004  
FILING DATE: 18-NOV-1996

NAME: HENRY A. MARZULLO, JR  
REGISTRATION NUMBER: 20,910  
REFERENCE/DOCKET NUMBER: P-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (614) 753-4200

TELEPHONE: (914) 723-4300  
TELEFAX: (914) 723-4301  
INFORMATION FOR SEO ID NO: 3

```

;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 119 Amino acid residues
;

```

TYPE: Amino acid.  
STRANDEDNESS: Unknown

```

;      TOPOLOGY:  Unknown.
;      MOLECULE TYPE:  Protein
;      HYDROPHOBICITY:  0.00

```

```

1  APOPHYLICAL: NO
2  ANTI-SENSE: NO
3  FRAGMENT TYPE: -N Terminal fragment

```

ORIGINAL SOURCE:  
TISSUE TYPE: Animal cells.  
CELL TYPE: MCO # 3D 340 F CTV

```

1  CDD LINE:  NSC - SR 2/0 - CHO
2
3  IMMEDIATE SOURCE:
4
5  CLONE:  Sub-clone for CIA
6
7  FEATURE:
8
9  IDENTIFICATION METHOD:  By similarity with known sequence

```

OTHER INFORMATION:	Sequence corresponding to the humanized
OTHER INFORMATION:	variant of sub-clone for C1A recognizing human CD6, particu-
OTHER INFORMATION:	to the variable region of its heavy chain.
US-08-875-674A-3	

Query Match	77.9%;	Score 501.5;	DB 4;	Length 119;
Best Local Similarity	82.0%;	Pred. No. 3.7e-46;		
Matches 100; Conservative	1;	Mismatches 18;	Indels 3;	Gaps 1.

**QY**

**db**

**1 EVQLAESGGGIVKPGSKLKSCAASGYTFSSITMSWVQTPEKKLEWATISSGSSTYY 60**

**1 EVDLVESGGGIHKPGSLKLSCAASGEKFRRYAMSWVRQAPEGKLEWATISSGSIIYY 60**

```
QY      61 PDSVKGKGFTRSDNAKNTLYLQSSLSRSEPTAMTYCTREGGFTTWNYFDWVGAGLTIVT 120
        |||||
db       61 PDSVKGKGFTRSDNWKNTLYLQSSLSRSEPTAMYCARROYDLD--YFDSWGQGTLIVT 117
```

Qy	121	SA	122
		:	
Db	118	SS	119

RESULT 5  
US-08-47

; Sequence 16, Application US/08475000  
; Patent No. 5811267

```

1  GENERAL INFORMATION:
2
3  APPLICANT: RING, DAVID B.
4
5  TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
6
7  TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
8
9  NUMBER OF SEQUENCES: 18
10
11  COMPLETION DATE: 19990601

```

1 CORRESPONDENCE ADDRESS:  
2 ADDRESSEE: CHIRON CORPORATION  
3 STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
4 CITY: Emeryville  
5 STATE: CA  
6 COUNTRY: USA

ZIP: 94662-8097  
COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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```

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: PatentIn Release
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/475,000  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:

NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914

REFERENCE/DOCKET NUMBER: 0  
TELECOMMUNICATION INFORMATION  
TELEPHONE: (510) 601-2585

TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid

```

Query Match	77.7%;	Score 500.5;	DB 2;	Length 119;
Best Local Similarity	79.5%;	Pred. No. 4.7e-46;		
Matches 97;	Conservative 10;	Mismatches 12;	Indels 3;	Gaps 1;

[illegible]

Db 61 PDSVKGRTFVSBDNAMSLYLQMSLSRSEDPTALYYCARYGAG---DAMFAWGGGTLVTV 117  
QY 121 SA 122  
118 SA 119

RESULT 6  
US-08-483-199-16  
Sequence 16, Application US/08483199  
Patent No. 5849877  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,199  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-199-16

Query Match 77.7%; Score 500.5; DB 2; Length 119;  
Best Local Similarity 79.5%; Pred. No. 4.7e-46;  
Matches 97; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVOLQSSGGGLVPRGSGIKLSGASGFTSSYTMWVROTPEKRLKLEWATISSGGSSITY 60  
Db 1 EVVVVSSGGLVPRGSGIKLSGASGFTSSYTMWVROTPEKRLKLEWATISSGGSSITY 60  
QY 61 PDSVKGRTFVSBDNAMSLYLQMSLSRSEDPTALYYCARYGAG---DAMFAWGGGTLVTV 120  
Db 61 PDSVKGRTFVSBDNAMSLYLQMSLSRSEDPTALYYCARYGAG---DAMFAWGGGTLVTV 117  
QY 121 SA 122  
Db 118 SA 119

RESULT 7  
US-08-484-508-16  
Sequence 16, Application US/08484508  
Patent No. 5948647  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,508  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-508-16

Query Match 77.7%; Score 500.5; DB 2; Length 119;  
Best Local Similarity 79.5%; Pred. No. 4.7e-46;  
Matches 97; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVOLQSSGGGLVPRGSGIKLSGASGFTSSYTMWVROTPEKRLKLEWATISSGGSSITY 60  
Db 1 EVVVVSSGGLVPRGSGIKLSGASGFTSSYTMWVROTPEKRLKLEWATISSGGSSITY 60  
QY 61 PDSVKGRTFVSBDNAMSLYLQMSLSRSEDPTALYYCARYGAG---DAMFAWGGGTLVTV 120  
Db 61 PDSVKGRTFVSBDNAMSLYLQMSLSRSEDPTALYYCARYGAG---DAMFAWGGGTLVTV 117  
QY 121 SA 122  
Db 118 SA 119

RESULT 8  
US-08-326-362-2  
Sequence 2, Application US/08326362  
Patent No. 5730981  
GENERAL INFORMATION:  
APPLICANT: Boserlet, Klaus  
APPLICANT: Seeman, Gerhard  
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,  
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/326,362  
FILING DATE: 17-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 08/032,863  
APPLICATION NUMBER: DE P 42 08 795.3  
FILING DATE: 19-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481-1276-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-326-362-2

Query Match 76.7%; Score 494; DB 1; Length 118;  
Best Local Similarity 79.5%; Pred. No. 2,3e-45;  
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 EVOLDSGGGLVPGGSLKLSCAAGFTSSYTMWVROTPKRLKLEWVATISSGGSTYY 60  
DB 1 QVQLQDSGGGLVPGGSLKLSCAASFTSTYAMSIVRQTPAKRLKLEWVATISSGGSTYY 60

QY 61 PDVSKGRFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGFTVMVFDVWGAGTLVTV 120  
DB 61 RDSVKGKFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGFTVMVFDVWGAGTLVTV 116

QY 121 SA 122  
DB 117 SS 118

RESULT 9  
US-08-579-378A-20  
Sequence 20, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co. Van Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8

FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheut, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-20

Query Match 76.1%; Score 490; DB 3; Length 135;  
Best Local Similarity 78.7%; Pred. No. 7,2e-45;  
Matches 96; Conservative 10; Mismatches 10; Indels 6; Gaps 2;

QY 1 EVOLDSGGGLVPGGSLKLSCAAGFTSSYTMWVROTPKRLKLEWVATISSGGSTYY 60  
DB 20 EVQLVESGGGLVPGGSLKLSCAAGFTSTYAMSIVRQTPAKRLKLEWVATISSGGSTYY 78  
QY 61 PDVSKGRFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGFTVMVFDVWGAGTLVTV 120  
DB 79 RDSVKGKFTISRDNKNTLYLQMSLSRSDTAMTYCTREGGFTVMVFDVWGAGTLVTV 133

QY 121 SA 122  
DB 134 SS 135

RESULT 10  
PCT-US96-13152-4  
Sequence 4, Application PC/TUS9613152  
GENERAL INFORMATION:  
APPLICANT: Martin, Ulrich, et al.  
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fa  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
ADDRESS: Acta: Norman D. Hanson  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Computer Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/13152  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/578,953  
FILING DATE: 27-DEC-95  
APPLICATION NUMBER: EP 95 112 895.8  
FILING DATE: 17-AUG-95  
APPLICATION NUMBER: EP 95 114 969.9  
FILING DATE: 19-SEP-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Norman D. Hanson  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 443  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-13152-4

Query Match 76.1%; Score 490; DB 5; Length 443;  
Best Local Similarity 78.7%; Pred. No. 3.3e-44;  
Matches 96; Conservative 10; Mismatches 10; Indels 6; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLKLEWYATISSGGSSTYY 60  
DB 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQAPKGLKLEWYATISSGGSSTYY 59  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSDTAMYYCTREGGFTVMWFDVWGAGTLVTV 120  
DB 60 PDSVKGRTISRDNKNTLYLQMSLSRSDTAMYYCTREGGFTVMWFDVWGAGTLVTV 114  
QY 121 SA 122  
DB 115 SS 116

## RESULT 11

US-08-553-497A-18  
Sequence 18, Application US/08553497A  
Patent No. 5844093

## GENERAL INFORMATION:

APPLICANT: KETTERBOROUGH, C. A.  
APPLICANT: BENDIG, MARY W.  
APPLICANT: ANSELI, KEITH H.  
APPLICANT: GUSOW, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MITJANS, FRANCESCA  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PIULATS, JAUME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553.497A  
FILING DATE: 17-NOV-1995

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33.302  
REFERENCE/DOCKET NUMBER: MERCK 1726

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-18

Query Match 76.0%; Score 489.5; DB 2; Length 239;  
Best Local Similarity 80.5%; Pred. No. 1.7e-44;  
Matches 99; Conservative 7; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLKLEWYATISSGGSSTYY 60  
DB 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYMSWVRQTPKRLKLEWYATISSGGSSTYY 60  
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSDTAMYYCTR-EGGFTVMWFDVWGAGTLVTV 119  
DB 61 PDSVKGRTISRDNKNTLYLQMSLSRSDTAMYYCTR-EGGFTVMWFDVWGAGTLVTV 116  
QY 120 VSA 122  
DB 117 VSS 119

## RESULT 12

US-08-356-272-3  
Sequence 3, Application US/08356272  
Patent No. 5766946

## GENERAL INFORMATION:

APPLICANT: Ciantigila Dr., Maurizio  
TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein P  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent and Trademark Department, Sandoz  
ADDRESS: Corporation  
STREET: 59 Route 10  
CITY: East Hanover  
STATE: N. J.  
COUNTRY: U. S. A.  
ZIP: 07936

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356.272  
FILING DATE: 15-DEC-1994

## CLASSIFICATION: 435

CLASSIFICATION: C12N5/20  
CLASSIFICATION: G01N33/574  
CLASSIFICATION: G01N33/577  
CLASSIFICATION: A61K39/295

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: IT RM92A000457  
FILING DATE: 17-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP93/01533  
FILING DATE: 16-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Battie, Carl W.

REGISTRATION NUMBER: 30.731

REFERENCE/DOCKET NUMBER: 118-8040

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 503-8177  
TELEFAX: (201) 503-8807  
TELEX: 240867

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-272-3

Query Match 75.8%; Score 486; DB 1; Length 123;  
Best Local Similarity 79.2%; Pred. No. 1e-44;  
Matches 99; Conservative 9; Mismatches 11; Indels 6; Gaps 3;

QY 1 EVOLQSSGGGLVYK-PGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 59  
DB 1 QVQLQESGGDLYWDPFGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 60  
QY 60 YPDSVGRFTISRDNAKNTLYLQWSSLRSSEDTAMYYCTR--EGGFTVMTFDWVGAGTL 117  
DB 61 FPDVSGRFTISRDNAKNTLYLQWSSLRSSEDTAMYYCARPAFRGYS--WFAWGGSTY 117  
QY 118 VTVSA 122  
DB 118 VTVSS 122

## RESULT 13

US-07-934-373C-4  
Sequence 4, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-4

Query Match 75.5%; Score 486; DB 2; Length 120;  
Best Local Similarity 77.0%; Pred. No. 1.7e-44;  
Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLQSSGGGLVYK-PGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 60

DB 1 EVOLQSSGGGLVYK-PGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 60  
QY 61 PDSVGRFTISRDNAKNTLYLQWSSLRSSEDTAMYYCTRGGGFTVMTFDWVGAGTLVTV 120  
DB 61 ADSVGRFTISRDSDSKNTLYLQWSSLRSSEDTAMYYCARPAFRGYS--YFDWVGAGTLVTV 118  
QY 121 SA 122  
DB 119 SS 120

## RESULT 14

US-08-437-642B-4  
Sequence 4, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-Aug-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-4

Query Match 75.5%; Score 486; DB 3; Length 120;  
Best Local Similarity 77.0%; Pred. No. 1.7e-44;  
Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLQSSGGGLVYK-PGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 60  
DB 1 EVOLQSSGGGLVYK-PGSLKLSCLASGFTSSYTMWVROTPEKRLKLEWVAITSSGGSSTY 60  
QY 61 PDSVGRFTISRDNAKNTLYLQWSSLRSSEDTAMYYCTRGGGFTVMTFDWVGAGTLVTV 120

Db 61 ADSVKRFTISRDSKNTLYLQMSLRADPAVYICARDGSAVS--YFDWVGSTLVTY 118  
 QY 121 SA 122  
 :  
 Db 119 SS 120

RESULT 15  
 US-08-146-206C-4  
 ; Sequence 4, Application US/08146206C  
 ; Patent No. 6407213  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carter, Paul J.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method for Making Humanized Antibodies  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Winpatin (genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/146,206C  
 ; FILING DATE: 17-NO. 6407213-1993  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/715272  
 ; FILING DATE: 14-JUN-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER: 40,378  
 ; REFERENCE/DOCKET NUMBER: P0709P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1994  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 120 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-08-146-206C-4

Query Match 75.5%; Score 486; DB 4; Length 120;  
 Best Local Similarity 77.0%; Pred. No. 1.7e-44;  
 Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLIKLSCAASGFTFSSTYMSWVRQTPKRLKLEWVAITISGGSTYY 60  
 :  
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSPTDYAMSWVRQAPGKLEWVAVISNGSDTY 60  
 :  
 QY 61 PDSYKGRFTISRDNKNTLYLQMSLRSEDTAMVYCTRSGGAGFTVNTYFPDWAGTLYTV 120  
 :  
 Db 61 ADSVKRFTISRDSKNTLYLQMSLRADPAVYICARDGSAVS--YFDWVGSTLVTY 118  
 :  
 QY 121 SA 122  
 :  
 Db 119 SS 120

Search completed: November 7, 2003, 07:30:10  
 Job time : 17.9172 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 14.5047 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_138\_249

Perfect score: 584  
Sequence: 1 ENVLTPSPASLAVSLGGRAT.....QQSNEDPLTFGGGTRLEIKR 112

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	532	91.1	111	1	IG kappa chain V r
2	517	88.5	107	1	IG kappa chain V r
3	514	88.0	115	2	IG kappa chain V r
4	513	87.8	107	2	IG kappa chain V r
5	511	87.5	131	1	IG kappa chain V r
6	501	85.8	111	2	IG kappa chain V r
7	494	84.6	111	2	IG kappa chain V r
8	490	83.9	132	1	IG kappa chain V r
9	489	83.7	111	1	IG kappa chain V r
10	468	80.1	111	1	IG kappa chain V r
11	467	80.0	111	1	IG kappa chain V r
12	465	79.6	111	1	IG kappa chain V r
13	462	79.1	111	1	IG kappa chain V r
14	460	78.8	112	2	IG kappa chain V r
15	458	78.4	111	1	IG kappa chain V r
16	458	78.4	218	1	IG kappa chain V r
17	457	78.3	111	1	IG kappa chain V r
18	457	78.3	218	1	IG kappa chain V r
19	456	78.1	111	1	IG kappa chain V r
20	456	78.1	111	1	IG kappa chain V r
21	455	77.9	210	2	IG kappa chain V r
22	454	77.7	111	2	IG kappa chain V r
23	451	77.2	112	2	IG kappa chain V r
24	450	77.1	111	1	IG kappa chain V r
25	450	77.1	112	2	IG kappa chain V r
26	450	77.1	112	2	IG kappa chain V r
27	445	76.2	131	2	IG kappa chain V r
28	444	76.0	131	2	IG kappa chain V r
29	441	75.5	96	2	IG light chain V r

30	440.5	75.4	110	1	KVMS10	IG kappa chain V r
31	440	75.3	111	1	KVMS80	IG kappa chain V r
32	439	75.2	111	1	KVMS50	IG kappa chain V r
33	434	74.3	111	2	PL0081	IG kappa chain V r
34	433	74.1	111	2	S09963	IG kappa chain V-J
35	433	74.1	111	2	S09969	IG kappa chain V-J
36	423.5	72.5	95	2	S25177	IG kappa chain V r
37	423	72.4	109	2	PH0093	IG kappa chain V r
38	422	72.3	108	1	KVMS54	IG kappa chain V r
39	421	72.1	111	2	S09966	IG kappa chain V r
40	420	71.9	140	2	PN0446	IG kappa chain V-J
41	414	70.9	91	2	S25462	IG kappa chain pre
42	413.5	70.8	110	2	S24288	IG kappa chain V r
43	412	70.5	111	1	KVMS13	IG kappa chain V r
44	407	69.7	102	2	PH1076	IG light chain V r
45	404	69.2	102	2	PH1079	IG light chain V r

## ALIGNMENTS

## RESULT 1

IG kappa chain V regions (PC3741, T111) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 21-Jan-2000  
C/Accession: A93204; A93822; A01934  
R/Weigert, M.; Gattamatta, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A/Reference number: A93204; PMID:79073152; PMID:103003  
A/Contents: PC3741  
A/Accession: A93204  
A/Molecule type: protein  
A/Residues: 1-111 <NR1>  
R/McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A/Title: Mechanisms of antibody diversity: multiple genes encode structurally related A/Reference number: A93822; PMID:79012520; PMID:99744  
A/Contents: T111  
A/Accession: A93822  
A/Molecule type: protein  
A/Residues: 1-111 <NR1>  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer  
F/16-94/Domain: immunoglobulin homology <IMM>  
F/23-92/Disulfide bonds: #status predicted

Query Match 91.1%; Score 532; DB 1; Length 111;  
Best Local Similarity 94.5%; Pred. No. 1.6e-41;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VLTPSPASLAVSLGGRATISCRASEVDYGVNFMFMWQOIRPOPKLITRASNESGI 62  
Db 3 VLTPSPASLAVSLGGRATISCRASEVDYGVNFMFMWQOIRPOPKLITRASNESGI 62  
QY 63 PARFGSGGRTDFTLTINPEADVDVATYYCQSNEDPLTFGGGTRLEIKR 111  
Db 63 PARFGSGGRTDFTLTINPEADVDVATYYCQSNEDPLTFGGGTRLEIKR 111

## RESULT 2

S26343  
IG kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26343  
R/Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A/Title: Antibodies that are specific for a single amino acid interchange in a protein A/Reference number: S26309; PMID:91341421; PMID:1908510



F:21-131/Domain: Ig kappa chain precursor V region #status experimental <M>  
 F:36-114/Domain: immunoglobulin homology <IMM>  
 F:43-112/Disulfide bonds: #status predicted

Query Match 87.5%; Score 511; DB 1; Length 131;  
 Best Local Similarity 89.9%; Pred. No. 1.5e-39;  
 Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 62  
 DB 23 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGV 82  
 QY 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 111  
 DB 83 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 131

RESULT 6  
 D45722  
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (F)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: D45722  
 R:Simpton, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu  
 U. Vitol. 67, 489-496, 1993  
 A>Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
 A:Reference number: A45722; MUID:93100833; PMID:677958  
 A:Accession: D45722  
 A>Status: preliminary, not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-111 <SIM>  
 A>Note: sequence extracted from NCBI backbone (NCBI:120592)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 501; DB 2; Length 111;  
 Best Local Similarity 88.1%; Pred. No. 1e-38;  
 Matches 96; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 62  
 DB 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGV 62  
 QY 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 111  
 DB 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 111

RESULT 7  
 S09965  
 Ig kappa chain V-J region (106-108) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
 C:Accession: S09965  
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
 Eur. J. Immunol. 20, 771-777, 1990  
 A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie  
 A:Reference number: S09965; MUID:90269328; PMID:2347362  
 A:Accession: S09965  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RET>  
 A:Cross-references: EMBL:X51853; NID:955394; PIDN:CA93146.1; PID:9930230  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 494; DB 2; Length 111;  
 Best Local Similarity 88.1%; Pred. No. 4.4e-38;  
 Matches 96; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 62  
 DB 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGV 62

DB 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 62  
 QY 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 111  
 DB 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 111

RESULT 8  
 KMW532  
 Ig kappa chain precursor V regions (MOPC 321, TBPC 124) - mouse (tentative sequence)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-May-1979 #sequence\_revision 31-May-1979 #text\_change 31-Mar-2000  
 C:Accession: A90412; A90373; A90374; A01933  
 R:Burssten, Y.; Schechter, I.  
 Biochemistry 17, 2392-2400, 1978  
 A>Title: Primary structures of N-terminal extra peptide segments linked to the variabl  
 A:Reference number: A90412; MUID:78235887; PMID:98179  
 A:Contents: MOPC 321  
 A:Accession: A90412  
 A:Molecule type: protein  
 A:Residues: 1-37 <BUR>  
 A>Note: this precursor was synthesized in a cell-free system directed by mRNA isolated  
 R:McKean, D.; Potter, M.; Hood, L.  
 Biochemistry 12, 749-759, 1973  
 A>Title: Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.  
 A:Reference number: A90373; MUID:73140224; PMID:4120629  
 A:Contents: MOPC 321  
 A:Accession: A90373  
 A:Molecule type: protein  
 A:Residues: 21-133 <MCK>  
 A>Note: the partial sequence of the C region of this Bence Jones protein was also dete  
 R:McKean, D.; Potter, M.; Hood, L.  
 Biochemistry 12, 760-771, 1973  
 A>Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains  
 A:Reference number: A90374; MUID:73140225; PMID:4651517  
 A:Contents: TBPC 124  
 A:Accession: A90374  
 A:Molecule type: protein  
 A:Residues: 21-131 <MC2>  
 A>Note: the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-T  
 A:Comment: The MOPC 321 sequence is shown.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-132/Product: Ig kappa chain V regions (MOPC 321, TBPC 124) #status predicted <M>  
 F:36-114/Domain: immunoglobulin homology <IMM>  
 F:43-112/Disulfide bonds: #status predicted

Query Match 83.9%; Score 490; DB 1; Length 132;  
 Best Local Similarity 78.2%; Pred. No. 1.2e-37;  
 Matches 86; Conservative 20; Mismatches 4; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 62  
 DB 23 VLTQSPASLAVSLGQRATISCRASESDVSIGYVFMHWYQOIPGQPKLLIYRASNLSESGI 82  
 QY 63 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 112  
 DB 83 PARFSGSGSRITDFTLTINPEADVAITYCOQSNEDPLTFGNGRLLEIK 132

RESULT 9  
 E53285  
 Ig kappa chain V and J regions, monoclonal antibody OHP 4B2.2.1 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
 C:Accession: E53285  
 R:Sawada, J.; Minisawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
 Mol. Immunol. 28, 1063-1072, 1991  
 A>Title: Molecular characterization of monoclonal anti-steroid antibodies: primary str

and their pH-reactivity profiles

A:Reference number: A53285; MUID:92017897; PMID:1922102  
 A:Accession: E53285  
 A:Status: preliminary  
 A:Molecule type: DNA; protein  
 A:Residues: 1-111 <SAM>  
 A:Cross-references: GR:D12731; NID:g2220542; PIND:BA02222.1; PID:g2220543  
 A>Note: sequence extracted from NCBI backbone (NCIN:63307, NCIR:63311)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 489; DB 2; Length 111;  
 Best Local Similarity 84.4%; Pred. No. 1.3e-37;  
 Matches 92; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 DB 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111  
 DB 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111

#### RESULT 10

KYMS83  
 Ig kappa chain V region (PC7183) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: B01937; A01937  
 R:Weigert, M.; Gattalman, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152; PMID:103003  
 A:Accession: B01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 80.1%; Score 468; DB 1; Length 111;  
 Best Local Similarity 82.6%; Pred. No. 1e-35;  
 Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 DB 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111  
 DB 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111

#### RESULT 11

KYMS43  
 Ig kappa chain V region (PC7043) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
 C:Accession: A01937; S42187; S42184; S42190; S42189; S42188; S42191; S42192  
 R:Weigert, M.; Gattalman, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152; PMID:103003  
 A:Accession: A01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 R:Mo, J.A.; Bona, C.A.; Holmahl, R.  
 Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with sp  
 A:Reference number: S42176; MUID:94009207; PMID:7691608  
 A:Accession: S42187  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MOJ>  
 A:Cross-references: EMBL:Z25444; NID:g407832; PIND:CA080931.1; PID:g407833  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MOH>  
 A:Cross-references: EMBL:Z25458; NID:g407844; PIND:CA080945.1; PID:g407845  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42190  
 A:Molecule type: DNA  
 A:Residues: 13-99 <MOF>  
 A:Cross-references: EMBL:Z25450; NID:g407838; PIND:CA080937.1; PID:g407839  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42189  
 A:Molecule type: DNA  
 A:Residues: 15-99 <MOA>  
 A:Cross-references: EMBL:Z25448; NID:g407836; PIND:CA080935.1; PID:g407837  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42188  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MOZ>  
 A:Cross-references: EMBL:Z25446; NID:g407834; PIND:CA080933.1; PID:g407835  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42191  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MOY>  
 A:Cross-references: EMBL:Z25452; NID:g407840; PIND:CA080939.1; PID:g407841  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42192  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MOO>  
 A:Cross-references: EMBL:Z25454; NID:g407842; PIND:CA080941.1; PID:g407843  
 A>Note: V-kappa-21E; anti-collagen  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 80.0%; Score 467; DB 1; Length 111;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-35;  
 Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 DB 3 VLTQSPASIVAVSLGQRAITISCRASESVDSYGYNFMHWYQOIPQPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111  
 DB 63 PARFSGSGSRPTFTLTINPEADVAITYCCQSNEDPLFTFGTGLEIK 111

#### RESULT 12

KYMS08  
 Ig kappa chain V region (PC6308) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: C01937; A01937  
 R:Weigert, M.; Gattalman, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152; PMID:103003  
 A:Accession: C01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 80.0%; Score 467; DB 1; Length 111;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-35;  
 Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

C/Keywords: heterotetramer; immunoglobulin  
F/16-94/Domain: immunoglobulin homology <IMM>  
F/23-92/Disulfide bonds: #status predicted

Query Match 79.6%; Score 465; DB 1; Length 111;  
Best Local Similarity 82.6%; Pred. No. 1.9e-35;  
Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSICQARTISCRASESVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSICQARTISCRASKSVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPYEADVAITYCOQSNEDPFTFGTGLRLEIK 111  
|||||  
DB 63 PARFSGSGSGTDFLTINHPVEEDDAITYCOQSNEDPFTFGTGLRLEIK 111

## RESULT 13

KVM575

Ig kappa chain V region (PC7175) - mouse (tentative sequence)  
C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-2000  
C/Accession: B01938; A01938

R/Weigert, M.; Garmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978

A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A/Reference number: A93204; MUID:79073152; PMID:103003

A/Accession: B01938

A/Molecule type: protein

A/Residues: 1-111 <WEI>

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-94/Domain: immunoglobulin homology <IMM>  
F/23-92/Disulfide bonds: #status predicted

Query Match 79.1%; Score 462; DB 1; Length 111;  
Best Local Similarity 80.7%; Pred. No. 3.5e-35;  
Matches 88; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSICQARTISCRASESVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSICQARTISCRASKSVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPYEADVAITYCOQSNEDPFTFGTGLRLEIK 111  
|||||  
DB 63 PARFSGSGSGTDFLTINHPVEEDDAITYCOQSNEDPFTFGTGLRLEIK 111

## RESULT 14

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)  
C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S19972

R/Weissenborn, W.; Rietmueler, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.  
A/Reference number: S19963

A/Accession: S19972

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-112 <WEI>

A/Cross-references: EMBL:X65094; NID:G52290; PIDN:CAA46222.1; PID:G52291

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-94/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 460; DB 2; Length 112;  
Best Local Similarity 80.8%; Pred. No. 5.4e-35;  
Matches 89; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSICQARTISCRASESVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSICQARTISCRASKSVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPYEADVAITYCOQSNEDPFTFGTGLRLEIK 112  
|||||  
DB 63 PARFSGSGSGTDFLTINHPVEEDDAITYCOQSNEDPFTFGTGLRLEIK 112

## RESULT 15

KVM569

Ig kappa chain V region (PC7769) - mouse  
C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C/Accession: B01937; A01937

R/Weigert, M.; Garmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978

A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A/Reference number: A93204; MUID:79073152; PMID:103003

A/Accession: B01937

A/Molecule type: protein

A/Residues: 1-111 <WEI>

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-94/Domain: immunoglobulin homology <IMM>  
F/23-92/Disulfide bonds: #status predicted

Query Match 78.4%; Score 458; DB 1; Length 111;  
Best Local Similarity 80.7%; Pred. No. 8.2e-35;  
Matches 88; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSICQARTISCRASESVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSICQARTISCRASKSVDSYGVFMHMYQOIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPYEADVAITYCOQSNEDPFTFGTGLRLEIK 111  
|||||  
DB 63 PARFSGSGSGTDFLTINHPVEEDDAITYCOQSNEDPFTFGTGLRLEIK 111

Search completed: November 7, 2003, 07:36:20  
Job time: 14.6047 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 8.07477 Seconds  
(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_138\_249

Sequence: 1 ENVLTPSPASLAVSLGQRT.....QQSNEDPPLFGGTRLEIKR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	532 91.1	111 1	KV3H_MOUSE	P01660 mus musculu
2	517 88.5	111 1	KV3K_MOUSE	P01663 mus musculu
3	512 87.7	111 1	KV3J_MOUSE	P01662 mus musculu
4	511 87.5	131 1	KV3I_MOUSE	P01661 mus musculu
5	490 83.9	132 1	KV3F_MOUSE	P01658 mus musculu
6	483 82.7	112 1	KV3G_MOUSE	P01659 mus musculu
7	468 80.1	111 1	KV3N_MOUSE	P01666 mus musculu
8	467 80.0	111 1	KV3M_MOUSE	P01665 mus musculu
9	465 79.6	111 1	KV3O_MOUSE	P01668 mus musculu
10	462 79.1	111 1	KV3S_MOUSE	P01667 mus musculu
11	458 78.4	111 1	KV3Q_MOUSE	P01669 mus musculu
12	457 78.3	111 1	KV3L_MOUSE	P01664 mus musculu
13	456 78.1	111 1	KV3R_MOUSE	P01670 mus musculu
14	456 78.1	111 1	KV3T_MOUSE	P01672 mus musculu
15	450 77.1	111 1	KV3U_MOUSE	P01673 mus musculu
16	440.5 75.4	110 1	KV3P_MOUSE	P01668 mus musculu
17	440 75.3	111 1	KV3A_MOUSE	P01654 mus musculu
18	439 75.2	111 1	KV3D_MOUSE	P01657 mus musculu
19	432.5 74.1	112 1	KV3B_MOUSE	P01655 mus musculu
20	431 73.8	111 1	KV3C_MOUSE	P01656 mus musculu
21	422 72.3	108 1	KV3V_MOUSE	P01674 mus musculu
22	412 70.5	111 1	KV3E_MOUSE	P01657 mus musculu
23	380 65.1	114 1	KV4A_HUMAN	P01625 mus musculu
24	375 64.2	134 1	KV4C_HUMAN	P06314 homo sapien
25	372 63.7	108 1	KV5P_MOUSE	P01649 mus musculu
26	370.5 63.4	133 1	KV4B_HUMAN	P06313 homo sapien
27	358.5 61.4	129 1	KV3H_HUMAN	P04237 homo sapien
28	354 60.6	129 1	KV1W_HUMAN	P04431 homo sapien
29	353 60.4	108 1	KV1N_HUMAN	P01606 homo sapien
30	352.5 60.4	129 1	KV3L_HUMAN	P01815 homo sapien
31	352 60.3	108 1	KV1H_HUMAN	P01600 homo sapien
32	352 60.3	108 1	KV1M_HUMAN	P01605 homo sapien
33	350.5 60.0	109 1	KV3B_HUMAN	P01620 homo sapien

34	350.5	60.0	109 1	KV3D_HUMAN	P01622 homo sapien
35	350.5	60.0	129 1	KV3M_HUMAN	P01816 homo sapien
36	349	59.8	108 1	KV1Y_HUMAN	P08032 homo sapien
37	348.5	59.7	129 1	KV4A_MOUSE	P01680 mus musculu
38	346	59.2	108 1	KV1V_HUMAN	P01607 homo sapien
39	345	59.1	108 1	KV1O_HUMAN	P04430 homo sapien
40	344.5	59.0	113 1	KV2D_HUMAN	P01617 homo sapien
41	343	58.7	109 1	KV1F_HUMAN	P01598 homo sapien
42	342.5	58.6	108 1	KV1P_HUMAN	P01624 homo sapien
43	342	58.6	108 1	KV1B_HUMAN	P01608 homo sapien
44	341	58.4	108 1	KV1E_HUMAN	P01594 homo sapien
45	341	58.4	108 1	KV1E_HUMAN	P01597 homo sapien

## ALIGNMENTS

## RESULT 1

ID	KV3H_MOUSE	STANDARD	PRT	111 AA.
AC	P01660:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region PC 3741/TEPC 111.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RM	[1]			
RP	SEQUENCE (PC 3741).			
RX	MEDLINE=79073152; PubMed=103003;			
RA	Wiegert M., Gattalian L., Loh E., Schilling J., Hood L.E.;			
RT	"Rearrangement of genetic information may produce immunoglobulin			
RT	diversity.";			
RL	Nature 276:785-790(1978).			
RM	[2]			
RP	SEQUENCE (TEPC 111).			
RX	MEDLINE=79012520; PubMed=99744;			
RA	McLean D.J., Bell M., Potter M.;			
RT	"Mechanisms of antibody diversity: multiple genes encode structural			
RT	related mouse kappa variable regions.";			
CC	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).			
DR	-I- MISCRLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.			
DR	PIR, A93204; KWS37.			
DR	HSP, P01679; ZFBU.			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003006; Ig MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART: SM00406; IgV_1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 23			FRAMEWORK-1.
FT	DOMAIN 24 38			COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 39 53			FRAMEWORK-2.
FT	DOMAIN 54 60			COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61 92			FRAMEWORK-3.
FT	DOMAIN 93 101			COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 102 111			FRAMEWORK-4.
FT	DISULFID 23 92			BY SIMILARITY.
FT	NON TER 111 111			
SQ	SEQUENCE 111 AA; 12099 MW; EC46C9D2S9213BE4 CRC64;			

Query Match 91.1%; Score 532; DB 1; Length 111;  
Best Local Similarity 94.5%; Pred. No. 1.6e-49;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	3	VLTQSPASLAVSLGQRTISCRASSTSYSGINPMHWYQITGQPPKLIYASNLSEGI	62
DB	3	VLTQSPASLAVSLGQRTISCRASSTSYSGINPMHWYQITGQPPKLIYASNLSEGI	62
QY	63	PARFSGSGSRFDITLINFVEADVAITYYCCQSNEDPPLFGGTRLEIKR	111

Db 63 PARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPYTGGTKEIK 111

## RESULT 2

KV3K MOUSE STANDARD; PRT; 111 AA.

ID KV3K MOUSE

AC P01663;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OK

RE SEQUENCE.

RA MEDLINE=79073152; PubMed=103003;

RA Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

diversity."

RL Nature 276:785-790 (1978).

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-1like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DISULFID

FT NON TER

SEQUENCE

111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match

Best Local Similarity 88.5%; Score 517; DB 1; Length 111;

Matches 98; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 VLTQSPASLVSLGQRATISCRASESVSYGNFMHWYQOIPGPPKLLITRASNLBSGI 62

Db 3 VLTQSPASLVSLGQRATISCRASESVSYGNFMHWYQOIPGPPKLLITRASNLBSGV 62

QY 63 PARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPYTGGTKEIK 111

Db 63 PARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPYTGGTKEIK 111

RESULT 3

KV3J MOUSE

ID KV3J MOUSE

AC P01662;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OK

RE SEQUENCE (ABPC 22).

RA MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;

RT "Mechanisms of antibody diversity: multiple genes encode structurally

related mouse kappa variable regions."

REL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).

RP SEQUENCE (PC 9245).

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

diversity."

RL Nature 276:785-790 (1978).

CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-1like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DISULFID

FT NON TER

SEQUENCE

111 AA; 12041 MW; D7DF0609303453CB CRC64;

Query Match

Best Local Similarity 87.7%; Score 512; DB 1; Length 111;

Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLVSLGQRATISCRASESVSYGNFMHWYQOIPGPPKLLITRASNLBSGI 62

Db 3 VLTQSPASLVSLGQRATISCRASESVSYGNFMHWYQOIPGPPKLLITRASNLBSGV 62

QY 63 PARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPYTGGTKEIK 111

Db 63 PARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPYTGGTKEIK 111

RESULT 4

KV3I MOUSE

ID KV3I MOUSE

AC P01661;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OK

RE SEQUENCE OF 1-35.

RX MEDLINE=78235867; PubMed=98179;

RA Burstein Y., Schachter I.;

RT "Primary structures of N-terminal extra peptide segments linked to

the variable and constant regions of immunoglobulin light chain

precursors: implications on the organization and controlled

expression of immunoglobulin genes."

RL Biochemistry 17:2392-2400 (1978).

RE SEQUENCE OF 21-131.

RX MEDLINE=73140225; PubMed=4691517;

RA McKean D.J., Potter M., Hood L.E.;

RT "Mouse immunoglobulin chains. Pattern of sequence variation among

kappa chains with limited sequence differences."

RL Biochemistry 12:760-771 (1973).

RE REVISIONS.

RX MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions."?  
 Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).  
 DR PIR: B90412; KXMSM6.  
 DR HSSP: P01679; 2RFJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003066; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 131  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON TER 131  
 SQ SEQUENCE 131 AA; 14291 MW; D212C9F08DC860A CRC64;  
 Query Match 87.5%; Score 511; DB 1; Length 131;  
 Best Local Similarity 89.9%; Pred. No. 3,2e-47;  
 Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 3 VLTPSPASLAVSLGQRTATISCRASESVDSYGVNFMFMVYQOIPQPKLIIYRASNL25GI 62  
 DB 23 VLTPSPASLAVSLGQRTATISCRASESVDSYGVNFMFMVYQOIPQPKLIIYRASNL25GI 62  
 QY 63 PARFSGSGSRFTFTLTINPEADVAITYCCQGSNEDPLTFGTGLRIK 111  
 DB 83 PARFSGSGSRFTFTLTINPEADVAITYCCQGSNEDPLTFGTGLRIK 111  
 ID KX3F\_MOUSE STANDARD; PRT; 132 AA.  
 AC P01658;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 321 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-37.  
 RA MEDLINE=78235887; PubMed=981179;  
 RA Burstein Y.; Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 RT the variable and constant regions of immunoglobulin light chain  
 RT precursors: implications on the organization and controlled  
 RT expression of immunoglobulin genes.";  
 RT Biochemistry 17:2392-2400 (1978).  
 RN [2]  
 RP SEQUENCE OF 21-132.  
 RA MEDLINE=73140224; PubMed=4120629;  
 RA McKean D.J.; Potter M.; Hood L.E.;  
 RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa  
 RT chain.";  
 RT Biochemistry 12:749-759 (1973).  
 CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS  
 CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT  
 CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY  
 CC RESIDUES.  
 DR FTR: A90412; KYMS32.  
 DR HSSP: P01679; 2RFJ.  
 DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003066; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Bence-Jones protein; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 132  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON TER 132  
 SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBB9 CRC64;  
 Query Match 83.9%; Score 490; DB 1; Length 132;  
 Best Local Similarity 78.2%; Pred. No. 5.5e-45;  
 Matches 86; Conservative 20; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 VLTPSPASLAVSLGQRTATISCRASESVDSYGVNFMFMVYQOIPQPKLIIYRASNL25GI 62  
 DB 23 VLTPSPASLAVSLGQRTATISCRASESVDSYGVNFMFMVYQOIPQPKLIIYRASNL25GI 62  
 QY 63 PARFSGSGSRFTFTLTINPEADVAITYCCQGSNEDPLTFGTGLRIK 112  
 DB 83 PARFSGSGSRFTFTLTINPEADVAITYCCQGSNEDPLTFGTGLRIK 132  
 ID KX3G\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01659;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region TEPC 124.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J.; Potter M.; Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences.";  
 RT Biochemistry 12:760-771 (1973).  
 DR HSSP: P01679; 2RFJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003066; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT SIGNAL 1 23  
 FT CHAIN 24 38  
 FT DOMAIN 24 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 112  
 SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DB8E89771 CRC64;  
 Query Match 82.7%; Score 483; DB 1; Length 112;  
 Best Local Similarity 78.2%; Pred. No. 2.5e-44;  
 Matches 86; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 DB 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 112  
 DB 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 112

## RESULT 7

KV3M\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01665;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region PC 7183.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 RL PIR; A01937; KXMS83.  
 DR HSSP; P01679; 2EBU.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_V.1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR FROSTITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11952 MW; 2058B5B0C306D31 CRC64;

Query Match 80.1%; Score 468; DB 1; Length 111;  
 Best Local Similarity 82.6%; Pred. No. 9.5e-43;  
 Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 DB 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 111  
 DB 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 111

## RESULT 8

KV3M\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01665;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region PC 7043.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 RL PIR; A01937; KXMS83.  
 DR HSSP; P80362; 1MTL.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_V.1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 80.0%; Score 467; DB 1; Length 111;  
 Best Local Similarity 82.6%; Pred. No. 1.2e-42;  
 Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 DB 3 VLTGSPASLAVSLGGRATISCRASESDSYGNFMHWYQOIPGPPKLLIYRASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 111  
 DB 63 PARFSGSGSRDFTLTINPVADVATYCCQSNEDPLTFGTGTRLEIKR 111

## RESULT 9

KV3M\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01667;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region PC 6308.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 RL PIR; C01937; KXMS08.  
 DR HSSP; P80362; 1MTL.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IG\_V.1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.



DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 11964 MW; E2BAD98AD965562 CRC64;

Query Match 78.3%; Score 457; DB 1; Length 111;  
 Best Local Similarity 81.7%; Pred. No. 1,4e-41;  
 Matches 89; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 DB 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVEADVATYYCQSNEDPLTFTGTRLEIK 111  
 DB 63 PARFSGSGSGTDFTLTINHPVEEDATYYCQSNEDPLTFTGTRLEIK 111

RESULT 13  
 KV3U\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01670;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region PC 6684.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR; A01938; KIMS84.  
 DR HSBP; P80362; IWTU.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12039 MW; 1E4698834A858526 CRC64;

Query Match 78.1%; Score 456; DB 1; Length 111;  
 Best Local Similarity 80.7%; Pred. No. 1.8e-41;  
 Matches 88; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 DB 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVEADVATYYCQSNEDPLTFTGTRLEIK 111  
 DB 63 PARFSGSGSGTDFTLTINHPVEEDATYYCQSNEDPLTFTGTRLEIK 111

RESULT 14  
 KV3U\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01672;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region PC 7940.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR PIR; C01938; KIMS40.  
 DR HSBP; P80362; IWTU.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON TER 111 111  
 SQ SEQUENCE 111 AA; 12038 MW; E38A82306084352E CRC64;

Query Match 78.1%; Score 456; DB 1; Length 111;  
 Best Local Similarity 79.8%; Pred. No. 1.8e-41;  
 Matches 87; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 DB 3 VLTQSPASLAIVSLGQRATISCRASESVDSYGVNFMHWYQIIPQPPKLLIYASNLSEGI 62  
 QY 63 PARFSGSGSRDFTLTINPVEADVATYYCQSNEDPLTFTGTRLEIK 111  
 DB 63 PARFSGSGSGTDFTLTINHPVEEDATYYCQSNEDPLTFTGTRLEIK 111

RESULT 15  
 KV3U\_MOUSE STANDARD; PRT; 111 AA.  
 ID P01673;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region PC 2485/PC 4039.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX  NCB1_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=79073152; PubMed=103003;
RA  Weigert M, Gataiutan L, Joh E, Schilling J, Hood L.E.;
RT  "Rearrangement of genetic information may produce immunoglobulin
RL  diversity.";
CC  Nature 276:785-790(1978).
DR  PIR; A01939; KMS85.
DR  HSSP; P01679; 2PB1.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KM  Immunoglobulin V region.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 39 53 FRAMEWORK-2.
FT  DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 61 92 FRAMEWORK-3.
FT  DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 102 111 FRAMEWORK-4.
FT  DISULFID 23 92 BY SIMILARITY.
FT  NON_TER 111 111
SQ  SEQUENCE 111 AA; 11986 MW; BF38C59AA7858467 CRC64;

Query Match 77.1%; Score 450; DB 1; Length 111;
Best Local Similarity 78.9%; Pred. No. 7.6e-41;
Matches 86; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY  3 VLTQSPASLAVSIGQRATISCRASESVDSYGFNFHMWYCOIPQGPXKLIYRASNLESGI 62
    |||||
Db  3 VLTQSPASLAVSIGQRATISCRASESVDSYGFNFHMWYCOIPQGPXKLIYRASNLESGI 62
    |||||

QY  63 PARFSGSGSRTDFTLTINPEADVDVATYYCOQSNEDPLTFTGTLEIK 111
    |||||
Db  63 PARFSGSGSRTDFTLTINPEADVDVATYYCOQSNEDPLTFTGTLEIK 111
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 Job time : 8.07477 secs

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OM, protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 36.9346 Seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992B-86\_COPY\_138\_249  
Perfect score: 584

Sequence: 1 ENVTQSPASLAVSLGQRAT.....QQSNEDPLTFGTGTRLEIKR 112

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

### Listing first 45 summaries

```

1:  sp archaea:*
SPREMBL_23:*
2:  sp archaea:*
3:  sp bacteria:*
4:  sp fungi:*
5:  sp human:*
6:  sp invertibrate:*
7:  sp mammal:*
8:  sp mhc:*
9:  sp organelle:*
10: sp phage:*
11: sp plant:*
12: sp rodent:*
13: sp virus:*
14: sp vertebrate:*
15: sp unclassified:*
16: sp virus:*
17: sp bacteriap:*
18: sp archaeap:*

```

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	457	78.3	111	11	Q9Z0E9	Q9Z0E9 mus musculus
2	412	70.5	103	11	Q9ULB0	Q9J1B0 mus musculus
3	358.5	61.4	109	4	Q9ULI78	Q9ULI78 homo sapien
4	358	61.3	108	4	Q9ULI70	Q9ULI70 homo sapien
5	357.5	61.2	107	4	Q9GSA9	Q9GSA9 homo sapien
6	357	61.1	108	4	Q9ULV77	Q9ULI77 homo sapien
7	356	61.0	234	4	Q8NEK1	Q8NEK1 homo sapien
8	352.5	60.4	238	11	Q8VCIC6	Q8VCIC6 mus musculus
9	350.5	60.0	112	11	Q8KIIF2	Q8KIIF2 mus musculus
10	349.5	59.8	107	4	Q9ULB1	Q9ULB1 mus musculus
11	347.5	59.5	238	11	Q99M37	Q9ULH7 homo sapien
12	345.5	59.2	112	11	Q8KIF3	Q99M37 mus musculus
13	345	59.1	108	4	Q9ULB3	Q8KIF3 mus musculus
14	344.5	59.0	114	11	Q8KIF1	Q9ULB3 homo sapien
15	343.5	58.8	239	4	Q8NEKO	Q8KIF1 mus musculus
16	343	58.7	108	4	Q9ULI79	Q8NEKO homo sapien Q9ULI79 homo sapien

17	339.5	58.1	239	4	Q8TC00	Q8TC00	homo sapien
18	337.5	57.8	109	4	Q9TAS5	Q9TAS5	homo sapien
19	336.5	57.5	239	11	Q8VC55	Q8VC55	mus musculus
20	334.5	57.3	109	4	Q9UL86	Q9UL86	homo sapien
21	330	56.5	214	11	Q9TAS5	Q9TAS5	mus musculus
22	329.5	56.4	116	5	Q9U410	Q9U410	schistosoma
23	329	56.3	114	4	Q9UL80	Q9UL80	homo sapien
24	328	56.2	234	11	Q9UWFA	Q9UWFA	mus musculus
25	326.5	55.9	112	11	Q8K1F0	Q8K1F0	mus musculus
26	326.5	55.9	134	11	Q8VDD0	Q8VDD0	mus musculus
27	323	55.3	234	11	Q8R062	Q8R062	mus musculus
28	322	55.1	101	11	Q9UL78	Q9UL78	mus musculus
29	322	55.1	107	11	Q9ER29	Q9ER29	mus musculus
30	320.5	54.9	104	11	Q9UL82	Q9UL82	mus musculus
31	315.5	54.0	235	11	Q9UL12	Q9UL12	mus musculus
32	313	53.6	233	11	Q9UWS9	Q9UWS9	mus musculus
33	313	53.6	234	11	Q8VCP0	Q8VCP0	mus musculus
34	310	53.1	108	11	Q8VUJ0	Q8VUJ0	mus musculus
35	310	53.1	234	11	Q8R028	Q8R028	mus musculus
36	308.5	52.8	239	11	Q8R0F8	Q8R0F8	mus musculus
37	305	52.2	116	4	Q96PF6	Q96PF6	homo sapien
38	304	52.1	298	11	Q9QYF0	Q9QYF0	mus musculus
39	302	51.7	99	11	Q9UL74	Q9UL74	mus musculus
40	302	51.7	109	11	Q9Z0E6	Q9Z0E6	mus musculus
41	301	51.5	97	11	Q9UL76	Q9UL76	mus musculus
42	298	51.0	218	11	Q9Z5S1	Q9Z5S1	mus musculus
43	290	49.7	109	6	Q9N0M5	Q9N0M5	oryzctolagus
44	289	49.5	107	11	Q9UL84	Q9UL84	mus musculus
45	284	48.6	127	11	Q9Z5S9	Q9Z5S9	mus musculus

## ALIGNMENTS

[illegible]

Db 63 PARFSGSGSDPTLTINHPVEEDATYTCQHSRELPTFGGTLEIK 111

## RESULT 2

Q9JL80 PRELIMINARY; PRT; 103 AA.

AC Q9JL80; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE Anti-myosin immunoglobulin light chain variable region  
 DE (Fragment).

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/c; PubMed=10992488;  
 RX MEDLINE=20448942; PubMed=10992488;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin."  
 RL Infect. Immun. 68:5803-5808(2000).

DR EMBL; AF206026; AAF69324.1; -.

DR HSSP; P80362; 1MTL.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 103

FT NON\_TER 103 103

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 70.5%; Score 412; DB 11; Length 103;

Best Local Similarity 76.7%; Pred. No. 2.2e-39;

Matches 79; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Db 9 ASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIPARPSG 68

1 ASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIPARPSG 60

QY 69 SGRSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 111

61 SGRSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 103

RESULT 3

Q9JL78 PRELIMINARY; PRT; 109 AA.

AC Q9JL78; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035036; AAD56272.1; -.

DR HSSP; P80362; 1MTL.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1 109  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52BC7BE197 CRC64;

Query Match 61.4%; Score 358.5; DB 4; Length 109;

Best Local Similarity 63.4%; Pred. No. 3.1e-33;

Matches 71; Conservative 17; Mismatches 21; Indels 3; Gaps 1;

QY 1 ENVLTQSPASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIP 60

1 ENVLTQSPASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIP 57

QY 61 GIPARPSGSGSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 112

58 GIPARPSGSGSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 109

RESULT 4

Q9JL70 PRELIMINARY; PRT; 108 AA.

AC Q9JL70; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035044; AAD56280.1; -.

DR HSSP; P01607; 1REI.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 108

FT NON\_TER 108 108

SQ SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 61.3%; Score 358; DB 4; Length 108;

Best Local Similarity 61.5%; Pred. No. 3.5e-33;

Matches 67; Conservative 19; Mismatches 19; Indels 4; Gaps 1;

QY 4 LTQSPASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIP 63

4 LTQSPASLAVSLGGRATISCRASESVSYGNFMHWYQOIFGQPKLLIYRASNLSEGIP 59

QY 64 ARFSGSGSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 112

60 ARFSGSGSDPTLTINHPVEADVATYTCQHSRELPTFGGTLEIK 108

RESULT 5

Q96SA9 PRELIMINARY; PRT; 107 AA.

AC Q96SA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
DE variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal monoclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody V region genes."  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -.  
DR InterPro; IPR007110; IG\_1ike.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;  
  
Query Match 61.2%; Score 357.5; DB 4; Length 107;  
Best Local Similarity 63.3%; Pred. No. 3.9e-33;  
Matches 69; Conservative 20; Mismatches 15; Indels 5; Gaps 2;  
  
QY 4 LTQSPASLAVSICQRTICRASESDSYGNFMHWYQIQPQPPPLIYRASNLSSGIP 63  
DB 4 MTQSPSLASVSDRVTITCRASQSSSY---LNMVQKPGKAPPLIYAASSLQSGVP 59  
64 ARFSGSGSRDFTLTINPEADVDVATYYCQSQNEDPLTGTGRLRIK 112  
60 SRFSGSGSGTFTLTITSSLSQPEDPAFYVYCOQSYSTWTEGKVEIKR 107  
  
RESULT 6  
Q9UL77 PRELIMINARY; PRT; 108 AA.  
ID Q9UL77;  
AC Q9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; -.  
DR HSSP; P01607; IRET.  
DR InterPro; IPR007110; IG\_1ike.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

QY 4 LTQSPASLAVSICQRTICRASESDSYGNFMHWYQIQPQPPPLIYRASNLSSGIP 63  
DB 4 MTQSPSLASVSDRVTITCRASQSSSY---LNMVQKPGKAPPLIYAASSLQSGVP 59  
64 ARFSGSGSRDFTLTINPEADVDVATYYCQSQNEDPLTGTGRLRIK 112  
60 SRFSGSGSGTFTLTITSSLSQPEDPAFYVYCOQSYSTWTEGKVEIKR 108  
  
RESULT 7  
Q9NEK1 PRELIMINARY; PRT; 234 AA.  
ID Q9NEK1;  
AC Q9NEK1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Lung;  
RA Straussberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BE030813; AAB30813.1; -.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00407; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
DR PROSITE; PSS0290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25530 MW; 6316BDEF8D132F8 CRC64;  
  
Query Match 61.0%; Score 356; DB 4; Length 224;  
Best Local Similarity 62.5%; Pred. No. 1.6e-32;  
Matches 70; Conservative 20; Mismatches 18; Indels 4; Gaps 1;  
  
QY 1 ENVTQSPASLAVSICQRTICRASESDSYGNFMHWYQIQPQPPPLIYRASNLSSGIP 60  
DB 21 EIVMTQSPALTSVSGERATISCRASQSVTSN---LNMVQKPGKAPPLIYAASSLQSGVP 76  
61 GIPARFSGSGSRDFTLTINPEADVDVATYYCQSQNEDPLTGTGRLRIK 112  
77 GIPARFSGSGSGTFTLTITSSLSQPEDPAFYVYCOQSYSTWTEGKVEIKR 128  
  
RESULT 8  
Q9VC16 PRELIMINARY; PRT; 238 AA.  
ID Q9VC16;  
AC Q9VC16;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 26.2 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;

RA Strausberg R.;  
 RL Submitted (JSC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019760; AAH19760.1; -  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2. Hom.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 KM SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 60.4%; Score 352.5; DB 11; Length 238;  
 Best Local Similarity 63.1%; Pred. No. 4,1e-33;  
 Matches 70; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 3 VLTQSPASLAVSGQRATISCRASES-VDSYGNFMHWYQIQGPCKLLIYRASNLISG 61  
 DB 22 VMTQTPSLVSLDQASISCRSSQSLVHSGNWTYLLHWYIQKQGPCKLLIYKSNRFSG 81  
 QY 62 IPAFSGSGSRPTDFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 112  
 DB 82 VPAFSGSGSGTDTFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 132

## RESULT 9

ID 08K1F2 PRELIMINARY; PRT; 112 AA.  
 AC 08K1F2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Tsuchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;  
 RT "Immune proteolytic antibodies: Failed D-VIPase response to the D-  
 RT epsilon-oligomer of VIP and identification of L-VIPase VL domains";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516283; AAM64201.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT SEQUENCE 112 AA; 11953 MW; 4716B87FADE543ED CRC64;

Query Match 60.0%; Score 350.5; DB 11; Length 112;  
 Best Local Similarity 60.9%; Pred. No. 2,6e-32;  
 Matches 67; Conservative 17; Mismatches 21; Indels 5; Gaps 1;

QY 3 VLTQSPASLAVSGQRATISCRASES-VDSYGNFMHWYQIQGPCKLLIYRASNLISG 62  
 DB 3 VLTQSPASLAVSGQRATISCRASES-VDSYGNFMHWYQIQGPCKLLIYKSNRFSG 57  
 QY 63 PAFSGSGSRPTDFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 112  
 DB 58 PAFSGSGSGTDTFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 107

RESULT 10  
 Q9UL81 PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 OS (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AR035033; BAB56269.1; -  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 FT SEQUENCE 107 AA; 11501 MW; 070549FDB0754748 CRC64;

Query Match 59.8%; Score 349.5; DB 4; Length 107;  
 Best Local Similarity 60.6%; Pred. No. 3,2e-32;  
 Matches 66; Conservative 23; Mismatches 15; Indels 5; Gaps 2;

QY 4 LTQSPASLAVSGQRATISCRASES-VDSYGNFMHWYQIQGPCKLLIYRASNLISG 63  
 DB 4 LTQSPASLAVSGQRATISCRASES-VDSYGNFMHWYQIQGPCKLLIYKSNRFSG 59  
 QY 64 PAFSGSGSRPTDFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 112  
 DB 60 PAFSGSGSGTDTFTLTINPEADVATYCCQSNEDPLTFGTGLEIKR 107

## RESULT 11

ID 09NM37 PRELIMINARY; PRT; 238 AA.  
 AC 09NM37;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 26.3 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002035; AAH02035.1; -  
 DR HSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 KM SEQUENCE 238 AA; 26344 MW; FB2B06A0B0801330A CRC64;

Query Match 59.5%; Score 347.5; DB 11; Length 238;  
 Best Local Similarity 62.2%; Pred. No. 1,5e-31;  
 Matches 69; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

QY 3 VLTGSPASLAVSLGQRATISCRASBS-VDSYGNFMHWYQOIPGQPKLLIYRASNLBSG 61  
 DB 22 VMTQVPLSLVPSLGGDASISCRSSQSIYASNNATLEWLTQRPQSPKLLIYKVSRRSG 81  
 QY 62 IPARFSGSGSRDTFTLTINPVEADVATYCCQSNEDPLTFGTGRLTEIKR 112  
 DB 82 VDPFRFSGSGSGDTFTLKISRVRABDLGVYTCFGSHVPTFGSGTKLEIKR 132

## RESULT 12

Q8K1F3 PRELIMINARY; PRT; 112 AA.  
 ID 08K1F3  
 AC 08K1F3  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RT "Immune proteolytic antibodies: Failed D-VIPase response to the D-  
 entactinomer of VIP and identification of L-VIPase VL domains.";  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516282; AAM64200.1; -  
 DR InterPro; IPR003599; IG\_1.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 59.2%; Score 345.5; DB 11; Length 112;  
 Best Local Similarity 61.8%; Pred. No. 9.8e-32;  
 Matches 68; Conservative 15; Mismatches 22; Indels 5; Gaps 1;

QY 3 VLTGSPASLAVSLGQRATISCRASBSVDSYGNFMHWYQOIPGQPKLLIYRASNLBSG 62  
 DB 3 VLTGSPALMSASPGKRVITSCSSSV-----SYMYWQOKFGSSDPKFWIYRTSYLASGV 57  
 QY 63 PARFSGSGSRDTFTLTINPVEADVATYCCQSNEDPLTFGTGRLTEIKR 112  
 DB 58 PARFSGSGSGTSLTISMEADATYCCQYHSYPTFGSGTKLEIKR 107

## RESULT 13

Q9UL83 PRELIMINARY; PRT; 108 AA.  
 ID Q9UL83  
 AC Q9UL83  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,  
 RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 CLin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035031; AAD56267.1; -  
 DR HSSP; P80362; 1MTL.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92BBA36EEA CRC64;

Query Match 59.1%; Score 345; DB 4; Length 108;  
 Best Local Similarity 61.6%; Pred. No. 1.1e-31;  
 Matches 69; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

QY 1 ENVTGSPASLAVSLGQRATISCRASBSVDSYGNFMHWYQOIPGQPKLLIYRASNLBSG 60  
 DB 1 EIVMTGSPATLSVSGERATISCRASQSVSSN---LAWYQOKFGQAPRLIYCASTRAT 56  
 QY 61 GIPARFSGSGSRDTFTLTINPVEADVATYCCQSNEDPLTFGTGRLTEIKR 112  
 DB 57 GIPARFSGSGSGTFTLTISLQPEDPRAVYCCQHYNNWPTFGSGTKVDIKR 108

## RESULT 14

Q8K1F1 PRELIMINARY; PRT; 114 AA.  
 ID 08K1F1  
 AC 08K1F1  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RT "Immune proteolytic antibodies: Failed D-VIPase response to the D-  
 entactinomer of VIP and identification of L-VIPase VL domains.";  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516284; AAM64202.1; -  
 DR InterPro; IPR003599; IG\_1.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3BEFD1 CRC64;

Query Match 59.0%; Score 344.5; DB 11; Length 114;  
 Best Local Similarity 60.9%; Pred. No. 1.3e-31;  
 Matches 67; Conservative 17; Mismatches 23; Indels 3; Gaps 1;

QY 3 VLTGSPASLAVSLGQRATISCRASBSVDSYGNFMHWYQOIPGQPKLLIYRASNLBSG 62  
 DB 3 VLTGSPALMSASPGKRVITSCSSSV---SYLHWYQOKFGSGSPKFWIYRTSYLASGV 59  
 QY 63 PARFSGSGSRDTFTLTINPVEADVATYCCQSNEDPLTFGTGRLTEIKR 112  
 DB 60 PARFSGSGSGTSLTISMEADATYCCQYHSYPTFGSGTKLEIKR 109



GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17; Search time 48.2991 Seconds  
(without alignments)  
368.069 Million cell updates/sec

Title: US-09-661-992b-86\_COPY\_138\_249

Sequence: 1 ENVLQSPASLVSLGQRAT.....QQSNEDPLRFGCTRIEIKR 112

Scoring table: ELOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	100.0	249	22	AA1980.435
2	573	98.1	294	22	AA1981.437
3	573	98.1	294	22	AA1982.437
4	569	97.4	325	22	AA1983.438
5	543	93.0	249	22	AA1984.436
6	542	92.8	112	12	AA1985.439
7	542	92.8	112	12	AA1986.439
8	531	90.9	111	15	AA1987.494
9	528	90.4	131	17	AA1988.443

10	528	90.4	131	19	AA1989.468
11	526	90.1	112	22	AA1990.480
12	526	90.1	112	22	AA1991.480
13	526	90.1	112	22	AA1992.480
14	524	89.7	131	13	AA1993.480
15	521	89.2	131	18	AA1994.480
16	518	88.7	112	12	AA1995.480
17	517	88.5	112	12	AA1996.480
18	517	88.5	112	12	AA1997.480
19	513	87.8	121	17	AA1998.480
20	513	87.8	121	17	AA1999.480
21	509	87.0	121	15	AA2000.480
22	508	87.0	121	15	AA2001.480
23	507	86.8	120	15	AA2002.480
24	506	86.6	121	14	AA2003.480
25	505	86.5	134	23	AA2004.480
26	501	85.8	112	15	AA2005.480
27	501	85.8	112	15	AA2006.480
28	500	85.6	112	17	AA2007.480
29	500	85.6	112	17	AA2008.480
30	498	85.3	110	15	AA2009.480
31	496	84.9	132	12	AA2010.480
32	495	84.8	260	16	AA2011.480
33	494	84.6	112	23	AA2012.480
34	493	84.4	112	19	AA2013.480
35	492	84.2	215	16	AA2014.480
36	491	84.1	112	16	AA2015.480
37	491	84.1	149	17	AA2016.480
38	491	84.1	252	17	AA2017.480
39	491	84.1	271	17	AA2018.480
40	491	84.1	495	22	AA2019.480
41	490	83.9	107	18	AA2020.480
42	488.5	83.6	132	14	AA2021.480
43	485	83.0	329	22	AA2022.480
44	479	82.0	108	22	AA2023.480
45	475	81.3	108	22	AA2024.480

#### ALIGNMENTS

RESULT 1	AA1980.435	standard; Protein; 249 AA.
ID	AA1980.435	
AC	AA1980.435	
XX	21-JUN-2001	(first entry)
DT		
XX		
DB	Anti-FIX/FIXA antibody 198/AB2 scFv.	
XX		
KW	Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;	
KW	Factor VII cofactor; blood coagulation disorder; haemophilia A;	
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.	
OS	Chimeric - Mus musculus.	
XX		
OS	Chimeric - Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Label= VH	1..122
FT	Region	98..102
FT	Label= CDR3	123..136
FT	Peptide	137..249
FT	Protein	Label= Linker
FT	Region	Label= VL
FT		230..238
FT		Label= CDR3
PN	WO200119992-A2.	
XX		
PD	22-MAR-2001.	

Monoclonal antibody  
Synthetic antibody  
Antibody scFv8 lig  
Synthetic antibody  
p64-k protein pro  
Light chain of Mm  
Chimeric MAb 9.2.2  
TSH receptor antib  
Monoclonal antib  
Mab NM-01 light ch  
Sequence of the mo  
Mature NM-01 varia  
Sequence of the li  
Sequence of the va  
Anti-Streptococcus  
Human IGE receptor  
Sequence of the mo  
Variable light cha  
Anti-human FasL an  
Light chain variab  
Kappa light chain  
Anti-CS Mab N19/8  
Veneered 1B4 light  
Light chain variab  
Monoclonal antibod  
Human IGE receptor  
FvKC-II-VL region.  
FvKC-II-KEX2. Chi  
Double-head antio  
Light chain variab  
Mouse 4C10 anti-Id  
SNV-env leader/hum  
Synthetic antibody  
Synthetic antibody

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XX 13-SEP-2000; 2000MO-EP08936.
PF 14-SEP-1999; 99AT-0001576.
PR (BAXT ) BAXTER AG.
PA
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX WPI; 2001-290358/30.
DR N-PSDB; AAF30725.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Claim 12; Fig 16; 138pp; English.
XX
CC The present sequence is that of a single chain Fv (scFv) derivative
CC of antibody 198/AB2, comprising the heavy (VH) and light (VL) chain
CC variable regions of 198/AB2 joined by an artificial, flexible linker
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 198/AB2 VH and VL regions and cloning in vector pDAP2. 198/AB2 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of FVIIIa inhibitors. This allows for rapid blood coagulation even
CC in the absence of FVIII or FVIIIa, and in the case of FVIII
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis.
CC
SQ Sequence 249 AA;
Query Match 100.0%; Score 584; DB 22; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.2e-42;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENVLTGSPALAVSLGGRATISCRASESVDSYGNFMHWYQQLPGQPKLLIRASNLBSGI 60
DB 138 ENVLTGSPALAVSLGGRATISCRASESVDSYGNFMHWYQQLPGQPKLLIRASNLBSGI 197
QY 61 GIPARFSGSSRDPTLTINPVADVATYCCQSNEDPTFGTGRLEIKR 112
DB 198 GIPARFSGSSRDPTLTINPVADVATYCCQSNEDPTFGTGRLEIKR 249

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FT Protein /label= Mature_protein
FT 23..271
FT /label= scFv
FT Region 23..144
FT /label= VH
FT Misc-difference 76
FT /note= "encoded by GGN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..274
FT /label= Spacer
FT Protein 275..286
FT /label=Myc_tag
FT Peptide 287..288
FT /label= Spacer
FT Peptide 289..294
FT /label= His_tag
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX WPI; 2001-290358/30.
XX N-PSDB; AAF30732.
XX
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Example 18; Fig 34; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a PelB
XX leader; a single chain Fv (scFv) derivative of antibody 198/BI
XX comprising the heavy (VH) and light (VL) chain variable regions of
XX 198/BI joined by an artificial, flexible linker peptide; a spacer;
XX a Myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.
XX 198/BI is an example of anti-human Factor IX (FIX)/activated Factor
XX IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and
XX their derivatives, including scFv fragments, have FVIIIa cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FVIIIa inhibitors. This allows for rapid blood coagulation even
XX in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor
XX patients. The antibodies and derivatives are used in a claimed
XX pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis. The scFv-myc-tag fusion was expressed in E. coli. It
XX exhibited FVIII-like activity.
XX
SQ Sequence 294 AA;
Query Match 98.1%; Score 573; DB 22; Length 294;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VLTGSPALAVSLGGRATISCRASESVDSYGNFMHWYQQLPGQPKLLIRASNLBSGI 62
DB 162 VLTGSPALAVSLGGRATISCRASESVDSYGNFMHWYQQLPGQPKLLIRASNLBSGI 221
QY 63 PARFSGSSRDPTLTINPVADVATYCCQSNEDPTFGTGRLEIKR 112
DB 222 PARFSGSSRDPTLTINPVADVATYCCQSNEDPTFGTGRLEIKR 271

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```

RESULT 3
AAB20437
ID AAB20437 standard; Protein; 732 AA.
XX
AC AAB20437;
XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
XX
KM Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KM alkaline phosphatase.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Synthetic.
OS Chimeric - Escherichia coli.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..732
FT /label= Mature_protein
FT Protein 23..271
FT /label= scFv
FT Region 23..144
FT /label= VH.
FT Misc-difference 76
FT /note= "encoded by GGN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..275
FT /label= Spacer
FT Protein 276..725
FT /label= Alkaline_phosphatase
FT Peptide 726..732
FT /label= His_tag
XX
XX WO20011992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000MO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F,
XX WPI; 2001-290358/30.
XX N-PSDB; AAB30727.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Example 16; Fig 26; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a Pe1B
XX leader; a single chain Fv (scFv) derivative of antibody 198/B1
XX comprising the heavy (VH) and light (VL) chain variable regions of
XX 198/B1 joined by an artificial, flexible linker peptide; a spacer;
XX Escherichia coli alkaline phosphatase; and a C-terminal His
XX affinity tag. 198/B1 is an example of anti-human Factor IX
XX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
XX Anti-FIX/FIXa antibodies and their derivatives, including scFv
XX fragments, have FVIII cofactor activity or FIXa activating
XX activity. Administration leads to an increase in the procoagulant

```

```

CC activity of FIXa, even in the presence of FVIII inhibitors. This
CC allows for rapid blood coagulation even in the absence of FVIII or
CC FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The
CC scFv-alkaline phosphatase was expressed in E. coli. It exhibited
CC FVIII-like activity.
XX
XX SQ Sequence 732 AA;
XX
XX Query Match 98.1%; Score 573; DB 22; Length 732;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-41;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 VLTPSPASLAVSLGQRTATSCASPSVSYGNPMHMYQIGQPPKLLIYASNLSEGI 62
XX |||||
XX DB 162 VLQSPASLAVSLGQRTATSCASPSVSYGNPMHMYQIGQPPKLLIYASNLSEGI 221
XX |||||
XX QY 63 PARFGSGSRDPTFTLTINPEVADVATYCCQSNEDPLTFGTLEIR 112
XX |||||
XX DB 222 PARFGSGSRDPTFTLTINPEVADVATYCCQSNEDPLTFGTLEIR 271
XX |||||
XX
XX RESULT 4
XX AAB20438
XX ID AAB20438 standard; Protein; 325 AA.
XX
XX AC AAB20438;
XX
XX DT 21-JUN-2001 (first entry)
XX
XX DE Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
XX
XX KM Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
XX KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX KM bivalent antibody; plasmid pZap-198A2#102.
XX
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Synthetic.
XX OS Chimeric - Escherichia coli.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..22
XX /label= Signal_peptide
XX /note= "Pe1B leader"
XX FT Protein 23..325
XX /label= Mature_protein
XX FT Protein 23..271
XX /label= scFv
XX FT Region 23..144
XX /label= VH
XX FT Misc-difference 76
XX /note= "encoded by GGN"
XX FT Peptide 145..159
XX /label= Linker
XX FT Region 160..271
XX /label= VL
XX FT Misc-difference 166
XX /note= "encoded by TMT"
XX FT Peptide 181
XX /note= "encoded by TCN"
XX FT Peptide 272..274
XX /label= Spacer
XX FT Protein 275..284
XX /label= Hinge
XX FT Protein 285..319
XX /label= Helix
XX FT Peptide 320..325
XX /label= His_tag
XX
XX WO20011992-A2.

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XX PD 22-MAR-2001.
XX PF 13-SEP-2000; 2000WO-EP08936.
XX PR 14-SEP-1999; 99AT-0001576.
XX (BAXT ) BAXTER AG.
XX PI Schefflinger F, Kerschbaumer R, Falkner F, Dornier F,
XX DR N-PSDB; AAF30728.
XX PT WPI: 2001-290358/30.
XX PS New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Example 16; Fig 28; 138pp; English.
XX
XX The present sequence is that of a bivalent miniantibody comprising
XX a FcB2 leader peptide, the single chain Fv (scFv) fragment of
XX antibody 198/B1 (subclone AB2), an amphipathic helical structure
XX and a C-terminal 6His tag. The protein was expressed in
XX Escherichia coli from plasmid pZ19198AB2#102 (see AAF30728).
XX Antibody 198/B1 is an example of anti-human factor IX
XX (FIX)/activated factor IX (FIXa) antibodies of the invention.
XX Anti-FIX/FIXa antibodies and their derivatives have FvIIIA cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FvIIIA inhibitors. This allows for rapid blood coagulation even
XX in the absence of FvIII or FvIIIA, and in the case of FvIII
XX inhibitor patients. The antibodies and derivatives are used in a
XX claimed pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis. The bivalent miniantibody exhibited FvIII-like
XX activity.
XX
XX Sequence 325 AA;
SO
XX
XX Query Match 97.4%; Score 569; DB 22; Length 325;
XX Best Local Similarity 99.1%; Pred. No. 5.5e-41;
XX Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 VTQSPASIAVSLGORATISCRASESVDSYGFNFHMWYQIQPGPPKLLIYRASNLSEGI 62
DB 162 VLTQSPASIAVSLGORATISCRASESVDSYGFNFHMWYQIQPGPPKLLIYRASNLSEGI 221
QY 63 PARFSGSGSRDFTLTINPVADVAITYCCQSNEDPILFTGTGLEIKR 112
DB 222 PARFSGSGSRDFTLTINPVADVAITYCCQSNEDPILFTGTGLEIKR 271
RESULT 5
AAB20436
ID AAB20436 standard; Protein: 249 AA.
XX
XX AAB20436;
XX
XX 21-JUN-2001 (first entry)
XX
XX Anti-FIX/FIXa antibody 198/A1 scFv.
XX
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX Factor VIII cofactors; blood coagulation disorder; haemophilia A;
XX haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
XX
XX Chimeric - Mus musculus.
XX
XX Chimeric - Synthetic.
XX
XX Key Location/Qualifiers
XX Protein 1..122
XX /label= VH
FT

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FT Region 99..111
FT /label= CDR3
FT Peptide 123..136
FT /label= Linker
FT Protein 137..249
FT /label= VL
FT Region 230..238
FT /label= CDR3
FT Misc-difference 142
FT /note= "encoded by ACN"
FT Misc-difference 224
FT /note= "encoded by GCN"
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP08936.
XX
XX 14-SEP-1999; 99AT-0001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX Schefflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX WPI: 2001-290358/30.
XX N-PSDB; AAF30726.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
XX Example 10; Fig 17; 138pp; English.
XX
XX The present sequence is that of a single chain Fv (scFv) derivative
XX of antibody 198/A1, comprising the heavy (VH) and light (VL) chain
XX variable regions of 198/A1 joined by an artificial, flexible linker
XX peptide. The scFv was obtained by PCR amplification of cDNAs for
XX 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is
XX an example of anti-human factor IX (FIX)/activated factor IX (FIXa)
XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
XX including scFv and CDR3 fragments, have factor VIIIA (FvIIIA) cofactor
XX activity or FIXa activating activity. Administration leads to an
XX increase in the procoagulant activity of FIXa, even in the presence
XX of FvIIIA inhibitors. This allows for rapid blood coagulation even
XX in the absence of FvIII or FvIIIA, and in the case of FvIII
XX inhibitor patients. The antibodies and derivatives are used in a
XX claimed pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis.
XX
XX Sequence 249 AA;
SO
XX
XX Query Match 93.0%; Score 543; DB 22; Length 249;
XX Best Local Similarity 96.3%; Pred. No. 7e-39;
XX Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 LTQSPASIAVSLGORATISCRASESVDSYGFNFHMWYQIQPGPPKLLIYRASNLSEGI 63
DB 141 LTQSPASIAVSLGORATISCRASESVDSYGFNFHMWYQIQPGPPKLLIYRASNLSEGI 200
QY 64 ARFSGSGSRDFTLTINPVADVAITYCCQSNEDPILFTGTGLEIKR 112
DB 201 ARFSGSGSRDFTLTINPVADVAITYCCQSNEDPILFTGTGLEIKR 249
RESULT 6
AAR13089
ID AAR13089 standard; Protein: 112 AA.
XX
XX AAR13089;
XX
XX 25-MAR-2003 (updated)
FT

```

DT 09-JAN-2003 (updated)  
 DT 01-OCT-1991 (first entry)  
 XX  
 DE Murine 1B4 light chain-2 variable region.  
 XX  
 KM Monoclonal antibody; complementarily determining region; CDR;  
 KM integrin; hybridoma 1B4; protein REI; Gal/REI; Ig.  
 XX  
 OS Mus sp.  
 PN EP438312-A.  
 PN EP440351-A.  
 XX  
 PD 24-JUL-1991.  
 XX  
 PF 17-JAN-1991; 91EP-0300367.  
 XX  
 PR 20-DEC-1990; 90US-0627421.  
 PR 19-JAN-1990; 90US-0467692.  
 XX  
 PA (MERI) MERCK & CO INC.  
 PA (LAMM/) LAM M P.  
 XX  
 PI Law MF, Mark GE, Schmidt JA, Singer II;  
 PI MPI; 1991-216985/30.  
 DR N-PSDB; AAQ12684.  
 XX  
 PT New recombinant immunoglobulin(s) reactive with leukocyte CD18  
 PT antigen - comprise heavy chain framework and murine  
 PT complementarity regions useful in treatment of inflammation  
 XX  
 PS Disclosure; Fig 25; 77pp; English.  
 XX  
 CC A recombinant human Ig comprises a human heavy chain framework  
 CC and murine CDRs (with the heavy chain framework mutated at sites  
 CC near the CDRs), a human light chain framework and murine CDRs.  
 CC It has a mean IC50 nearly equal to that of the murine monoclonal  
 CC antibody from which the CDRs were derived. It is designated  
 CC mutated Gal/REI. The human Ig is capable of binding to a human  
 CC CD18 integrin.  
 CC The murine CDRs are obt'd. from murine hybridoma 1B4  
 CC (ATCC HB 10164). The light chain framework is derived from  
 CC human myeloma protein REI (EP-239400).  
 CC See also AAQ12682-84.  
 CC (Updated on 09-JAN-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 SQ Sequence 112 AA;  
 Query Match 92.8%; Score 542; DB 12; Length 112;  
 Best Local Similarity 94.5%; Pred. No. 3.9e-39;  
 Matches 104; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 VLTQSPALAVSLGQRATISCRASESDYSGYFMHWYQQIIPGQPPKLLIYRASNLSSGI 62  
 DB 3 VLTQSPALAVSLGQRATISCRASESDYSGYFMHWYQQIIPGQPPKLLIYRASNLSSGI 62  
 QY 63 PARFSGSGSRRTDFTLTINPVEADVAITYCOQSNEDPLTGTGRLRIKR 112  
 DB 63 PARFSGSGSRRTDFTLTINPVEADVAITYCOQSNEDPLTGTGRLRIKR 112  
 RESULT 7  
 ABB77332 standard; Protein; 112 AA.  
 AC ABB77332;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 KM Mouse 1B4 light chain variable region SEQ ID NO 37.  
 XX

KM Mouse; human; immunoglobulin; antigenicity; immunogenicity.  
 XX  
 OS Mus sp.  
 XX  
 PN US2002034765-A1.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 16-MAR-2001; 2001US-0810502.  
 XX  
 PR 19-AUG-1993; 93US-0109187.  
 PR 01-MAR-1996; 96US-0609218.  
 PR 01-AUG-1997; 97US-0905280.  
 PR 17-MAY-1991; 91US-0702217.  
 XX  
 PA (MERI) MERCK & CO INC.  
 XX  
 PI Daugherty BL, Mark GE, Fadlan EA;  
 PI WPI; 2002-338924/37.  
 DR  
 XX  
 PT Identifying and replacing immunoglobulin surface amino acid residues  
 PT useful for converting the antigenicity of a first mammalian species to  
 PT a second mammalian species -  
 XX  
 PS Example 1; Fig 12; 36pp; English.  
 XX  
 CC The invention relates to identifying differences (I) in mammalian species  
 CC specific surface amino acid residues on an immunoglobulin which converts  
 CC the antigenicity of a first mammalian species to a second mammalian  
 CC species. The new method is used for identifying and replacing  
 CC immunoglobulin surface amino acid residues which converts the  
 CC antigenicity of a first mammalian species to that of a second mammalian  
 CC species. The method simultaneously reduces the immunogenicity and  
 CC strictly preserves ligand binding properties. The replacement of exterior  
 CC amino acid residues has no effect on the ligand binding properties but  
 CC greatly alters immunogenicity. The present sequence is that of a PCR  
 CC primer used in the construction of the "venetized" 1B4 heavy and light  
 CC chain variable regions plus those necessary to fuse the human signal and  
 CC intronic sequences onto these variable regions. The present sequence is  
 CC that of the mouse 1B4 light chain variable region.  
 CC  
 SQ Sequence 112 AA;  
 Query Match 92.8%; Score 542; DB 23; Length 112;  
 Best Local Similarity 94.5%; Pred. No. 3.9e-39;  
 Matches 104; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 VLTQSPALAVSLGQRATISCRASESDYSGYFMHWYQQIIPGQPPKLLIYRASNLSSGI 62  
 DB 3 VLTQSPALAVSLGQRATISCRASESDYSGYFMHWYQQIIPGQPPKLLIYRASNLSSGI 62  
 QY 63 PARFSGSGSRRTDFTLTINPVEADVAITYCOQSNEDPLTGTGRLRIKR 112  
 DB 63 PARFSGSGSRRTDFTLTINPVEADVAITYCOQSNEDPLTGTGRLRIKR 112  
 RESULT 8  
 AAR47494  
 ID AAR47494 standard; Protein; 111 AA.  
 AC AAR47494;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 06-JUL-1994 (first entry)  
 XX  
 DE Murine anti-CD18 Ab 60.3 light chain.  
 XX  
 KM Monoclonal antibody; Mab; heavy chain; light chain;  
 KM constant region; variable region; amplification; primer;  
 KM polymerase chain reaction; PCR; chimera; Ig;  
 KM immunoglobulin; humanised antibody; leucocyte; integrin.  
 XX

OS Mus sp.  
 XX EP578515-A2.  
 XX 12-JAN-1994.  
 PD  
 XX  
 PF 24-MAY-1993; 93EP-0401328.  
 XX  
 XX 26-MAY-1992; 92US-0888233.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX  
 PI Björketh J, Harris LJ, Hsiao K, Ku-Chuan H;  
 XX  
 XX WPI; 1994-010334/02.  
 DR N-PSDB; AAC55002.  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 XX building, by computer database searching  
 PS  
 XX Disclosure; Page 21; 68pp; English.  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR), and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was  
 CC expressed in tissue culture (A9.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 Mab. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (IgG1, kappa). The humanised proteins were again  
 CC expressed in A9.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig  
 CC (updated on 25-MAR-2003 to correct FN field.)  
 XX  
 XX SQ Sequence 111 AA;  
 Query Match 90.3%; Score 531; DB 15; Length 111;  
 Best Local Similarity 94.5%; Pred. No. 3.4e-38;  
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLBSGI 62  
 DB 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLBSGI 62  
 QY 63 PARFSGSGSRFTDFTLTINPVEADVAITYCOQSNEDPFTFGGTLEIK 111  
 DB 63 PARFSGSGSRFTDFTLTINPVEADVAITYCOQSNEDPFTFGGTLEIK 111  
 RESULT 9  
 ID AAW01143 standard; Protein; 131 AA.  
 XX  
 XX AAW01143;  
 AC  
 XX  
 DT 10-FBB-1997 (first entry)  
 XX  
 XX Mab 1.4 light chain, directed against type II phospholipase A2.  
 DX  
 XX Monoclonal antibody; phospholipase; myocardial infarction;  
 KM

KM pancreatitis; cerebral infarction; acute kidney failure; colitis;  
 KM chronic rheumatism; adult respiratory distress syndrome;  
 KM cardiac shock; treatment; preclinical testing; disease; hybridoma.  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH Binding-site 44..58  
 FT Binding-site /label= CDR 1  
 FT Binding-site 74..80  
 FT Binding-site /label= CDR 2  
 FT Binding-site 113..121  
 FT Binding-site /label= CDR 3  
 XX  
 XX WO9620959-A1.  
 XX  
 XX 11-JUL-1996.  
 PD  
 XX  
 XX 27-DEC-1995; 95WO-JP02714.  
 PF  
 XX  
 XX 29-DEC-1994; 94JP-0340006.  
 PR  
 XX  
 XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
 PA  
 XX Kawauchi Y, Masuno Y, Takasaki J, Yasunaga T;  
 PI  
 XX WPI; 1996-333946/33.  
 DR N-PSDB; AAT40803.  
 XX  
 XX Monoclonal antibody inhibiting type II phospholipase A2 activity -  
 PT for treatment of myocardial and cerebral infarction  
 PS  
 XX Claim 6; Figure 10; 69pp; Japanese.  
 XX  
 XX Monoclonal antibodies which inhibit type II phospholipase A2 are  
 CC useful in the treatment of myocardial infarction, cerebral  
 CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,  
 CC pancreatitis, adult respiratory distress syndrome and colitis. The  
 CC antibodies were generated by immunising Balb/C mice with recombinant  
 CC human type II phospholipase A2. Spleen cells from the mice were  
 CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas  
 CC obtained were screened for phospholipase A2 inhibitory activity.  
 CC Active clones were isolated including 12H5, 1.4 and 10.1. These  
 CC were cultured and the antibody isolated from the culture  
 CC supernatant by precipitation with ammonium sulphate and purification  
 CC on a column of protein A-Sepharose CL4B. Because the antibody acts  
 CC on the primate and mouse forms of enzyme as well as human it is  
 CC particularly suitable for preclinical testing.  
 XX  
 XX SQ Sequence 131 AA;  
 Query Match 90.4%; Score 528; DB 17; Length 131;  
 Best Local Similarity 92.7%; Pred. No. 7.2e-38;  
 Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 VLTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLBSGI 62  
 DB 23 VLTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLBSGI 82  
 QY 63 PARFSGSGSRFTDFTLTINPVEADVAITYCOQSNEDPFTFGGTLEIK 111  
 DB 63 PARFSGSGSRFTDFTLTINPVEADVAITYCOQSNEDPFTFGGTLEIK 131  
 RESULT 10  
 ID AAW44168 standard; Protein; 131 AA.  
 XX  
 XX AAW44168;  
 AC  
 XX  
 DT 16-JUN-1998 (first entry)  
 XX  
 XX Monoclonal antibody 1.4 light chain against type II phospholipase A2.  
 DX  
 XX



DT 24-OCT-2001 (first entry)  
 XX Antibody scfv8 light chain variable region.  
 XX  
 XX Anticardial; antiviral; cytostatic; immunomodulatory;  
 KW antibody; gene therapy; HIV; human immunodeficiency virus; tumour;  
 KW metabolic disorder; immune disorder; auto-immune disorder; lysosome;  
 KW antibody light chain variable region; scfv8.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200149713-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 29-DEC-2000; 2000MO-IT00554.  
 XX  
 PR 30-DEC-1999; 99IT-RM00803.  
 XX  
 PA (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.  
 PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.  
 XX  
 PI Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;  
 FI WPI: 2001-50255/55.  
 DR  
 XX  
 XX Peptides which are able to confer stability and solubility to an  
 PT antibody comprising these peptides, useful for treating pathologies  
 PT (e.g. tumour) associated with accumulation of a molecule inside or  
 PT outside a human, or animal cell -  
 XX  
 PS Disclosure; Fig 4; 109pp; English.  
 XX  
 CC The invention relates to peptides which are able to confer stability and  
 CC solubility to an antibody comprising these peptides. The peptides  
 CC are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4  
 CC present within a variable region of an antibody which makes the antibody  
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to  
 CC H-FR4 are present within the variable region of the heavy chain of an  
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order  
 CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and  
 CC peptides having the sequences of L-FR1 to L-FR4 are present within  
 CC the variable region of the light chain of an antibody, covalently  
 CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-  
 CC (L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and  
 CC polynucleotides (e.g. by gene therapy) are useful for the manufacture  
 CC of a medicament for the treatment of pathologies associated with  
 CC accumulation of a molecule inside or outside a human, animal cell  
 CC or plant cell. The pathologies are infectious (e.g. viral infections such  
 CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and  
 CC immune (especially auto-immune) pathologies. The present sequence  
 CC represents the antibody scfv8 light chain variable region, used as  
 CC a basis for making mutant antibodies.  
 XX  
 XX Sequence 112 AA;  
 SQ  
 Query Match 90.1%; Score 526; DB 22; Length 112;  
 Best Local Similarity 93.6%; Pred. No. 9.1e-38;  
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 4 LTSPASAVSLGPRATISCASSSVSYGYNFMHWQIQFGPPKLIYRASNLSEGIP 63  
 DB 4 LTSPASAVSLGPRATISCASSSVSYGYNFMHWQIQFGPPKLIYRASNLSEGIP 63  
 QY 64 ARFGSGSRDTFTLTINPEADVAITYCOQSNEDPITFGGTLETKR 112  
 DB 64 ARFGSGSRDTFTLTINPEADVAITYCOQSNEDPITFGGTLETKR 112  
 RESULT 13  
 AAU07497  
 ID AAU07497 standard; Protein; 252 AA.  
 XX

AC AAU07497;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX  
 XX Synthetic antibody scfv(F8).  
 DE  
 XX  
 XX Anticardial; antiviral; cytostatic;  
 KW immunomodulatory; antibody; gene therapy; HIV; light chain;  
 KW human immunodeficiency virus; tumour; metabolic disorder;  
 KW immune disorder; auto-immune disorder; scfv(F8);  
 KW cucumber mosaic virus.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200149713-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 29-DEC-2000; 2000MO-IT00554.  
 XX  
 PR 30-DEC-1999; 99IT-RM00803.  
 XX  
 PA (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.  
 PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.  
 XX  
 PI Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;  
 FI WPI: 2001-50255/55.  
 DR N-PSDB; AAS11887.  
 XX  
 XX Peptides which are able to confer stability and solubility to an  
 PT antibody comprising these peptides, useful for treating pathologies  
 PT (e.g. tumour) associated with accumulation of a molecule inside or  
 PT outside a human, or animal cell -  
 XX  
 PS Example 1; Page 81; 109pp; English.  
 XX  
 CC The invention relates to peptides which are able to confer stability and  
 CC solubility to an antibody comprising these peptides. The peptides  
 CC are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4  
 CC present within a variable region of an antibody which makes the antibody  
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to  
 CC H-FR4 are present within the variable region of the heavy chain of an  
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order  
 CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and  
 CC peptides having the sequences of L-FR1 to L-FR4 are present within  
 CC the variable region of the light chain of an antibody, covalently  
 CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-  
 CC (L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and  
 CC polynucleotides (e.g. by gene therapy) are useful for the manufacture  
 CC of a medicament for the treatment of pathologies associated with  
 CC accumulation of a molecule inside or outside a human, animal cell  
 CC or plant cell. The pathologies are infectious (e.g. viral infections such  
 CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and  
 CC immune (especially auto-immune) pathologies. The present sequence  
 CC represents the synthetic antibody scfv(F8) which is used as a basis  
 CC for constructing synthetic antibodies incorporating the peptides of the  
 CC invention.  
 XX  
 XX Sequence 252 AA;  
 SQ  
 Query Match 90.1%; Score 526; DB 22; Length 252;  
 XX

Best Local Similarity 93.6%; Pred. No. 2e-37;  
Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSSGIP 63  
DB 144 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSSGIP 203

QY 64 ARFSGSGSRITDFTLTINPEADVATYYCQGSNEDPLFTGTGTRLEIKR 112  
DB 204 ARFSGSGSRITDFTLTINPEADVATYYCQGSNEDPLFTGTGTRLEIKR 252

## RESULT 14

AAK29008  
ID AAK29008 standard; Protein; 131 AA.

XX AAK29008;

DT 25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

DE p64-k4 protein product.

XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KM heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;  
KM plasmid; p64-k4; p64-h2.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein /note="Signal peptide"

FT Protein /note="Mature peptide"

XX WO9229759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-UP00544.

XX 25-APR-1991; 91JP-0095476.

XX 19-FEB-1992; 92JP-0032084.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Bending MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;

XX WPI; 1992-398882/48.

XX N-PSDB; AAQ30757.

PT Reconstituted human antibody to human interleukin-6 receptor -  
PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions

PS Disclosure; Page 124-125; 207pp; Japanese.

CC The sequences given in AAK29008-09 were encoded by plasmids which were  
CC used in example to illustrate the production of a human antibody which  
CC recognizes human interleukin-6 receptor (IL-6R). The antibody  
CC comprises light (L) chain and heavy (H) chain variable regions which  
CC were derived from a mouse monoclonal antibody produced from the  
CC hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 131 AA;

Query Match 89.7%; Score 524; DB 13; Length 131;  
Best Local Similarity 92.7%; Pred. No. 1.6e-37;  
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSSGIP 62  
|||||

DB 23 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSSGIP 82

QY 63 PARFSGSGSRITDFTLTINPEADVATYYCQGSNEDPLFTGTGTRLEIKR 111  
DB 83 PARFSGSGSRITDFTLTINPEADVATYYCQGSNEDPLFTGTGTRLEIKR 131

## RESULT 15

AAK30278  
ID AAK30278 standard; Protein; 131 AA.

XX AAK30278;

DT 07-JUL-1998 (first entry)

DE Light chain of MUM4TS.11.

XX MUM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition;  
KM initial hyperplasia; vasculature; restenosis; angioplasty; light chain.  
XX Mus sp.

XX Key Location/Qualifiers

FT Protein /note="Mature protein"

FT Binding-site 43..58

FT Binding-site /note="Complementarity determining region 1"

FT Binding-site 73..80

FT Binding-site /note="Complementarity determining region 2"

FT Binding-site 112..120

FT Binding-site /note="Complementarity determining region 3"

XX WO9737029-A1.

XX 09-OCT-1997.

XX 19-MAR-1997; 97WO-US04198.

XX 22-MAR-1996; 96US-0621751.

XX (BOE) BOEHRINGER MANNHEIM GMBH.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Chang CN, Landolfi NF, Martin U;

XX WPI; 1997-503114/46.

XX N-PSDB; AAT90985.

PT Antibodies to platelet derived growth factor beta receptor - inhibit  
PT PDGF-BB-induced proliferation of cells expressing the receptor, used  
PT particularly for inhibiting intimal hyperplasia

PS Claim 11; Fig 7B; 87pp; English.

CC This is the amino acid sequence for the light chain of MUM4TS.11, a  
CC novel antibody which specifically binds to the platelet derived  
CC growth factor receptor (PDGF-R beta), but not within the fifth  
CC extracellular Ig-like domain, where the antibody inhibits PDGF  
CC BB-induced proliferation of a cell expressing the PDGF beta receptor.  
CC The antibody can be used in a method of inhibiting intimal hyperplasia  
CC in the vasculature of a mammal. The antibodies can be used for the  
CC treatment of disorders related to PDGF activity such as disorders  
CC involving proliferation of smooth muscle cells, and including  
CC restenosis following angioplasty.

XX Sequence 131 AA;

Query Match 89.2%; Score 521; DB 18; Length 131;  
Best Local Similarity 92.7%; Pred. No. 2.8e-37;  
Matches 101; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSSGIP 62  
|||||

Db 23 VLTQSPSLAVSLGQRATISCRASESVDSYGNSEFMWYQQKPKQLIYRASNLSEGI 82

QY 63 PARFSGSGSRDPFTLTINPVPAADVATYYCQGSNEDPLTGTGTLEIK 111

Db 83 PARFSGSGSRDPFTLTINPVPAADVATYYCQGSNEDPPTFGGTLEIK 131

Search completed: November 7, 2003, 07:27:03  
Job time : 49,2991 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 98.243 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992B-86\_COPY\_138\_249  
Perfect score: 584  
Sequence: 1 ENVIQTSPMSIAVSLGQRA.....QQSNEDPLFGCTRIETKR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Published Applications AA.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	542	92.8	112	9 US-09-810-502-37	Sequence 37, Appl
2	527	90.2	112	10 US-09-144-886-81	Sequence 81, Appl
3	526	90.1	112	12 US-10-169-351-32	Sequence 32, Appl
4	526	90.1	252	12 US-10-169-351-49	Sequence 49, Appl
5	525	89.9	112	10 US-09-144-886-80	Sequence 80, Appl
6	521	89.2	112	10 US-09-144-886-87	Sequence 87, Appl
7	514	88.0	112	12 US-10-169-351-103	Sequence 103, Appl
8	513	87.8	112	10 US-09-144-886-86	Sequence 86, Appl
9	513	87.8	112	10 US-09-144-886-85	Sequence 85, Appl
10	509	87.2	112	10 US-09-144-886-85	Sequence 85, Appl
11	505	86.5	134	9 US-09-881-823-2	Sequence 2, Appl
12	499	85.4	112	10 US-09-144-886-94	Sequence 94, Appl
13	494	84.6	112	9 US-09-810-502-36	Sequence 36, Appl
14	487.5	83.5	112	12 US-10-169-351-81	Sequence 81, Appl
15	479	82.0	108	12 US-10-169-351-48	Sequence 48, Appl

16	476	81.5	111	12 US-10-160-506-77	Sequence 77, Appl
17	475	81.3	108	12 US-10-169-351-44	Sequence 44, Appl
18	474	81.2	108	12 US-10-169-351-46	Sequence 46, Appl
19	473	81.0	108	12 US-10-169-351-38	Sequence 38, Appl
20	472	80.8	108	12 US-10-169-351-42	Sequence 42, Appl
21	471.5	80.7	112	12 US-10-160-506-82	Sequence 82, Appl
22	471	80.7	108	12 US-10-169-351-36	Sequence 36, Appl
23	471	80.7	108	12 US-10-169-351-40	Sequence 40, Appl
24	467	80.0	238	12 US-10-384-933-11	Sequence 11, Appl
25	467	80.0	238	15 US-10-216-484-11	Sequence 11, Appl
26	466	79.8	132	10 US-09-879-461-2	Sequence 2, Appl
27	464	79.5	238	10 US-09-903-327A-4	Sequence 4, Appl
28	462	79.1	108	12 US-10-169-351-109	Sequence 109, Appl
29	459	78.6	112	15 US-10-194-975-115	Sequence 115, Appl
30	445	76.2	129	9 US-09-839-447A-2	Sequence 2, Appl
31	445	76.2	129	15 US-10-153-271-2	Sequence 2, Appl
32	445	76.2	238	12 US-10-384-933-54	Sequence 54, Appl
33	445	76.2	238	15 US-10-216-484-54	Sequence 42, Appl
34	444	76.0	112	15 US-10-148-844-42	Sequence 2, Appl
35	444	75.0	131	9 US-09-286-240-2	Sequence 2, Appl
36	443	75.0	269	14 US-10-027-770-2	Sequence 6, Appl
37	442	75.7	106	9 US-09-802-077-6	Sequence 6, Appl
38	442	75.7	106	9 US-09-802-077-6	Sequence 6, Appl
39	442	75.7	106	9 US-09-802-077-6	Sequence 6, Appl
40	442	75.7	269	14 US-09-925-179-6	Sequence 6, Appl
41	440.5	75.4	151	12 US-10-027-770-5	Sequence 5, Appl
42	437	74.8	131	10 US-09-879-461-58	Sequence 33, Appl
43	437	74.8	271	12 US-10-053-530-12	Sequence 58, Appl
44	437	74.8	271	15 US-10-207-655-12	Sequence 12, Appl
45	434	74.3	112	10 US-09-144-886-95	Sequence 95, Appl

#### ALIGNMENTS

RESULT 1  
US-09-810-502-37  
Sequence 37, Application US/09810502  
Patent No. US20020034765A1  
GENERAL INFORMATION:  
APPLICANT: Padlan, Eduardo A.  
Mark George E.  
Daugherty, Bruce L.  
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY  
OF ANTIBODY VARIABLE DOMAINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESS: Merck & Co., Inc.  
STREET: P. O. Box 2000, 126 B. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/810,502  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/905,280  
FILING DATE: 01-Aug-1997  
APPLICATION NUMBER: 08/609,218  
FILING DATE: 01-Mar-1996  
APPLICATION NUMBER: 08/109,187  
FILING DATE: 19-Aug-1993  
APPLICATION NUMBER: 07/702,217  
FILING DATE: 17-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark

REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18410CC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX: <UNKNOWN>  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-810-502-37

Query Match 92.8%; Score 542; DB 9; Length 112;  
Best Local Similarity 94.5%; Pred. No. 7.2e-44;  
Matches 104; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 VTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 62  
DB 3 VTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 62  
QY 63 PARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112  
DB 63 PARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112

## RESULT 2

US-09-144-886-81  
Sequence 81, Application US/09144886  
Patent No. US2002015114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amerisderfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
TITLE OF INVENTION: Botulinum Neurotoxins  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 81  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
OTHER INFORMATION: 1C9 region VL epitope 1  
US-09-144-886-81

Query Match 90.2%; Score 527; DB 10; Length 112;  
Best Local Similarity 93.6%; Pred. No. 1.9e-42;  
Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 63  
QY 64 ARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112  
DB 64 ARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112

## RESULT 3

US-10-169-351-32  
Sequence 32, Application US/10169351  
Publication No. US20030157090A1  
GENERAL INFORMATION:  
APPLICANT: BENVENUTO, EUGENIO  
APPLICANT: FRANCONI, ROSELLA  
APPLICANT: DESIDERIO, ANGIOLA

APPLICANT: TAVLADORAKI, PARASKEVI  
TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
TITLE OF INVENTION: WHICH INCLUDE THEM  
FILE REFERENCE: 4161-4  
CURRENT APPLICATION NUMBER: US/10/169,351  
PRIOR FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: PCT/IT00/00554  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: IT RM99A000803  
PRIOR FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: VL-F8 amino  
OTHER INFORMATION: acid sequence  
US-10-169-351-32

Query Match 90.1%; Score 526; DB 12; Length 112;  
Best Local Similarity 93.6%; Pred. No. 2.3e-42;  
Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 63  
QY 64 ARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112  
DB 64 ARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112

## RESULT 4

US-10-169-351-49  
Sequence 49, Application US/10169351  
Publication No. US20030157090A1  
GENERAL INFORMATION:  
APPLICANT: BENVENUTO, EUGENIO  
APPLICANT: FRANCONI, ROSELLA  
APPLICANT: DESIDERIO, ANGIOLA  
APPLICANT: TAVLADORAKI, PARASKEVI  
TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
TITLE OF INVENTION: WHICH INCLUDE THEM  
FILE REFERENCE: 4161-4  
CURRENT APPLICATION NUMBER: US/10/169,351  
PRIOR FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: PCT/IT00/00554  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: IT RM99A000803  
PRIOR FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 252  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: scrv(F8)  
OTHER INFORMATION: amino acid sequence  
US-10-169-351-49

Query Match

90.1%; Score 526; DB 12; Length 252;  
Best Local Similarity 93.6%; Pred. No. 5.6e-42;  
Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 63  
DB 144 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPQOPPKLLIYRASNLSESGIP 203  
QY 64 ARFSGSGSRDFTLTINPEADVDVATYYCOQSNEDPLTFGTGTRLEIKR 112

Db 204 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 252

## RESULT 5

US-09-144-886-80  
; Sequence 80, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117050  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-80

Query Match 89.9%; Score 525; DB 10; Length 112;  
Best Local Similarity 92.7%; Pred. No. 2.9e-42;  
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
QY 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112  
DB 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112

## RESULT 6

US-09-144-886-87  
; Sequence 87, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117050  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-87

Query Match 89.2%; Score 521; DB 10; Length 112;  
Best Local Similarity 91.7%; Pred. No. 6.9e-42;  
Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
QY 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112  
DB 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112

## RESULT 7

US-10-169-351-103  
; Sequence 103, Application US/10169351  
; Publication No. US20030157090A1  
; GENERAL INFORMATION:  
; APPLICANT: BEVENUTO, EUGENIO  
; APPLICANT: FRANCONI, ROSELA  
; APPLICANT: DESIDERIO, ANGELA  
; APPLICANT: TAVLADORAKI, PARASKEVI  
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
; FILE OF INVENTION: WHICH INCLUDE THEM  
; FILE REFERENCE: 4161-4  
; CURRENT APPLICATION NUMBER: US/10/169,351  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: PCT/IT00/00564  
; PRIOR FILING DATE: 2000-12-29  
; PRIOR APPLICATION NUMBER: IT RM99A000803  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 103  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VL-F8 amino  
US-10-169-351-103

Query Match 88.0%; Score 514; DB 12; Length 112;  
Best Local Similarity 92.7%; Pred. No. 3.1e-41;  
Matches 101; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
QY 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112  
DB 64 ARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPWTFGGKTLEIKR 112

## RESULT 8

US-09-144-886-84  
; Sequence 84, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117050  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-84

Query Match 87.8%; Score 513; DB 10; Length 112;  
Best Local Similarity 89.9%; Pred. No. 3.9e-41;  
Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63  
DB 4 LTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQOIPGQPKLLIYRASNLSEGP 63

Db 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63  
QY 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112  
Db 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112

RESULT 9  
US-09-144-886-86  
; Sequence 86, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: C39 region VL epitope 2  
US-09-144-886-86

Query Match 87.8%; Score 513; DB 10; Length 112;  
Best Local Similarity 89.0%; Pred. No. 3.9e-41;  
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63  
Db 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63  
QY 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112  
Db 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112

RESULT 10  
US-09-144-886-85  
; Sequence 85, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: 1F1 region VL epitope 2  
US-09-144-886-85

Query Match 87.2%; Score 509; DB 10; Length 112;  
Best Local Similarity 89.0%; Pred. No. 9.3e-41;  
Matches 97; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63  
Db 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63

QY 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112  
Db 64 ARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112

RESULT 11  
US-09-881-823-2  
; Sequence 2, Application US/09881823  
; Patent No. US20020068066A1  
; GENERAL INFORMATION:  
; APPLICANT: SHI, WENYUAN  
; APPLICANT: ANDERSON, MAXWELL  
; APPLICANT: MORRISON, SHERIE  
; APPLICANT: TRINH, RYAN  
; APPLICANT: WIMS, LETITIA  
; APPLICANT: CHEN, LI  
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries  
; FILE REFERENCE: 22851-032  
; CURRENT APPLICATION NUMBER: US/09/881,823  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 07/378,577  
; PRIOR FILING DATE: 1999-08-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-881-823-2

Query Match 86.5%; Score 505; DB 9; Length 134;  
Best Local Similarity 89.1%; Pred. No. 2.7e-40;  
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 3 VITGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 62  
Db 23 VITGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 82  
QY 63 PARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 112  
Db 83 PARFSGSGSRDFTLTINPEADVAATYCCQSNEDPFTFGTGRLEIKR 132

RESULT 12  
US-09-144-886-94  
; Sequence 94, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 94  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: 2B6 region VL epitope 3  
US-09-144-886-94

Query Match 85.4%; Score 499; DB 10; Length 112;  
Best Local Similarity 88.0%; Pred. No. 8.1e-40;  
Matches 95; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63  
Db 4 LTGSPASIAVSLGQRATISCRASESVDSYGNFMHMYQKRGQPKLLIYASNLSSGVP 63

Db 4 LTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGVP 63  
QY 64 ARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 111  
Db 64 ARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 111

RESULT 13  
US-09-810-502-36

Sequence 36 Application US/09810502  
Patent No. US20020034765A1  
GENERAL INFORMATION:  
APPLICANT: Padlan, Eduardo A.  
Mark, George B.  
Daugherty, Bruce L.  
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY  
OF ANTIBODY VARIABLE DOMAINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/810,502  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/905,280  
FILING DATE: 01-Aug-1997  
APPLICATION NUMBER: 08/609,218  
FILING DATE: 01-Mar-1996  
APPLICATION NUMBER: 08/109,187  
FILING DATE: 19-Aug-1993  
APPLICATION NUMBER: 07/702,217  
FILING DATE: 17-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18410CC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-810-502-36

Query Match 84.6%; Score 494; DB 9; Length 112;  
Best Local Similarity 87.3%; Pred. No. 2.4e-39;  
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 3 VTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGI 62  
Db 3 VTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGI 62  
QY 63 PARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 112  
Db 63 PARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 112

RESULT 14  
US-10-160-506-81  
Sequence 81 Application US/10160506  
Publication No. US20030161832A1  
GENERAL INFORMATION:  
APPLICANT: Bardear, Neil H.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
FILE REFERENCE: 10448-162001  
CURRENT APPLICATION NUMBER: US/10/160,506  
CURRENT FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: 60/324,100  
PRIOR FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: 60/362,612  
PRIOR FILING DATE: 2002-03-08  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 81  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-160-506-81

Query Match 83.5%; Score 487.5; DB 12; Length 112;  
Best Local Similarity 87.3%; Pred. No. 9.9e-39;  
Matches 96; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 3 VTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGI 62  
Db 3 VTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGI 62  
QY 63 PARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 111  
Db 63 PARFGSGSGRTDFTLLINVEADVAITYCCQSNEDPLTFGTGRLLEIK 112

RESULT 15  
US-10-169-351-48  
Sequence 48 Application US/10169351  
Publication No. US20030157090A1  
GENERAL INFORMATION:  
APPLICANT: BENVENUTO, EUGENIO  
APPLICANT: FRANCONI, ROSELLA  
APPLICANT: DESIDERIO, ANGIOLA  
APPLICANT: TAVLADORAKI, PARASKEVI  
TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
FILE REFERENCE: 4161-4  
CURRENT APPLICATION NUMBER: US/10/169,351  
CURRENT FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: PCT/IT00/00554  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: IT RM99A000803  
PRIOR FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 48  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: VL-CMV/2G  
US-10-169-351-48

Query Match 82.0%; Score 479; DB 12; Length 108;  
Best Local Similarity 87.2%; Pred. No. 6e-38;  
Matches 95; Conservative 3; Mismatches 7; Indels 4; Gaps 1;  
QY 4 LTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGIP 63  
Db 4 LTOSPASLAVSLGQRTATSCRASBSVDSYGNFMHWYQKRGQPKLLIYASNLBSGIP 63

Db 4 LTQSPASLAVSIGQRATISCRASBSV---HNVMHWYQKRGQPPKLLIYRALNLESQIP 59

OY 64 AAFSGSGSRDFTLTINPVEADVAFTYCOOSNEDPLTFGTGRLEIKR 112  
|||||  
Db 60 AAFSGSGSRDFTLTINPVEADVAFTYCOOSRRPMTFGGTGRLEIKR 108  
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Search completed: November 7, 2003, 08:16:54  
Job time : 39.243 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 16.486 Seconds  
(without alignments)  
288.098 Million cell updates/sec

Title: US-09-661-992B-86\_COPY\_138\_249

Perfect score: 584  
Sequence: 1 ENVTQSPASIVSLQGRAT.....QSNEDPLTFTGTREIKR 112

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCITUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	524	89.7	131 1	US-08-137-117D-33 Sequence 33, Appl
2	524	89.7	131 2	US-08-436-717-33 Sequence 33, Appl
3	521	89.2	131 2	US-08-621-751A-10 Sequence 10, Appl
4	513	87.8	121 1	US-08-111-080-18 Sequence 18, Appl
5	513	87.8	121 1	US-08-111-080-22 Sequence 22, Appl
6	513	87.8	121 1	US-08-211-980-18 Sequence 18, Appl
7	513	87.8	121 1	US-08-211-980-22 Sequence 22, Appl
8	513	87.8	121 5	PCT-US92-07111-17 Sequence 17, Appl
9	513	87.8	121 5	PCT-US93-07967-18 Sequence 18, Appl
10	513	87.8	121 5	PCT-US93-07967-22 Sequence 22, Appl
11	510	87.3	120 1	US-08-111-080-26 Sequence 26, Appl
12	510	87.3	120 5	PCT-US93-07967-26 Sequence 26, Appl
13	510	87.3	120 5	PCT-US93-07967-26 Sequence 26, Appl
14	508	87.0	111 1	US-08-275-053-11 Sequence 11, Appl
15	508	85.6	112 3	US-09-065-059-13 Sequence 13, Appl
16	492	84.2	215 4	US-09-170-769A-4 Sequence 4, Appl
17	491	84.1	149 4	US-08-894-922A-6 Sequence 6, Appl
18	491	84.1	252 2	US-08-894-922A-14 Sequence 14, Appl
19	491	84.1	271 2	US-08-894-922A-14 Sequence 14, Appl
20	470	80.5	106 4	US-09-170-769A-25 Sequence 25, Appl
21	466	79.8	132 2	US-08-483-636-2 Sequence 2, Appl
22	466	79.8	132 2	US-08-483-636-2 Sequence 2, Appl
23	454	77.7	111 1	US-08-491-845-8 Sequence 8, Appl
24	454	77.7	131 2	US-08-621-751A-14 Sequence 14, Appl
25	450	77.4	131 3	US-08-579-378A-14 Sequence 25, Appl
26	450	77.4	131 1	US-08-137-117D-25 Sequence 25, Appl
27	450	77.1	131 2	US-08-436-717-25 Sequence 25, Appl

28	445	76.2	129 4	US-09-556-605-2 Sequence 2, Appl
29	444	76.0	113 2	US-08-553-497A-6 Sequence 6, Appl
30	442	75.7	106 3	US-08-466-151-6 Sequence 6, Appl
31	442	75.7	106 4	US-08-466-151-6 Sequence 6, Appl
32	442	75.7	113 2	US-08-553-497A-10 Sequence 10, Appl
33	440.5	75.4	151 4	US-09-318-786-33 Sequence 33, Appl
34	440	75.3	111 1	US-07-634-728-54 Sequence 54, Appl
35	440	75.3	111 1	US-08-477-728-54 Sequence 54, Appl
36	440	75.3	111 1	US-08-474-040-54 Sequence 54, Appl
37	440	75.3	111 1	US-08-487-200-54 Sequence 54, Appl
38	440	75.3	111 3	US-08-484-537-54 Sequence 54, Appl
39	440	75.3	131 1	US-07-634-728-67 Sequence 67, Appl
40	440	75.3	131 1	US-08-477-728-67 Sequence 67, Appl
41	440	75.3	131 1	US-08-474-040-67 Sequence 67, Appl
42	440	75.3	131 3	US-08-487-200-67 Sequence 67, Appl
43	440	75.3	131 3	US-08-484-537-67 Sequence 67, Appl
44	438	75.0	120 1	US-08-111-080-24 Sequence 24, Appl
45	438	75.0	120 1	US-08-211-980-24 Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-08-137-117D-33  
Sequence 33, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-33

Query Match 89.7%; Score 524; DB 1; Length 131;  
Best Local Similarity 92.7%; Pred. No. 6, 5e-51;  
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 62  
DB 23 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 82  
QY 63 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPLTGTGTRLEIK 111  
DB 83 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPPTFGAGTKLEK 131

## RESULT 2

US-08-436-717-33  
Sequence 33, Application US/08436717  
Patent No. 581790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AACK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5339  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-33

Query Match 89.7%; Score 524; DB 2; Length 131;  
Best Local Similarity 92.7%; Pred. No. 6, 5e-51;  
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 62  
DB 23 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 82  
QY 63 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPLTGTGTRLEIK 111  
DB 83 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPPTFGAGTKLEK 131

## RESULT 3

US-08-621-751A-10  
Sequence 10, Application US/08621751A  
Patent No. 5862644  
GENERAL INFORMATION:  
APPLICANT: Chang, Chung N.  
APPLICANT: Landolfi, Nicholas F.  
APPLICANT: Martin, Ulrich  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER LLP  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,751A  
FILING DATE: 22-MAR-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 321152000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 484-0792  
TELEX: 706141 MRSN FOER SFO  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-621-751A-10

Query Match 89.2%; Score 521; DB 2; Length 131;  
Best Local Similarity 92.7%; Pred. No. 1, 4e-50;  
Matches 101; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 62  
DB 23 VLTPSPASLAVSLGQRTATISCRASESVDSYGNFMHMYQOIPGQPKLLIYRASNLSSGI 82  
QY 63 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPLTGTGTRLEIK 111  
DB 83 PARFSGSGSRDPTLTINPVEADVATYYCCQSNEDPPTFGAGTKLEK 131

## RESULT 4

US-08-111-080-18  
Sequence 18, Application 08/111080

```

; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohio, Teuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; FAX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-18
;
; Query Match      87.8%; Score 513; DB 1; Length 121;
; Best Local Similarity 89.1%; Pred. No. 9.9e-50;
; Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
;
; QY      3 VLTQSPASLVAVSLOQRATISCRASESDSYGNFMHWYQOIPQOPKLLIYRASNLSEGI 62
;         |||||
; DB      3 VLTQSPASLVAVSLOQRATISCRASESDSYGNFMHWYQOIPQOPKLLIYRASNLSEGI 62
;
; QY      63 PARFSGSGSRTPDFTLTINPVADVDVATYYCQGSNEDPLTFGTGRLRIKR 112
;         |||||
; DB      63 PARFSGSGSRTPDFTLTIDPVADDAATYYCQGNNEDEPLTFGTGRLRIKR 112
;
; RESULT 5
; US-08-111-080-22
; Sequence 22, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohio, Teuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago

```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; FAX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-22
;
; Query Match      87.8%; Score 513; DB 1; Length 121;
; Best Local Similarity 89.1%; Pred. No. 9.9e-50;
; Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
;
; QY      3 VLTQSPASLVAVSLOQRATISCRASESDSYGNFMHWYQOIPQOPKLLIYRASNLSEGI 62
;         |||||
; DB      3 VLTQSPASLVAVSLOQRATISCRASESDSYGNFMHWYQOIPQOPKLLIYRASNLSEGI 62
;
; QY      63 PARFSGSGSRTPDFTLTINPVADVDVATYYCQGSNEDPLTFGTGRLRIKR 112
;         |||||
; DB      63 PARFSGSGSRTPDFTLTIDPVADDAATYYCQGNNEDEPLTFGTGRLRIKR 112
;
; RESULT 6
; US-08-211-980-18
; Sequence 18, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohio, Teuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980

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FILING DATE: 424  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA: PCT/US92/07111  
APPLICATION NUMBER: 24-AUG-1992  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borum, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-18

Query Match 87.8%; Score 513; DB 1; Length 121;  
Best Local Similarity 89.1%; Pred. No. 9.9e-50;  
Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLVAVSGLQRTATISCRASESVDSYGNFMFMWYQIQPQPKLLIYASNLSEGI 62  
DB 3 VLTQSPASLVAVSGLQRTATISCRASESVDSYGNFMFMWYQIQPQPKLLIYASNLSEGV 62  
QY 63 PARFSGSGSRDFTLTINPVEADVDVATYYCOQSNEDPLTFGTREIRK 112  
DB 63 PARFSGSGSRDFTLTIDPVEADDAATYYCOQNNEDPLTFGTREIRK 112

RESULT 7  
US-08-211-980-22  
Sequence 22, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohio, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borum  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borum, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-22

Query Match 87.8%; Score 513; DB 1; Length 121;  
Best Local Similarity 89.1%; Pred. No. 9.9e-50;  
Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLVAVSGLQRTATISCRASESVDSYGNFMFMWYQIQPQPKLLIYASNLSEGI 62  
DB 3 VLTQSPASLVAVSGLQRTATISCRASESVDSYGNFMFMWYQIQPQPKLLIYASNLSEGV 62  
QY 63 PARFSGSGSRDFTLTINPVEADVDVATYYCOQSNEDPLTFGTREIRK 112  
DB 63 PARFSGSGSRDFTLTIDPVEADDAATYYCOQNNEDPLTFGTREIRK 112

RESULT 8  
PCT-US92-07111-17  
Sequence 17, Application PC/TUS9207111  
GENERAL INFORMATION:  
APPLICANT: Ohio, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 19920824  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-07111-17

Query Match 87.8%; Score 513; DB 5; Length 121;  
Best Local Similarity 89.1%; Pred. No. 9.9e-50;  
Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLVAVSGLQRTATISCRASESVDSYGNFMFMWYQIQPQPKLLIYASNLSEGI 62

Db 3 VLTGSPASLAVSLGQRTATISCRASESVDSYGNFPMHYQKPKQSPKLLIYASNLSESV 62  
QY 63 PARFSGSGSRDTFTLTINPYEADVDVATYYCQSNEDPLTFGTGTRLEIKR 112  
Db 63 PARFSGSGSRDTFTLTIDPVEADDAATYYCQNNEDPLTFGTGTRLEIKR 112

## RESULT 9

PCT-US93-07967-18  
Sequence 18, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borum, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-18

Query Match 87.8%; Score 513; DB 5; Length 121;  
Best Local Similarity 89.1%; Pred. No. 9.9e-50;  
Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
QY 3 VLTGSPASLAVSLGQRTATISCRASESVDSYGNFPMHYQKPKQSPKLLIYASNLSESV 62  
Db 3 VLTGSPASLAVSLGQRTATISCRASESVDSYGNFPMHYQKPKQSPKLLIYASNLSESV 62  
QY 63 PARFSGSGSRDTFTLTINPYEADVDVATYYCQSNEDPLTFGTGTRLEIKR 112  
Db 63 PARFSGSGSRDTFTLTIDPVEADDAATYYCQNNEDPLTFGTGTRLEIKR 112

## RESULT 10

PCT-US93-07967-22  
Sequence 22, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borum, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-22

Query Match 87.8%; Score 513; DB 5; Length 121;  
Best Local Similarity 89.1%; Pred. No. 9.9e-50;  
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
QY 3 VLTGSPASLAVSLGQRTATISCRASESVDSYGNFPMHYQKPKQSPKLLIYASNLSESV 62  
Db 3 VLTGSPASLAVSLGQRTATISCRASESVDSYGNFPMHYQKPKQSPKLLIYASNLSESV 62  
QY 63 PARFSGSGSRDTFTLTINPYEADVDVATYYCQSNEDPLTFGTGTRLEIKR 112  
Db 63 PARFSGSGSRDTFTLTIDPVEADDAATYYCQNNEDPLTFGTGTRLEIKR 112

## RESULT 11

US-08-111-080-26  
Sequence 26, Application 08/111080  
Patent No. 5558865  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/111,080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-080-26

Query Match 87.3%; Score 510; DB 1; Length 120;  
Best Local Similarity 89.1%; Pred. No. 2,1e-49;  
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLTQSPASIAVLGQRTATISCRASESDYSGYNFMHWYQIIPQPPKLLIYRASNLSEGI 62  
DB 3 VLTQSPASIAVLGQRTATISCRASESDYSGYNFMHWYQIIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPEADVDATYYCOQSNEDPLTFGTGRLEIKR 112  
DB 63 PARFSGSGSRDFTLTINPEADVDATYYCOQSNEDPLTFGTGRLEIKR 112

RESULT 12  
US-08-211-980-26  
Sequence 26, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457

FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-26

Query Match 87.3%; Score 510; DB 1; Length 120;  
Best Local Similarity 89.1%; Pred. No. 2,1e-49;  
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLTQSPASIAVLGQRTATISCRASESDYSGYNFMHWYQIIPQPPKLLIYRASNLSEGI 62  
DB 3 VLTQSPASIAVLGQRTATISCRASESDYSGYNFMHWYQIIPQPPKLLIYRASNLSEGI 62

QY 63 PARFSGSGSRDFTLTINPEADVDATYYCOQSNEDPLTFGTGRLEIKR 112  
DB 63 PARFSGSGSRDFTLTINPEADVDATYYCOQSNEDPLTFGTGRLEIKR 112

RESULT 13  
PCT-US93-07967-26  
Sequence 26, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
PCT-US93-07967-26

Query Match 87.3%; Score 510; DB 5; Length 120;  
Best Local Similarity 89.1%; Pred. No. 2.1e-49;  
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
|||||

QY 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 112  
|||||  
DB 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 112  
|||||

RESULT 14  
US-08-275-053-11  
Sequence 11, Application US/08275053  
Patent No. 5607847

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Recombinant human anti-human immunodeficiency  
virus antibody.

TITLE OF INVENTION: virus antibody.

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/275,053

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/01798

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-275-053-11

Query Match 87.0%; Score 508; DB 1; Length 111;  
Best Local Similarity 89.0%; Pred. No. 3.2e-49;  
Matches 97; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
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DB 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
|||||

QY 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 111  
|||||  
DB 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 111  
|||||

RESULT 15  
US-09-065-059-13  
Sequence 13, Application US/09065059  
Patent No. 6068841

GENERAL INFORMATION:

APPLICANT: SEINO, Ken-ichiro

APPLICANT: KAWAGAKI, No. 6068841uhiko

APPLICANT: YAGITA, Hideo

APPLICANT: OKUMURA, Ko

APPLICANT: NAKATA, Motomi

TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDermott, Will & Emery

STREET: 99 Canal Center Plaza

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/065,059

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Bucca Ph.D., Daniel

REGISTRATION NUMBER: P-42,368

REFERENCE/DOCKET NUMBER: 50356-151

TELEPHONE: 703-518-5100

TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-065-059-13

Query Match 85.6%; Score 500; DB 3; Length 112;  
Best Local Similarity 87.3%; Pred. No. 2.5e-48;  
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
|||||  
DB 3 VLTQSPASLAVSLGQRTATISCRASESVDSYGNFMFMWYQIIPQOPKLLIYRASNLSEGI 62  
|||||

QY 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 112  
|||||  
DB 63 PARFSGSGSRDTFTLTINPEADVDVATYYCOQSNEDPLTFGGTGRLEIK 112  
|||||

Search completed: November 7, 2003, 07:30:11  
Job time: 17.4486 secs

! FINDPATTERNS on geneseq: \* allowing 0 mismatches  
! 1 CXXYGNSPKGFAYXXC

November 7, 2003 07:46 ..

1 AAB20444 ck: 623 len: 16 ! Aab20444 Anti-Flx/FixA antibody CDR3. 6/200  
1: CXXYGNSPKGFAYXXC  
CXXYGNSPKGFAYXXC

Databases searched:

Geneseq-Aa, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003

Total finds: 1  
Total length: 158,726,570  
Total sequences: 1,107,863  
CPU time: 02:53.22

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! FINDPATTERNS on geneseq.* allowing 0 mismatches
!      1 CXXYGNSPKGFAYXC      November 7, 2003 07:51 ..
GENESECP2001S:AAB20444 ck: 623 len: 16 finds: 1 1 Aab20444 Anti-Flx/FixA antiB
\\End of list
Databases searched:
  Geneseq-AA, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003
Total finds:      1
Total length:    158,726,570
Total sequences: 1,107,863
CPU time:        05:00.84
  
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!!AA SEQUENCE 1.0
ID AAB20444 standard; peptide; 16 AA.
XX
AC AAB20444;
XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody CDR3.
XX
KM Factor IX; FIX; Factor IXa; antibody; procoagulant;
KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KM complementarily determining region; CDR.
XX
OS Mus musculus.
XX
Key Location/Qualifiers
FH Misc-difference /note= "any amino acid"
FT Misc-difference 3 /note= "any amino acid"
FT Misc-difference 14 /note= "any amino acid"
FT Misc-difference 15 /note= "any amino acid"
FT Misc-difference 15 /note= "any amino acid"
XX
W020011992-A2.
XX
PN 22-MAR-2001.
XX
PD 13-SEP-2000; 2000MO-EP08936.
XX
PF 14-SEP-1999; 99AT-0001576.
XX
PR (BAXT ) BAXTER AG.
XX
PA Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX
PI WPI; 2001-290358/30.
XX
DR New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -
XX
XX Claim 7; Page 74; 138pp; English.
XX
PS The present sequence is that of complementarily determining
CC region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or
CC anti-activated factor IX (FIXa) activity. Such antibodies
CC and their derivatives (including those that comprise the present
CC CDR3 peptide) have Factor VIIa (FVIIa) cofactor activity or FIXa
CC activating activity. Administration of the antibodies or their
CC derivatives leads to an increase in the procoagulant activity of
CC FIXa, even in the presence of FVIIa inhibitors. This allows for
CC rapid blood coagulation even in the absence of FVIII or FVIIa, and
CC in the case of FVIII inhibitor patients. The antibodies or their
CC derivatives are used in a claimed pharmaceutical composition for
CC treating patients with blood coagulation disorders, especially
CC haemophilia A and haemorrhagic diathesis.
XX
SQ Sequence 16 AA;

```

AAB20444 Length: 16 November 7, 2003 08:14 Type: P Check: 623 ..

1 CXXYGNPKG PAYXXC



```
> O <
O | | O Intelligence
> O <
```

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "seq105-1ss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "new.key":

Selected sequence key from "new.key":  
seq105 (AA) ID seq105 AA preliminary pattern

1 followed by

- 2 c any character
- 2 any character
- 2 ygmshkfyay
- 2 any character
- 2 any character
- 2 c

Selected data banks and files:

Data bank : Issued\_AA , all entries

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	File Options:	
Find non-matching hits only	No	Indirect file	No
Report key used	Yes	Sequence or key file	No
Note position of hit	Yes	List of hits	Yes
Display full annotations	Yes	Hit display	Yes
Sequence context	50	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:01:34.06	00:01:37.00
Number of sequences searched:		328807
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

! FINDPATTERNS on plr:\* allowing 0 mismatches  
! 1 CXYGNSPKGPAYXXC

November 7, 2003 07:41 ..

Databases searched:

NBRF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003

Total finds: 0  
Total length: 96,168,682  
Total sequences: 283,308  
CPU time: 54.01

! FINDPATTERNS on swp:\* allowing 0 mismatches

! 1 CXXYGNPKGFAYXXC

November 7, 2003 07:42 ..

Databases searched:

SWISS-PROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003  
 SPTREMBL, Release 23.0, Released on 4Mar2003, Formatted on 7Mar2003

Total finds: 0  
 Total length: 305,079,309  
 Total sequences: 958,388  
 CPU time: 03:26.62

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 2.0721 Seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-105

Perfect score: 80

Sequence: 1 CXXYGNSPKGFAYXC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	55.0	205	2	T19356
2	44	55.0	306	1	S59863
3	42	52.5	109	2	F30607
4	42	52.5	166	2	T39586
5	42	52.5	568	1	A55377
6	42	52.5	626	2	B70749
7	41	51.2	389	2	H90083
8	41	51.2	429	2	D70763
9	41	51.2	453	2	S75579
10	41	51.2	1866	1	GNWE2C
11	41	51.2	2515	2	A41519
12	40	50.0	107	2	AH3499
13	40	50.0	109	1	K3HUGO
14	40	50.0	359	2	T47208
15	40	50.0	382	2	S51425
16	40	50.0	382	2	T39451
17	40	50.0	384	2	A31398
18	40	50.0	395	1	S27257
19	40	50.0	395	2	A37118
20	40	50.0	395	2	S65800
21	40	50.0	404	2	T34085
22	40	50.0	404	2	T34084
23	39.5	49.4	1787	2	AC2009
24	39.5	49.4	1800	2	AT1918
25	39	48.8	218	2	F84170
26	39	48.8	318	2	H86342
27	39	48.8	401	2	H82175
28	39	48.8	503	1	S64019
29	38	47.5	92	2	S37519

30	38	47.5	92	2	S37517	Ig kappa chain V r
31	38	47.5	96	2	T07138	probable metalloa
32	38	47.5	109	2	G30601	Ig kappa chain V-I
33	38	47.5	109	2	D30601	Ig kappa chain V-I
34	38	47.5	110	2	S20635	Ig kappa chain V r
35	38	47.5	118	2	T03036	Ig light chain - h
36	38	47.5	128	2	S20636	Ig kappa chain V r
37	38	47.5	351	2	C36470	Wnt-4 protein - mo
38	38	47.5	352	2	A49146	developmental regu
39	38	47.5	402	2	D90034	hypothetical prote
40	38	47.5	488	2	AD0735	conserved hypothet
41	38	47.5	488	2	AG0621	probable bacteriop
42	38	47.5	488	2	B96521	protein r21p18.20
43	38	47.5	583	2	B87204	probable acyl-CoA
44	38	47.5	588	2	UC7206	phosphoprotein Pho
45	37	46.2	92	2	S37514	Ig kappa chain V r

## ALIGNMENTS

### RESULT 1

T19356

hypothetical protein C17E4.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T19356

R:Percy, C.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19113

A:Accession: T19356

A:Molecule type: DNA

A:Residues: 1-205 <WII>

A:Cross-references: EMBL:Z81037, PIDN:CA902750.1, GSPDB:GN00019, CESP:C17E4.5

A:Experimental source: clone C17E4

A:Gene: CESP:C17E4.5

A:Map position: 1

A:Introns: 22/3, 120/2

Query Match

Best Local Similarity 55.0%, Score 44; DB 2; Length 205;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db

1 CXXYGNSPKGFAY 13

111 CDRFGHKGKGFAY 123

RESULT 2

S59863

polya binding protein II - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Nov-1999

C:Accession: S59863

R:Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jenoe, P.; Lustig, A.; Wahle, E.

Ig kappa chain V r  
probable metalloa  
Ig kappa chain V-I  
Ig kappa chain V-I  
Ig kappa chain V r  
Ig light chain - h  
Ig kappa chain V r  
Wnt-4 protein - mo  
developmental regu  
hypothetical prote  
conserved hypothet  
probable bacteriop  
protein r21p18.20  
probable acyl-CoA  
phosphoprotein Pho  
Ig kappa chain V r

Nucleic Acids Res. 23, 4034-4041, 1995

A:Title: Isolation of genomic and cDNA clones encoding bovine poly(a) binding protein I

A:Reference number: S59863; MUID:96071160; PMID:7479061

A:Accession: S59863

A:Molecule type: mRNA

A:Status: preliminary; nucleic acid sequence not shown, translation not shown

A:Cross-references: EMBL:X89969, NID:G1055677, PIDN:CA62006.1, PID:G1051125

Ig kappa chain V r  
probable metalloa  
Ig kappa chain V-I  
Ig kappa chain V-I  
Ig kappa chain V r  
Ig light chain - h  
Ig kappa chain V r  
Wnt-4 protein - mo  
developmental regu  
hypothetical prote  
conserved hypothet  
probable bacteriop  
protein r21p18.20  
probable acyl-CoA  
phosphoprotein Pho  
Ig kappa chain V r

Nucleic Acids Res. 23, 4034-4041, 1995

A:Title: Isolation of genomic and cDNA clones encoding bovine poly(a) binding protein I

A:Reference number: S59863; MUID:96071160; PMID:7479061

A:Accession: S59863

A:Molecule type: mRNA

A:Status: preliminary; nucleic acid sequence not shown, translation not shown

A:Cross-references: EMBL:X89969, NID:G1055677, PIDN:CA62006.1, PID:G1051125

OY 1 CXXYGNSPKGFAY 13  
| : |||||  
Db 205 CDKFGHPKGFAY 217

## RESULT 3

ig kappa chain V-III region (Bor) - human (fragment)  
F30607  
C/Species: Homo sapiens (man)  
C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
C/Accession: F30607  
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold  
J. Immunol. 142, 3158-3163, 1989  
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantib  
C/Keywords: heterodimer; immunoglobulin  
A/Accession: F30601; MUID:89215279; PMID:2496160  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-109 <CON>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 52.5%; Score 42; DB 2; Length 109;  
Best Local Similarity 63.6%; Pred. No. 3.4;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CXXYGNSPKGF 11  
| : |||||  
Db 89 CQYGNSPQTF 99

## RESULT 4

rna binding protein - fission yeast (Schizosaccharomyces pombe)  
T39586  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T39586  
R/Volckert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, August 1997  
A/Reference number: Z21865  
A/Accession: T39586  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-166 <VOL>  
A/Cross-references: EMBL:Z99759; PIDD:CAH16904.1; GSPDB:GN00067; SPDB:SPBC16B9.12c  
A/Experimental source: strain 972h-; cosmid c16B9  
C/Genetics:  
A/Gene: SPDB:SPBC16B9.12c  
A/Map position: 2  
A/Introns: 12/3; 97/2; 126/3

Query Match 52.5%; Score 42; DB 2; Length 166;  
Best Local Similarity 53.8%; Pred. No. 5.2;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXXYGNSPKGFAY 13  
| : |||||  
Db 88 CDKFGHPKGFAY 100

## RESULT 5

CPE-binding protein - African clawed frog  
A55377  
N/Alternate names: cytoplasmic polyadenylation element-binding protein  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C/Accession: A55377  
R/Hake, L.E.; Richter, J.D.  
Cell 79, 617-627, 1994  
A/Title: CPEB is a specificity factor that mediates cytoplasmic polyadenylation during X  
A/Reference number: A55377; MUID:95042759; PMID:7954828  
A/Accession: A55377

A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-568 <HAK>  
A/Cross-references: GB:U14169; NID:987224; PIDD:AAA0483.1; PID:6624634  
C/Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat homol  
F/314-386/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 52.5%; Score 42; DB 1; Length 568;  
Best Local Similarity 53.8%; Pred. No. 17;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXXYGNSPKGFAY 13  
| : |||||  
Db 353 CPEKGMPPKGFAY 365

## RESULT 6

probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain H37RV)  
B70749  
C/Species: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C/Accession: B70749  
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A/Reference number: A70500; MUID:98295987; PMID:9634230  
A/Accession: B70749  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-626 <COL>  
A/Cross-references: GB:Z74697; GB:AL123456; NID:93261602; PIDD:CAA98985.1; PID:9140596  
A/Experimental source: strain H37RV  
C/Genetics:  
A/Gene: fadD6  
C/Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology  
F/103-610/Domain: acetate-CoA ligase homology <ACL>

Query Match 52.5%; Score 42; DB 2; Length 626;  
Best Local Similarity 77.8%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YGNSPKGF 12  
| : |||||  
Db 73 YGSDPKGF 81

## RESULT 7

polyadenylate-binding protein (imported) - Guillardia theta nucleomorph  
H90083  
C/Species: nucleomorph Guillardia theta  
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C/Accession: H90083  
R/Douglas, S.; Zanner, S.; Fruhnholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; R  
Nature 410, 1091-1096, 2001  
A/Title: The highly reduced genome of an enslaved algal nucleus.  
A/Reference number: A99082; MUID:11323671; PMID:11323671  
A/Accession: H90083  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-389 <DOU>  
A/Cross-references: GB:AF165818; NID:913794428; PIDD:AAK39803.1; GSPDB:GN00150  
C/Genetics:  
A/Gene: pab1  
A/Map position: 1  
A/Genome: nucleomorph  
C/Keywords: nucleomorph

Query Match 51.2%; Score 41; DB 2; Length 389;  
Best Local Similarity 70.0%; Pred. No. 18;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13  
| : |||||  
DB 222 YNSIPKGFAY 231

## RESULT 8

D70763

threonine ammonia-lyase (BC 4.3.1.19) [liVA [similarity] - Mycobacterium tuberculosis (str

C/Species: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jun-2002

C/Accession: D70763

R/Col: S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Genies, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: D70763

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 14429 <COL>

A/Cross-references: GB:Z74020, GB:AL123456; NID:93261584; PIDN:CAA98332.1; PID:91403463

A/Experimental source: strain H37Rv

C/Genetics:

A/Gene: liVA

C/Superfamily: threonine dehydratase

C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phospho-66/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match

Best Local Similarity 51.2%; Score 41; DB 2; Length 429;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYNSPKGFAY 13  
| : |||||  
DB 88 CSSAGNHACGFAY 100

## RESULT 9

S75579

hypothetical protein sl10804 - Synechocystis sp. (strain PCC 6803)

C/Species: Synechocystis sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 02-Feb-2001

C/Accession: S75579

R/Kaneho, T.; Sato, S.; Kori, H.; Tanaka, A.; Asami, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
sp.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S75579

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1453 <KAN>

A/Cross-references: EMBL:D90911; GB:AB001339; NID:91653083; PIDN:BA18140.1; PID:9165322

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: hypothetical protein sl10804; translation elongation factor Tu homology

C/Keywords: GTP binding; nucleotide binding; P-loop

F/62-176/Domain: translation elongation factor Tu homology <ETU>

F/68-75/Region: nucleotide-binding motif A (P-loop)

F/173-176/Region: GTP-binding NKD motif

F/367-369/Region: GTP-binding SAK/L motif

Query Match

Best Local Similarity 100.0%; Score 41; DB 2; Length 453;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 10  
| : |||||

DB 224 YGNSPKGFAY 230

## RESULT 10

GNME2C

genome polyprotein B - cowpea aphid-borne mosaic virus

N/Comments: 24K viral proteinase (BC 3.4.22.-); 32K proteinase cofactor; 58K membrane-b

C/Species: cowpea aphid-borne mosaic virus, CABMV

C/Date: 18-Apr-1984 #sequence\_revision 18-Apr-1984 #text\_change 31-Mar-2000

C/Accession: A04211

R/Rimomoso, G.P.; Shanks, M.

EMBO J. 2, 2253-2258, 1983

A/Title: The nucleotide sequence of cowpea mosaic virus B RNA.

A/Reference number: A04211

A/Accession: A04211

A/Molecule type: genomic RNA

A/Residues: 1-1866 <LOM>

A/Note: the polyprotein is cleaved to give at least eight mature proteins; however, the

A/Note: the authors translated the codon AAU for residue 630 as Asp, GAG for 844 as Gly

C/Superfamily: cowpea aphid-borne mosaic virus genome polyprotein B

C/Keywords: cysteine proteinase; genome-linked protein; hydrolyase; membrane protein; nu

F/2-326/Product: 32K proteinase cofactor #status predicted <PCR>

F/327-919/Product: 58K membrane-binding protein #status predicted <MBP>

F/920-947/Product: genome-linked protein VPg #status predicted <VPG>

F/948-1155/Product: 24K viral proteinase #status predicted <VPT>

F/1156-1866/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match

Best Local Similarity 51.2%; Score 41; DB 1; Length 1866;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYNSPKGFAY 12  
| : |||||  
DB 285 CYNVGTNSKGFAY 296

## RESULT 11

A41519

posterior-group protein tudor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 24-Sep-1999

C/Accession: A41519; S19019

R/Golumbecki, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.

Genes Dev. 5, 2060-2070, 1991

A/Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel prot

A/Reference number: A41519; MUID:92038995; PMID:1936993

A/Accession: A41519

A/Molecule type: mRNA

A/Residues: 1-2515 <GOL>

A/Cross-references: GB:X62420; NID:98753; PIDN:CAA41286.1; PID:98754

C/Genetics:

A/Gene: tud

C/Superfamily: posterior-group protein tudor

Query Match

Best Local Similarity 51.2%; Score 41; DB 2; Length 2515;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 11  
| : |||||  
DB 2171 YGNSPKGFAY 2178

## RESULT 12

AH3499

hypothetical exported protein BME11982 [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C/Accession: AH3499

R/Belevichio, V.G.; Kapatral, V.; Redkar, R.U.; Patra, G.; Mijer, C.; Lee, T.; Ivanova,  
.; Mazur, M.; Goltzman, R.; Selkov, E.; Elzer, P.H.; Hagins, S.; O'Callaghan, D.; Detef  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AH3439  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-107 <KID>  
 A:Cross-references: GSI:AE008917, PTDN:AAE5353.1; PTD:917984034; GSPDB:GN00190  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BME11982  
 A:Map position: I



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CC EMBL; BC030719; AAH30719.1; -  
CC EMBL; BC030720; AAH30720.1; -  
CC EMBL; BC033602; AAH33602.1; ALT\_INIT.  
CC MGI; MGI:1351866; SLC21A12.  
CC InterPro; IPR004156; OATP\_Nterm.  
CC Pfam; PF03132; OATP\_C; 1.  
CC TIGRfams; TIGR00805; cat; 1.  
CC Transmembrane; Transport; Ion transport; Glycoprotein;  
KW Alternative splicing.  
FT TRANSMEM 103 123 POTENTIAL.  
FT TRANSMEM 142 162 POTENTIAL.  
FT TRANSMEM 171 191 POTENTIAL.  
FT TRANSMEM 231 251 POTENTIAL.  
FT TRANSMEM 265 285 POTENTIAL.  
FT TRANSMEM 311 331 POTENTIAL.  
FT TRANSMEM 387 407 POTENTIAL.  
FT TRANSMEM 426 446 POTENTIAL.  
FT TRANSMEM 456 476 POTENTIAL.  
FT TRANSMEM 581 601 POTENTIAL.  
FT TRANSMEM 627 647 POTENTIAL.  
FT TRANSMEM 670 690 POTENTIAL.  
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 566 566 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 629 632 SING -> TAWG (in isoform 2).  
FT VARSPPLIC 629 632 /FTID=VSP\_006157.  
FT VARSPPLIC 633 723 Missing (in isoform 2).  
FT VARSPPLIC 633 723 /FTID=VSP\_006158.  
SQ SEQUENCE 723 AA; 77668 MW; 0856B45F02C4EBAC CRC64;  
Query Match  
Best Local Similarity 53.8%; Score 43; DB 1; Length 723;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 CXXYGNSPKGRAXXC 16  
Db 94 CLOVNTPKGFLFPLC 109  
-----

RESULT 2  
ID S21C RAT STANDARD; PRT; 723 AA.  
AC Q99N01;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Solute carrier family, 21 member 12 (Sodium-independent organic anion transporter E) (Organic anion transporting polypeptide E) (OATP-E).  
GN SLC21A12 OR OATPE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=21216537; PubMed=11316767;  
RA Fujiwara K., Adachi H., Nishio T., Uno M., Tokui T., Okabe M., Onogawa T., Suzuki T., Asano N., Tanemoto M., Seki M., Shibata K., Suzuki M., Kondo Y., Nunoki K., Shimosegawa T., Iinuma K., Ito S., Matsuo S., Abe T.;  
RT "Identification of thyroid hormone transporters in humans: different molecules are involved in a tissue-specific manner";  
RL Endocrinology 142:2005-2012(2001).  
CC -1- FUNCTION: Mediates the Na(+)-independent transport of organic anions such as the thyroid hormone T3 (triiodo-L-tyronine) and of catecholamine.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.  
CC -----

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CC EMBL; AF239262; AAK30042.1; -  
CC InterPro; IPR004157; OATP\_Cterm.  
CC InterPro; IPR004156; OATP\_Nterm.  
CC Pfam; PF03137; OATP\_C; 1.  
CC Pfam; PF03132; OATP\_N; 1.  
CC TIGRfams; TIGR00805; cat; 1.  
CC Transmembrane; Transport; Ion transport; Glycoprotein.  
KW Transmembrane.  
FT TRANSMEM 103 123 POTENTIAL.  
FT TRANSMEM 143 163 POTENTIAL.  
FT TRANSMEM 171 191 POTENTIAL.  
FT TRANSMEM 234 254 POTENTIAL.  
FT TRANSMEM 268 288 POTENTIAL.  
FT TRANSMEM 314 334 POTENTIAL.  
FT TRANSMEM 387 407 POTENTIAL.  
FT TRANSMEM 426 446 POTENTIAL.  
FT TRANSMEM 486 476 POTENTIAL.  
FT TRANSMEM 581 601 POTENTIAL.  
FT TRANSMEM 627 647 POTENTIAL.  
FT TRANSMEM 669 689 POTENTIAL.  
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 566 566 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 723 AA; 77633 MW; DB857B514654497B CRC64;  
Query Match  
Best Local Similarity 43.8%; Score 43; DB 1; Length 723;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 CXXYGNSPKGRAXXC 16  
Db 94 CLOVNTPKGFLFPLC 109  
-----

RESULT 3  
ID PD26 MYCTU STANDARD; PRT; 583 AA.  
AC Q10976;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Purative fatty-acid--COA ligase fadD26 (BC 6.2.1.-) (Acyl--COA synthetase)  
GN FAD26 OR RV2930 OR MT2999 OR MYCY338.19.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37Kv;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers R., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence";  
RL Nature 393:537-544(1998).  
CC [2]  
CC SEQUENCE FROM N.A.  
CC STRAIN=CDC 1551 / Oshkosh;  
CC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Paterson J.F., Deboy R., Dodson R., Gwynn M.L., Haft D., Hickey E.,  
RA Kolonel J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Uitterlind T., Weidman J., Knouri H., Gill J., Mikula A.,  
RA Bishai W.,  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains",  
RL Submitted (Apr-2001) to the EMBL/GenBank/DBS databases.  
CC -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME  
CC FAMILY.  
CC -----  
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CC -----  
DR EMBL; Z74697; CAA98985.1; ALT INIT.  
DR EMBL; AE007122; AAK47327.1; -  
DR TIGR; MT2989; -  
DR Tuberculaet; Rv2930; -  
DR InterPro; IPR000873; AMP-bind.  
DR Pfam; PF00501; AMP-binding; 1.  
DR PROSITE; PS00455; AMP BINDING; FALSE NEG.  
KW Hypothetical protein; Ligase; Fatty acid metabolism;  
KW Complete proteome.  
SQ SEQUENCE 583 AA; 63043 MW; F970C6E19B217435 CRC64;

	Query Match	Best Local Similarity	Score 42:	DB 1:	Length 583:
	Matches	7:	Pred. No. 7:	Mismatches 1:	Indels 0:
QY	4	YGNSPKGF	12		
	:				
DB	30	YGNSPKGF	38		

THD1_MYCTU	STANDARD;	PRT;	429 AA.
AC Q10766;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DE Probable threonine dehydratase biosynthetic (EC 4.3.1.19) (threonine deaminase).			
DE ILVA OR RV1559 OR MT1610 OR MTCV48.06C.			
GN Mycobacterium tuberculosis.			
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX NCBI_TaxID=1773;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=H37R;			
RX MEDLINE=98295987; PubMed=9634230;			
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA Gordon S.V., Eigmeier K., Gao S., Barry C.E. III, Tekala F.,			
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,			
RA Hornsby T., Jasek K., Krogsh A., Molan J., Moule S., Murphy L.,			
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA Rutter S., Seeger K., Skellern S., Squares R.,			
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;			
RT "Deciphering the biology of Mycobacterium tuberculosis from the			
RT complete genome sequence."			
RL Nature 393:537-544 (1998).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CDC 1551 / Oshkosh;			
RA Fleischmann R., Doby R., Alland D., Eisen J.A., Carpenter L., White O.,			
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			

RA Delcher A., Utechtack T., Weidman J., Khouri H., Gill J., Mikula A.,  
RT Blahel W.,  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains." ;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
CC theonine in a two-step reaction. The first step is a dehydration  
CC of theonine, followed by rehydration and liberation of ammonia.  
CC -1- CATALYTIC ACTIVITY: L-theonine + 2-oxobutanoate + NH(3).  
CC -1- COFACTOR: Pyridoxal phosphate (by oxobutanoate).  
CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
CC -----  
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DR	EMBL	Z74020	CAA98332.1	-	-
DR	EMBL	AB007027	AAK45877.1	-	-
DR	PIR	D70763	D70763	-	-
DR	HSSP	P04968	ITDJ	-	-
DR	TIGR	MT1610	-	-	-
DR	TubercuList	Bv1559	-	-	-
DR	InterPro	IPR001926	B6 enzyme_beta	-	-
DR	InterPro	IPR000634	S/T_denhydrtse	-	-
DR	InterPro	IPR001721	Thrdh_C	-	-
DR	Pfam	PF00291	PALP_1	-	-
DR	Pfam	PF00585	Thx dehydrat_C_1	-	-
DR	PROSITE	PS00165	DEHYDRATASE_SER_THR_1	-	-
KW	Isolaccine biosynthesis; lyase; pyridoxal phosphate; Complete proteome.				
KW	BINDING				
FT	DOMAIN	66	66	PYRIDOXAL PHOSPHATE (BY SIMILARITY).	
FT	DOMAIN	145	149	FOLY-ALA.	
FT	DOMAIN	196	199	FOLY-GLY.	
SO	SEQUENCE	429 AA	45041 MW	DOCG1EC258AC521 CRC64	

Query Match	51.2%	Score 41;	DB 1;	Length 429;
Best Local Similarity	53.8%	Pred. No	7.7,	
Matches	7;	Conservative	1;	Mismatches 5;
				Indels 0;
				Gaps 0.
QY	1	CXYGNSKPKFAY	13	
Db	88	CSAGAGGAGFAY	100	

	RESULT 5
VGNB_CPMV	VGNB_CPMV
ID	VGNB_CPMV
AC	P03600;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Genome polypeptin B [contains: Protease cofactor; Membrane binding protein; VP6; Protease (EC 3.4.22.-); RNA polymerase (EC 2.7.7.48)].
OS	Compea mosaic virus (CPMV).
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
CC	Comovirus.
OX	NCBI_TaxID=12264;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Lomonosoff G.P., Shanks M.;
RT	"The nucleotide sequence of cowpea mosaic virus B RNA.";
BL	EMBO J. 2:2253-2258(1983).
CC	-1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC	{RNA}(N).
CC	-1- PFM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC	-1- SIMILARITY: TO OTHER COMOVIRUSES GENOME POLYPEPTIN B.
CC	-----
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EMBL; X00206; CAA25029.1; -.  
 DR PIR; A04211; GNM23C.  
 DR MEROPS; C03.003; -.  
 DR InterPro; IPR004004; Calic1 pol hel.  
 DR InterPro; IPR006065; RNA helicase.  
 DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
 DR InterPro; IPR01205; RNA\_pol\_PSD.  
 DR InterPro; IPR007094; RNA\_pol\_PSV1r.  
 DR Pfam; PF00680; RNA dep RNA pol; 1.  
 DR Pfam; PF00910; RNA helicase; 1.  
 DR PRINTS; PR00918; CALICITRUS.  
 DR Polypeptide; Transmembrane; Hydrolase; Protease; Transferase;  
 KM RNA-directed RNA polymerase; ATP-binding.  
 FT CHAIN 1 326  
 FT CHAIN 327 919  
 FT CHAIN 920 947  
 FT CHAIN 948 1155  
 FT CHAIN 1156 1866  
 FT NP BIND 494 501  
 FT ACT\_SITE 987 987  
 FT ACT\_SITE 1023 1023  
 FT ACT\_SITE 1113 1113  
 SQ SEQUENCE 1866 AA; 209809 MW; 0D4CD8A11C0B2976 CRC64;

Query Match 51.2%; Score 41; DB 1; Length 1866;  
 Best Local Similarity 58.3%; Pred. No. 32;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNSEKQPA 12  
 DB 285 CXXYGNSEKQPA 296

RESULT 6  
 TUD\_DROME STANDARD; PRT; 2515 AA.  
 AC P25823;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Maternal tudor protein.  
 GN TUD.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92038995; PubMed=1936993;  
 RA Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.,  
 RT "Tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel protein and an mRNA localized during mid-oogenesis.",  
 RL Genes Dev. 5:2060-2070(1991).  
 CC -1- PUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.  
 CC -1- MISCELLANEOUS: THE TUD mRNA ACCUMULATES WITHIN THE POSTERIOR REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES OF OOGENESIS.  
 CC -1- SIMILARITY: Contains 9 tudor domains.

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EMBL; X62420; CAA4286.1; -.  
 DR PIR; A41519; A41519.  
 DR HSP; Q16637; 1G5V.  
 DR FlyBase; FBgn0003891; tud.  
 DR GO; GO:0019090; Mitochondrial rRNA, mitochondrial export; IMP.  
 DR GO; GO:0007315; Ribosome assembly; IMP.  
 DR InterPro; IPR001097; Maternal\_tudor.  
 DR InterPro; IPR002999; Tudor.  
 DR Pfam; PF00567; TUDOR; 10.  
 DR SMART; SM00333; TUDOR; 10.  
 DR PROSITE; PS50304; TUDOR; 9.  
 KW Developmental protein; Repeat.  
 FT DOMAIN 455 513  
 FT DOMAIN 641 696  
 FT DOMAIN 1062 1122  
 FT DOMAIN 1355 1414  
 FT DOMAIN 1662 1718  
 FT DOMAIN 1839 1898  
 FT DOMAIN 2023 2082  
 FT DOMAIN 2211 2269  
 FT DOMAIN 2392 2451  
 SQ SEQUENCE 2515 AA; 285236 MW; 683C100D308BADA CRC64;

Query Match 51.2%; Score 41; DB 1; Length 2515;  
 Best Local Similarity 87.5%; Pred. No. 43;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKPF 11  
 DB 2171 YGNSPKPF 2178

RESULT 7  
 KV3G\_HUMAN STANDARD; PRT; 109 AA.  
 AC P04206;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region GOL (Rheumatoid factor).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86230578; PubMed=3086710;  
 RA Newkirk M., Chen P.F., Carson D.A., Posnett D., Capra J.D.,  
 RT "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotype group, in part predicted by its RT reactivity with anti-peptide antibodies.",  
 RL Mol. Immunol. 23:239-244(1986).  
 DR PIR; A01893; K3HUGO.  
 DR HSP; P80362; 1WTL.  
 DR GO; GO:000576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.

Query Match 50.0%; Score 40; DB 1; Length 109;  
 FT NON\_TER 23 89  
 FT DISURTD 109 109  
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Best Local Similarity 54.5%; Pred. No. 3.1;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSEKGF 11  
| | | | |  
89 CQVGSSEPSRF 99

RESULT 8  
METX SCHPO STANDARD; PRT; 382 AA.  
AC 060158;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
adenosyltransferase) (Adomet synthetase).  
GN SAM1 OR SPBC14F5.05C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Baktaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
[1]  
RN SEQUENCE FROM N.A., AND FUNCTION.  
RP MEDLINE=20083020; PubMed=10620770;  
RA Hilti N., Graub R., Jorg M., Arnold P., Schweingruber A.M.,  
Schweingruber M.E.;  
RT "Gene sam1 encoding adenosylmethionine synthetase: effects of its  
expression in the fission yeast Schizosaccharomycetes pombe.";  
RL Yeast 16:1-10(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21848401; PubMed=11859360;  
RC STRAIN=972;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
Holtroyd S., Hornsby T., Howarth S., Huckle E.D., Hunt S., Jagsels K.,  
James K., Jones L., Jones M., Leacher S., McDonald S., McLean J.,  
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odel C.,  
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,  
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
Woodward J., Voiclaert G., Aert R., Robben J., Grymopiez B.,  
Wetjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S.,  
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
Eger F., Zimmermann W., Weiler H., Wambutt K., Purnelle B.,  
Goffeau A., Cadieu B., Dreano S., Gloux S., Laureau V., Mottier S.,  
Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,  
Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Rhode G.,  
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
Cerrutti L., Lome T., McCamble W.R., Paulsen I., Potashkin J.,  
Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;  
RA "The genome sequence of Schizosaccharomycetes pombe.";  
RT Nature 415:871-880(2002).  
RL  
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP  
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2O) = phosphate +  
S-adenosyl-L-methionine.  
CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -1- PATHWAY: Activated methyl cycle.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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CC -----

DR EMBL, AJ001705; CA04941.1; -.  
DR EMBL, AJ023780; CA019323.1; -.  
DR PIR, T39451; T39451.  
DR HSP, P04384; IMXB.  
DR GenDB\_Spombe; SPBC14F5.05C; -.  
DR InterPro; IPR002133; S-Adomet synt.  
DR Pfam; PF00438; S-Adomet\_synt.1.  
DR Pfam; PF02772; S-Adomet\_synt2.1.  
DR Pfam; PF02773; S-Adomet\_syntD3.1.  
DR TIGRFAMs; TIGR01034; metK.1.  
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
KM Transferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;  
KM Metal-binding.  
FT NP BIND 118 123 ATP (POTENTIAL).  
FT METAL 18 18 MAGNESIUM (BY SIMILARITY).  
FT METAL 44 44 POTASSIUM (BY SIMILARITY).  
FT METAL 270 270 POTASSIUM (BY SIMILARITY).  
FT METAL 278 278 MAGNESIUM (BY SIMILARITY).  
FT BINDING 146 146 ATP (POTENTIAL).  
SQ SEQUENCE 382 AA; 41831 MW; 9970A9D1195C5738 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 382;  
Best Local Similarity 53.8%; Pred. No. 10;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXKC 16  
| | | | |  
Db 79 YDSEKGFYKTC 91

RESULT 9  
METX YEAST STANDARD; PRT; 382 AA.  
AC P10659;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 5-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine  
adenosyltransferase 1) (Adomet synthetase 1).  
GN SAM1 OR ETH10 OR YLR180W OR L9470.9.  
OS Saccharomycetes cerevisiae (Baker's Yeast).  
OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN  
RN SEQUENCE FROM N.A.  
RP MEDLINE=88059059; PubMed=3316224;  
RA Thomas D., Surdin-Kerjan Y.;  
RT "SAM1, the structural gene for one of the S-adenosylmethionine  
synthetases in Saccharomycetes cerevisiae. Sequence and expression.";  
RL J. Biol. Chem. 262:16704-16709(1987).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=S288c / AB972;  
RC MEDLINE=97313257; PubMed=9169871;  
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,  
Benes V., Ernekner M., Dellus H., Dubois E., Duysterhoft A.,  
Britten K.-D., Floeth M., Goffeau A., Heblin U., Heumann K.,  
Hous-Nelzel D., Hilbert H., Hilger F., Kleene K., Koester P.,  
Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,  
Mueller-Auer S., Neuwirth U., Obermaier B., Pirvandi E., Pohl T.M.,  
Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,  
Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,  
Underwood A.P., Urestratanz L.A., Vandenbol M., Verhaaselt P.,  
Vierdel S., Voet M., Voiclaert G., Voss R., Wambutt R., Weiler E.,  
Weiler H., Zimmermann F.K., Zollner A., Hani J., Hebeisel J.D.;  
RA "The nucleotide sequence of Saccharomycetes cerevisiae chromosome XII.";

```

RL Nature 367:87-90(1997).
RN [3]
RN SEQUENCE OF 157-162, 187-196 AND 253-258.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae."
RL FEMS Microbiol. Lett. 137:1-8(1996).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (by similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Heterotrimer.
CC -1- MISCELLANEOUS: IN YEAST, THERE ARE TWO GENES CODING FOR ADOMET
CC SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: J03477; AAA66932.1; -
DR EMBL: U1246; AAB67461.1; -
DR PIR: S51425; S51425.
DR HSSP: P04384; 1MXB.
DR SGD: S0004170; 1MXB.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0004476; F:methionine adenosyltransferase activity; IGI.
DR InterPro: IPR002133; S-AdoMet_synth.
DR Pfam: PF00438; S-AdoMet_synth2; 1.
DR Pfam: PF02772; S-AdoMet_synth2; 1.
DR Pfam: PF02773; S-AdoMet_synth3; 1.
DR TIGRfam: TIGR01034; metK; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding;
DR Magnesium; Potassium; Metal-binding.
DR NP BIND 118 123 ATP (POTENTIAL).
DR METAL 18 18 MAGNESIUM (BY SIMILARITY).
DR METAL 44 44 POTASSIUM (BY SIMILARITY).
DR METAL 270 270 POTASSIUM (BY SIMILARITY).
DR METAL 278 278 MAGNESIUM (BY SIMILARITY).
DR BINDING 146 146 ATP (POTENTIAL).
DR CONFLICT 246 246 A -> T (IN REF. 1).
DR CONFLICT 357 357 I -> F (IN REF. 1).
DR SEQUENCE 382 AA; 41018 MW; 18F828C89BE4706 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 382;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGAYXXC 16
DB 79 YDSAKGPDYKTC 91

RESULT 10
METL_YEAST STANDARD; PRT; 383 AA.
AC P19358;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (AdoMet synthetase 2).

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GN SAM2 OR ETH2 OR YDR502C OR D9719.8.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89218973; PubMed=3072475;
RA Thomas D., Rothstein R., Rosenberg N., Surdin-Kerjan Y.;
RT "SAM2 encodes the second methionine S-adenosyl transferase in
RT Saccharomyces cerevisiae: physiology and regulation of both
RT enzymes."
RL Mol. Cell. Biol. 8:5132-5139(1988).
RN [2]
RN SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Benito A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkeler-Smith S., Hyman R., Komp C., Lebkardt D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yellon M., Botstein D., Davis R.W.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RN ACETYLATION.
RA Garrett J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner U.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (by similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Heterotrimer.
CC -1- MISCELLANEOUS: IN YEAST, THERE ARE TWO GENES CODING FOR ADOMET
CC SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M23368; AAA35017.1; -
DR EMBL: U33057; AAB64944.1; -
DR PIR: A31398; A31398.
DR HSSP: P04384; 1MXB.
DR SGD: S0002910; SAM2.
DR InterPro: IPR002133; S-AdoMet_synth.
DR Pfam: PF00438; S-AdoMet_synth; 1.
DR Pfam: PF02772; S-AdoMet_synth2; 1.
DR Pfam: PF02773; S-AdoMet_synth3; 1.
DR TIGRfam: TIGR01034; metK; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding;
DR Acetylation; Magnesium; Potassium; Metal-binding.
DR NP BIND 0 0
DR METAL 19 19 MAGNESIUM (BY SIMILARITY).
DR METAL 45 45 POTASSIUM (BY SIMILARITY).
DR METAL 271 271 POTASSIUM (BY SIMILARITY).
DR METAL 279 279 MAGNESIUM (BY SIMILARITY).
DR MOD RES 1 1 ACETYLATION.
DR NP BIND 119 124 ATP (POTENTIAL).
DR BINDING 147 147 ATP (POTENTIAL).
DR SEQUENCE 383 AA; 42124 MW; 466879d27578e0b1 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 383;
Best Local Similarity 53.8%; Pred. No. 10;

```

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAVXXC 16  
DB 80 YDPSAKGFDYKTC 92

## RESULT 11

MEIK ASCIM STANDARD; PRT; 393 AA.

AC P50304;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-SEP-2003 (Rel. 41, Last annotation update)

DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine

adenosyltransferase) (Adomet synthetase).

OS Ascomycota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;

OC Pezizales; Ascombolaceae; Ascombolus.

OX NCBI\_TaxID=5191;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RN42;

RX MEDLINE=96200878; PubMed=8621082;

RA Maurino M.R., Goyon C., Rosa A.L.;

RT "Cloning and sequence of the Ascombolus immitis S-adenosyl-L-

methionine synthetase-encoding gene."

RU Gene 170:155-156(1996).

CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM

CC -1- METHIONINE AND ATP.

CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +

CC -1- dihydrophosphate + S-adenosyl-L-methionine.

CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and

CC -1- potassium ion per subunit (By similarity).

CC -1- PATHWAY: Activated methyl cycle.

CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.

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CC -----

CC EMBL: U21548; AAB03805.1; -.

CC HSSP: P04384; IMXB.

CC InterPro: IPR002133; S-Adomet synt.

CC Pfam: PF00438; S-Adomet synt. 1.

CC Pfam: PF02772; S-Adomet syntd2; 1.

CC Pfam: PF02773; S-Adomet syntd3; 1.

CC TIGRPFAMs: TIGR01034; metK; 1.

CC PROSITE: PS00376; ADOMET SYNTHETASE 1; 1.

CC PROSITE: PS00377; ADOMET SYNTHETASE 2; 1.

CC Transerferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;

CC Metal-binding.

CC NP BIND 127 132 ATP (POTENTIAL).

CC METAL 27 27 MAGNESIUM (BY SIMILARITY).

CC METAL 53 53 POTASSIUM (BY SIMILARITY).

CC METAL 279 279 POTASSIUM (BY SIMILARITY).

CC METAL 287 287 MAGNESIUM (BY SIMILARITY).

CC SEQUENCE 393 AA; 43010 MW; 88FB2F2F14B751C3 CRC64;

Query March 50.0%; Score 40; DB 1; Length 393;  
Best Local Similarity 53.8%; Pred. No. 11;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAVXXC 16  
DB 88 YDPSAKGFDYKTC 100

RESULT 12

MEIK HUMAN STANDARD; PRT; 395 AA.  
AC P31153;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine  
adenosyltransferase) (Adomet synthetase) (MAT-II).  
GN MAT2A OR MAT2A2 OR AMS2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=93050159; PubMed=1426236;  
RA Horikawa S., Tsukada K.;  
RT "Molecular cloning and developmental expression of a human kidney S-  
adenosylmethionine synthetase."

FEBS Lett. 312:37-41(1992).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marinsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sapleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulik S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Bailey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzyzanski M.I., Skalka U., Smilins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
CC -1- METHIONINE AND ATP.  
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
CC -1- dihydrophosphate + S-adenosyl-L-methionine.  
CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
CC -1- potassium ion per subunit (By similarity).  
CC -1- PATHWAY: Activated methyl cycle.  
CC -1- SUBUNIT: Homodimer.  
CC -1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT  
CC AND BETR ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY  
CC DISTRIBUTED IN EXTRAPARATIC TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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CC -----

CC EMBL: X68836; CAA48726.1; -.

CC EMBL: BC001686; AAH01686.1; -.

CC EMBL: BC001854; AAH01854.1; -.

CC FIR: S27257; S27257.

CC HSSP: P04384; IMXB.

CC Genew; HGNC:6904; MAT2A.

DR MIM; 601468; -  
 DR GO; GO:0004478; F-methionine adenosyltransferase activity; TRS.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF0438; S-AdoMet\_synth; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth2; 1.  
 DR Pfam; PF02773; S-AdoMet\_synth3; 1.  
 DR TIGRfam; TIGR01034; metX; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_2; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_1; 1.  
 DR TRANSFERASE; One-carbon metabolism; Magnesium; Potassium;  
 KM Metal-binding; Multigene family; ATP-binding;  
 FT NP BIND 131 136  
 FT METAL 31 31 MAGNESIUM (BY SIMILARITY).  
 FT METAL 57 57 POTASSIUM (BY SIMILARITY).  
 FT METAL 283 283 POTASSIUM (BY SIMILARITY).  
 FT METAL 281 281 MAGNESIUM (BY SIMILARITY).  
 FT BINDING 159 159 ATP (POTENTIAL).  
 SQ SEQUENCE 395 AA; 43660 MW; 2E7D1B91CC4F7BDD CRC64;  
 Query Match 50.0%; Score 40; DB 1; Length 395;  
 Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 4 YGNSPKGFAYXXC 16  
 DB 92 YDSSKSGFDYKTC 104  
 RESULT 13  
 METK NEUCR STANDARD; PRT; 395 AA.  
 AC P48466;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) [Methionine  
 adenosyltransferase] (AdoMet synthetase).  
 GN ETH-1.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5111;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Microbial;  
 RX MEDLINE=97002541; PubMed=884988;  
 RA Mautino M.R., Barra J.L., Rosa A.L.;  
 RT "eth-1, the Neurospora crassa locus encoding S-adenosylmethionine  
 synthetase: molecular cloning, sequence analysis and in vivo  
 overexpression".  
 RL Genetics 142:789-800 (1996).  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 METHIONINE AND ATP.  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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 CC -----  
 DR EMBL; U21547; AAC49260.1; -  
 DR PIR; S65800; S65800.  
 DR HSSP; P04384; IWK.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF00438; S-AdoMet\_synth; 1.

DR Pfam; PF02772; S-AdoMet\_synth2; 1.  
 DR Pfam; PF02773; S-AdoMet\_synth3; 1.  
 DR TIGRfam; TIGR01034; metX; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_2; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_1; 1.  
 DR TRANSFERASE; One-carbon metabolism; ATP-binding; Magnesium; Potassium;  
 KM Metal-binding;  
 FT NP BIND 130 135  
 FT METAL 30 30 MAGNESIUM (BY SIMILARITY).  
 FT METAL 56 56 POTASSIUM (BY SIMILARITY).  
 FT METAL 282 282 POTASSIUM (BY SIMILARITY).  
 FT METAL 290 290 MAGNESIUM (BY SIMILARITY).  
 FT BINDING 158 158 ATP (POTENTIAL).  
 SQ SEQUENCE 395 AA; 42986 MW; 8CF95CED9831AF0F CRC64;  
 Query Match 50.0%; Score 40; DB 1; Length 395;  
 Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 4 YGNSPKGFAYXXC 16  
 DB 91 YDSSKSGFDYKTC 103  
 RESULT 14  
 METK RAT STANDARD; PRT; 395 AA.  
 AC P18298;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) [Methionine  
 adenosyltransferase] (AdoMet synthetase) (MAT-II).  
 GN MAT2A OR AMS2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Kidney;  
 RX MEDLINE=90337979; PubMed=1696256;  
 RA Horikawa S., Saenga J., Shimizu K., Ozasa H., Tsukada K.;  
 RT "Molecular cloning and nucleotide sequence of cDNA encoding the rat  
 kidney S-adenosylmethionine synthetase".  
 RL J. Biol. Chem. 265:13683-13686 (1990).  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 METHIONINE AND ATP.  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT  
 FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA  
 AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY  
 DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM  
 PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY  
 REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
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CC -----  
 DR EMBL; J05571; AAA42106.1; -  
 DR EMBL; AB000717; BAA19170.1; -  
 DR EMBL; AB000716; BAA19170.1; JOINED.  
 DR PIR; A37118; A37118.  
 DR HSSP; P04384; 1MXB.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF00438; S-AdoMet\_synth; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth2; 1.  
 DR Pfam; PF02773; S-AdoMet\_synth3; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 DR Transferrase; One-carbon metabolism; Magnesium; Potassium;  
 KM Metal-binding; Multigene family; ATP-binding.  
 FT NP BIND 131 136  
 FT METAL 31 31 MAGNESIUM (BY SIMILARITY).  
 FT METAL 57 57 POTASSIUM (BY SIMILARITY).  
 FT METAL 283 283 POTASSIUM (BY SIMILARITY).  
 FT METAL 291 291 MAGNESIUM (BY SIMILARITY).  
 FT BINDING 159 159 ATP (POTENTIAL).  
 SQ SEQUENCE 395 AA; 43715 MW; 4DA9AFABF7D09CT9 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 395;  
 Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Oy 4 YGNSPKGFAYXXC 16  
 Db 92 YDSSKGFYKTC 104

RESULT 15  
 METK\_CAEEL  
 ID METK\_CAEEL STANDARD; PRT; 404 AA.  
 AC P50305;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Probable S-adenosylmethionine synthetase CO6E7.1 (EC 2.5.1.6)  
 DE (Methionine adenosyltransferase) (AdoMet synthetase).  
 GN CO6E7.1.  
 OS Caenorhabditis elegans.  
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 CC Rhabditidae; Pelodicerinae; Caenorhabditis.  
 CX NCBI\_taxid=6239;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA le T.T.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC dihydrophosphate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 CC 1 potassium ion per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR HSSP; P04384; 1MXB.  
 DR WormPep; CO6E7.1; CE03957.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF00438; S-AdoMet\_synth; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth2; 1.  
 DR Pfam; PF02773; S-AdoMet\_synth3; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 DR Hypothetical protein; Transferrase; One-carbon metabolism; Magnesium;  
 KM Potassium; Metal-binding; Multigene family; ATP-binding.  
 FT NP BIND 119 124  
 FT METAL 19 19 MAGNESIUM (BY SIMILARITY).  
 FT METAL 45 45 POTASSIUM (BY SIMILARITY).  
 FT METAL 271 271 POTASSIUM (BY SIMILARITY).  
 FT METAL 279 279 MAGNESIUM (BY SIMILARITY).  
 FT BINDING 147 147 ATP (POTENTIAL).  
 SQ SEQUENCE 404 AA; 44034 MW; 4F7891933B46E2C8 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 404;  
 Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Oy 4 YGNSPKGFAYXXC 16  
 Db 80 YDSSKGFYKTC 92

Search completed: November 7, 2003, 07:28:09  
 Job time : 2.15354 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 : Search time 5.27637 Seconds  
(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-105

Perfect score: 80  
Sequence: 1 CXXYGNPKGFAYXXC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protect:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44	55.0	120 11 Q920B8	Q920B8 mus musculi
2	44	55.0	205 5 Q93233	Q93233 ctenodactyl
3	44	55.0	292 11 Q8CCS6	Q8CCS6 mus musculi
4	44	55.0	302 11 Q35935	Q35935 mus musculi
5	44	55.0	306 4 Q43484	Q43484 homo sapien
6	44	55.0	306 6 Q28165	Q28165 bos taurus
7	43	53.8	294 16 Q8XN61	Q8XN61 clostridium
8	43	53.8	723 11 Q8BZT4	Q8BZT4 mus musculi
9	42	52.5	160 3 Q9UTU1	Q9UTU1 schizosacch
10	42	52.5	166 3 Q14327	Q14327 xenopus lae
11	42	52.5	296 13 Q9BZB7	Q9BZB7 homo sapien
12	42	52.5	491 4 Q9BZB7	Q9BZB7 homo sapien
13	42	52.5	559 13 Q9YX5	Q9YX5 brachydanio
14	42	52.5	559 13 Q9BZB5	Q9BZB5 carassius a
15	42	52.5	561 11 P70166	P70166 mus musculi
16	42	52.5	566 4 Q9BZB8	Q9BZB8 homo sapien

17	42	52.5	568 13 Q91572	Q91572 xenopus lae
18	42	52.5	600 13 Q93386	Q93386 brachydanio
19	42	52.5	833 3 Q13620	Q13620 schizosacch
20	41	51.2	389 8 Q9BRZ7	Q9BRZ7 guillardi
21	41	51.2	453 16 P74064	P74064 synecocyst
22	41	51.2	2515 16 Q9W238	Q9W238 drosophila
23	40	50.0	107 16 Q8IE96	Q8IE96 bruceella me
24	40	50.0	107 16 Q8FYV1	Q8FYV1 bruceella su
25	40	50.0	211 5 Q8MU02	Q8MU02 heterodera
26	40	50.0	291 5 Q9VTH9	Q9VTH9 drosophila
27	40	50.0	359 3 Q12642	Q12642 neurospora
28	40	50.0	385 3 Q9P842	Q9P842 candida alb
29	40	50.0	395 11 Q95057	Q95057 mus musculi
30	40	50.0	1312 16 Q98NH6	Q98NH6 rhizobium 1
31	39.5	49.4	570 5 Q9ML49	Q9ML49 clona savig
32	39.5	49.4	1787 16 Q8YWI8	Q8YWI8 anabaena sp
33	39.5	49.4	1800 16 Q8YFRO	Q8YFRO anabaena sp
34	39	48.8	218 17 Q9HSS2	Q9HSS2 halobacteri
35	39	48.8	318 10 Q9STN8	Q9STN8 arabidopsis
36	39	48.8	401 16 Q9KXK6	Q9KXK6 vibrio chol
37	39	48.8	594 5 Q97131	Q97131 leishmania
38	39	48.8	751 12 Q8QPH3	Q8QPH3 influenza a
39	38.5	48.1	120 12 Q9J5A6	Q9J5A6 fowlpox vir
40	38	47.5	95 10 Q24C39	Q24C39 solanum tub
41	38	47.5	223 16 Q98ND7	Q98ND7 rhizobium 1
42	38	47.5	224 5 Q9V308	Q9V308 drosophila
43	38	47.5	224 5 Q27926	Q27926 drosophila
44	38	47.5	252 5 P91951	P91951 heliocidari
45	38	47.5	402 16 Q99RS8	Q99RS8 staphylococ

#### ALIGNMENTS

RESULT 1	Q920B8	PRELIMINARY;	PRT;	120 AA.
ID	Q920B8			
AC	Q920B8			
DT	01-DEC-2001 (TREMURel. 19, Created)			
DT	01-DEC-2001 (TREMURel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMURel. 23, Last annotation update)			
DE	Pterin-mimicking anti-idiotypic heavy chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RY	[1]			
RP	SEQUENCE FROM N.A.			
RA	Artin J.D., Iape A., Jennings I.G., Horatius O., Cotton R.G.H.;			
RT	"Definition of the Idiotypic of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF307936; AA09420.1; -			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	SMART; SM00406; IG_V.1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE			
	120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;			
Query Match	55.0%; Score 44; DB 11; Length 120;			
Best Local Similarity	80.0%; Pred. No. 2.6;			
Matches	8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	4 YGNSPKGFAY 13			
DB	101 YGNSPKGFAY 110			

## RESULT 2

Q93233 PRELIMINARY; PRT; 205 AA.  
 AC Q93233;  
 DT 01-FEB-1997 (TRENBLREL. 02, Created)  
 DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
 DE C17E4.5 protein.  
 GN C17E4.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxId=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Percy C.M.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9069613; PubMed=9851916;  
 RA none;  
 RT "Genomic sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z81037; CAB02750.1; -.  
 DR WormPep; C17E4.5; CE08254.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rrm; 1.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS0102; RRM; 1.  
 DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
 SQ SEQUENCE 205 AA; 22603 MW; F6845A30DCPF7746 CRC64;

Query Match 55.0%; Score 44; DB 5; Length 205;  
 Best Local Similarity 53.8%; Pred. No. 4.6;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNPKGFAY 13  
 DB 111 CDKFGHPKGFAY 123

## RESULT 3

Q8CCS6 PRELIMINARY; PRT; 292 AA.  
 AC Q8CCS6;  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
 DE Poly.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
 RX MEDLINE=22354683; PubMed=1246851;  
 RA The FANTOM Consortium.  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RL EMBL; AK032172; BAC27741.1; -.  
 SQ SEQUENCE 292 AA; 31044 MW; 0874042BA4A60A2A CRC64;

Query Match 55.0%; Score 44; DB 11; Length 292;  
 Best Local Similarity 53.8%; Pred. No. 6.7;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNPKGFAY 13  
 DB 201 CDKFGHPKGFAY 213

## RESULT 4

O35935 PRELIMINARY; PRT; 302 AA.  
 AC O35935;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)  
 DE Poly(A) binding protein II.  
 GN PABP1 OR MPB1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=98094238; PubMed=9434149;  
 RA Lee Y.-J., Yang I.-C., Hahn Y., Lee Y., Chung J.H.;  
 RT "Genomic structure and expression of murine poly(A) binding protein II  
 RT gene."  
 RL Biochim. Biophys. Acta 1395:40-46(1998).  
 DR EMBL; U93050; AAC00210.1; -.  
 DR MGD; MGI:1859158; Pabp1.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rrm; 1.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS0102; RRM; 1.  
 DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
 SQ SEQUENCE 302 AA; 32296 MW; 2F0F6F7CC19C1986 CRC64;

Query Match 55.0%; Score 44; DB 11; Length 302;  
 Best Local Similarity 53.8%; Pred. No. 6.9;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNPKGFAY 13  
 DB 201 CDKFGHPKGFAY 213

## RESULT 5

O43484 PRELIMINARY; PRT; 306 AA.  
 AC O43484;  
 DT 01-JUN-1998 (TRENBLREL. 06, Created)  
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)  
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)  
 DE Poly(A) binding protein II (similar to poly(A)-binding protein,  
 DE nuclear 1).  
 GN PABP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9812579; PubMed=9462747;  
 RA Brails B., Boucharde J.-P., Xie Y.-G., Rochefort D.L., Chretien N.,  
 RA Tome F.M.S., Lafreniere R.G., Rommens J.M., Uyama E., Nohira O.,  
 RA Blumen S., Koryn A.D., Heutink P., Mathieu J., Durancieu A.,  
 RA Codere F., Fardieu M., Rouleau G.A.;  
 RT "Short GCG expansions in the PABP2 gene cause oculopharyngeal muscular  
 RT dystrophy."  
 RL Nat. Genet. 18:164-167(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026029; AAC39596.1; -.  
 DR EMBL; BC010939; AA010939.1; -.  
 DR Genew; HGNC:8565; PABPN1.

1D	Q9UT01	PRELIMINARY;	PRT;	160 AA.
AC	Q9UT01			
DT	01-MAY-2000 (TREMBArel.13, Created)			
DT	01-MAY-2000 (TREMBArel.13, Last sequence update)			
DT	01-MAR-2003 (TREMBArel.23, Last annotation update)			
DE	Hypothetical 18.1 kDa protein (Fragment).			
GN	2257512.			
OS	Schizosaccharomyces pombe (fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=968 H90;			
RX	MEDLINE=20223866; PubMed=10759889;			
RA	Hing D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,			
RA	Hiraka Y.;			

RT "Large-scale screening of intracellular protein localization in living  
RT fission yeast cells by the use of a GFP-fusion genomic DNA library."  
RL Genes Cells 5:169-190(2000).  
DR EMBL: AB028003; BAA87307.1; -.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00076; rrm; 1.  
DR SMART: SM00360; RRM; 1.  
DR PROSITE: PS0102; RRM; 1.  
DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
KW Hypothetical protein.  
FT NON\_TER 1  
FT SEQUENCE 160 AA; 18116 MW; 169A1FD5D5A94F5 CRC64;  
SQ

Query Match 52.5%; Score 42; DB 3; Length 160;  
Best Local Similarity 87.5%; Pred. No. 8.1;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSPKGFAY 13  
DB 58 NPKGFAY 65

RESULT 10  
014327 PRELIMINARY; PRT; 166 AA.

AC 014327;  
DT 01-JAN-1999 (TrEMBLrel. 09, Created)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative poly(a) binding protein.  
GN SPBC16B.12C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972h-;  
RA Volckaert G., Wood V., Rajandream M.A., Barrell B.G.;  
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z99789; CAB6904.1; -.  
DR GeneDB: Spombe; SPBC16B.12C; -.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00076; rrm; 1.  
DR SMART: SM00360; RRM; 1.  
DR PROSITE: PS0102; RRM; 1.  
DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
SQ SEQUENCE 166 AA; 18461 MW; A602B5EFC55600B8 CRC64;

Query Match 52.5%; Score 42; DB 3; Length 166;  
Best Local Similarity 53.8%; Pred. No. 8.5;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
DB 88 CDKFTGHPKGFAY 100

RESULT 11

09DDY9 PRELIMINARY; PRT; 296 AA.

AC 09DDY9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Poly(A) binding protein II.  
GN PABP1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kim J., Choi S., Han J.;  
RT "Developmental expression of Poly(A) Binding Protein II in Xenopus  
RT laevis."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF257236; AAG36902.1; -.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00076; rrm; 1.  
DR SMART: SM00360; RRM; 1.  
DR PROSITE: PS0102; RRM; 1.  
DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
SQ SEQUENCE 296 AA; 32449 MW; 319E1235DF493E3 CRC64;

Query Match 52.5%; Score 42; DB 13; Length 296;  
Best Local Similarity 53.8%; Pred. No. 16;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
DB 196 CDKFTGHPKGFAY 208

RESULT 12  
09BZB7 PRELIMINARY; PRT; 491 AA.

AC 09BZB7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytoplasmic polyadenylation element-binding protein short form.  
GN CPZB1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary, and Brain;  
RX MEDLINE=2112522; PubMed=11223249;  
RA Welk J.F., Charlesworth A., Smith G.D., MacNicol A.M.;  
RT "Identification and characterization of the gene encoding human  
RT cytoplasmic polyadenylation element binding protein."  
RL Gene 263:113-121(2001).  
DR EMBL: AF329403; AAK01240.1; -.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR PROSITE: PS0102; RRM; 2.  
SQ SEQUENCE 491 AA; 54162 MW; 561A40FEBD482262 CRC64;

Query Match 52.5%; Score 42; DB 4; Length 491;  
Best Local Similarity 53.8%; Pred. No. 27;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
DB 276 CPKGNMPKGFAY 288

RESULT 13

09YGX5 PRELIMINARY; PRT; 559 AA.

AC 09YGX5;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE ZOR-1.  
GN ZORRA OR ZOR-1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suzuki H., Maegawa S., Murakawa M., Hoshijima K., Shimura Y.,  
 RA Yasuda K., Inoue K.;  
 RT "Identification of zebrafish maternal RNA-binding proteins, ZOR-1 and  
 RT -2;"  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB01680; BA275637.1; -;  
 DR ZFIN; ZDB-GENE-990927-1; Zorba.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PSS0102; RRM; 1.  
 SQ SEQUENCE 559 AA; 62255 MW; 36CF42B1ACT0A377 CRC64;

Query Match 52.5%; Score 42; DB 13; Length 559;  
 Best Local Similarity 53.8%; Pred. No. 31;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNSPKGFAY 13  
 DB 344 CPEKGNMFKGYV 356

RESULT 14  
 Q9DED5 PRELIMINARY; PRT; 559 AA.  
 ID Q9DED5  
 AC Q9DED5;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Cytoplasmic polyadenylation element binding protein.  
 GN CPBB.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OC NCBI\_TaxId=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Katen Y., Yamashita M., Ogawa K., Nagahama Y.;  
 RT "Goldfish cytoplasmic polyadenylation element binding protein  
 RT (CPBB): its interaction with CPE of cyclin B mRNA and phosphorylation  
 RT by cdk and Eg2 protein kinases."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB044534; BAB19051.1; -;  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PSS0102; RRM; 1.  
 SQ SEQUENCE 559 AA; 62122 MW; 05507CE5D1568144 CRC64;

Query Match 52.5%; Score 42; DB 13; Length 559;  
 Best Local Similarity 53.8%; Pred. No. 31;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNSPKGFAY 13  
 DB 344 CPEKGNMFKGYV 356

RESULT 15  
 P70166 PRELIMINARY; PRT; 561 AA.  
 ID P70166  
 AC P70166;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Cytoplasmic polyadenylation element-binding protein (CPBB).  
 GN CPBB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=97121433; PubMed=8962099;  
 RA Gebauer F., Richter J.D.;  
 RT "Mouse cytoplasmic polyadenylation element binding protein: An  
 RT evolutionarily conserved protein that interacts with the cytoplasmic  
 RT polyadenylation elements of c-mos mRNA."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607 (1996).  
 DR EMBL; Y08260; CAA69588.1; -;  
 DR MGI; MGI:108442; Cpeb.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PSS0102; RRM; 2.  
 SQ SEQUENCE 561 AA; 61917 MW; CB7958885AB13FF6 CRC64;

Query Match 52.5%; Score 42; DB 11; Length 561;  
 Best Local Similarity 53.8%; Pred. No. 31;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CXXYGNSPKGFAY 13  
 DB 350 CPEKGNMFKGYV 362

Search completed: November 7, 2003, 07:34:37  
 Job time : 6.37637 secs

GenCore version 5.1.6  
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Om protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17 ; Search time 6.89387 Seconds  
(without alignments)  
368.069 Million cell updates/sec

Title:	US-09-661-992B-105
Perfect score:	80
Sequence:	1 CXXYGNSPKGFAYXXC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameter

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/Aa2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/Aa2003.DAT.*

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	72	90.0	16	22	AA820444	Anti-FIX/FIXa ant
2	66	82.5	242	22	AA820433	Anti-FIX/FIXa ant
3	58	72.5	10	22	AA820388	Anti-FIX/FIXa ant
4	44	55.0	365	19	AAW59884	Amino acid sequen
5	44	55.0	365	23	ABG95556	Human novel secre
6	42	52.5	132	23	ABP62116	Human immunopeti
7	42	52.5	626	22	AB866430	Protein encoded b
8	41	51.2	255	22	AB864427	Drosophila melano
9	40	50.0	107	23	ABG76564	HCV E1 antigen mor

45	38	47.5	351	24	ABU61105
44	38	47.5	351	24	ABU67445
43	38	47.5	351	24	ABU65941
42	38	47.5	351	24	ABU65608
41	38	47.5	351	24	ABU71151
40	38	47.5	351	22	AAW88899
39	38	47.5	351	22	AAU79053
38	38	47.5	351	21	AAV72733
37	38	47.5	351	21	AAV72722
36	38	47.5	351	21	AAV72707
35	38	47.5	351	21	AAV44275
34	38	47.5	351	20	AAV41719
33	38	47.5	351	19	AAW62767
32	38	47.5	235	24	ABP71366
31	38	47.5	224	22	ABBS8914
30	38	47.5	211	22	AAE09632
29	38	47.5	129	21	AAV43866
28	38	47.5	119	16	AAE82982
27	38	47.5	119	16	AAE82981
26	38	47.5	119	16	AAE82980
25	38	47.5	119	16	AAE82979
24	38	47.5	119	16	AAE82977
23	38	47.5	119	16	AAE82976
22	38	47.5	109	22	AAE82753
21	38	47.5	108	22	AAE82752
20	38	47.5	108	22	AAE82751
19	38	47.5	106	18	AAW31724
18	38	47.5	105	23	AAW31723
17	38	47.5	91	23	ABG77145
16	39	48.8	572	22	ABG31822
15	39	48.8	116	23	ABP08366
14	40	50.0	503	22	ABG28544
13	40	50.0	385	21	AAV50757
12	40	50.0	291	22	ABE63366
11	40	50.0	261	23	ABP43671
10	40	50.0	136	23	ABE62620

Human immunopeptid	Human immunop
Mechonine adenosy	Human immunop
Drosophila melanog	Human immunop
Candida albicans pr	Human immunop
Novel human diagno	Human immunop
Human ORF proteom	Human immunop
Novel human diagno	Human immunop
Anti-IGF-IR antibo	Human immunop
Anti-GD2 antibody	Human immunop
Alpha light chain	Human immunop
Human HIV-1 monoc	Human immunop
Anti-PPGL-1 antibo	Human immunop
Human HIV-1 monoc	Human immunop
LK6 heavy chain v	Human immunop
LK6 humanised VH	Human immunop
LK6 humanised VH	Human immunop
LK6 humanised VH	Human immunop
LK6 humanised VH	Human immunop
Human gene 3 encod	Human immunop
Drosophila melanog	Human immunop
Anti-PPGL-1 antibo	Human immunop
Signal transductio	Human immunop
Human PRO64 (PNC4	Human immunop
Human PRO64 (PNC4	Human immunop
Wnt-4AF and Wnt-5C	Human immunop
Wnt-4AF and Wnt-5C	Human immunop
Wnt-4AF and Wnt-5C	Human immunop
Wnt-4AF and Wnt-5C	Human immunop
Human PRO polypept	Human immunop
Human polypeptide	Human immunop
Human PRO64 protei	Human immunop
Human secreted/tra	Human immunop
Novel human secret	Human immunop
Human secreted/tra	Human immunop
Human PRO64 poly	Human immunop

XX 14-SEP-1999; 99AT-0001576.  
 XX (BAXT ) BAXTER AG.  
 XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 XX MPI, 2001-290358/30.  
 DR New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Claim 7; Page 74; 138pp; English.  
 XX  
 CC The present sequence is that of complementarity determining  
 CC region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or  
 CC anti-activated Factor IX (FIXa) activity. Such antibodies  
 CC and their derivatives (including those that comprise the present  
 CC CDR3 peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXa  
 CC activating activity. Administration of the antibodies or their  
 CC derivatives leads to an increase in the procoagulant activity of  
 CC FIXa, even in the presence of FVIIIa inhibitors. This allows for  
 CC rapid blood coagulation even in the absence of FVIII or FVIIIa, and  
 CC in the case of FVIII inhibitor patients. The antibodies or their  
 CC derivatives are used in a claimed pharmaceutical composition for  
 CC treating patients with blood coagulation disorders, especially  
 CC haemophilia A and haemorrhagic diathesis.  
 CC  
 SQ Sequence 16 AA;  
 Query Match 90.0%; Score 72; DB 22; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CXYGNSPKGFAYXXC 16  
 Db 1 CXYGNSPKGFAYXXC 16  
 RESULT 2  
 AAB20433  
 ID AAB20433 standard; Protein; 242 AA.  
 XX  
 AC AAB20433;  
 XX  
 DT 21-JUN-2001 (first entry)  
 DE Anti-FIX/FIXa antibody 193/AD3 scFv.  
 XX  
 KM Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;  
 KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..119  
 FT /label= VH  
 FT Region 98..108  
 FT /label= CDR3  
 FT Peptide 120..134  
 FT /label= Linker  
 FT Protein 135..242  
 FT /label= VL  
 FT Region 223..231  
 FT /label= CDR3  
 XX  
 PN MO20011992-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PI

PF 13-SEP-2000; 2000WO-EP08936.  
 XX  
 PR 14-SEP-1999; 99AT-0001576.  
 XX  
 XX (BAXT ) BAXTER AG.  
 XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 XX MPI, 2001-290358/30.  
 DR N-PSDB; AAF30723.  
 PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Claim 8; Fig 14; 138pp; English.  
 XX  
 CC The present sequence is that of a single chain Fv (scFv) derivative  
 CC of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain  
 CC variable regions of 193/AD3 joined by an artificial, flexible linker  
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
 CC 193/AD3 VH and VL regions and cloning in vector pDAP2. 193/AD3 is  
 CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)  
 CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,  
 CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIIIa inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis.  
 CC  
 SQ Sequence 242 AA;  
 Query Match 82.5%; Score 66; DB 22; Length 242;  
 Best Local Similarity 84.6%; Pred. No. 0.0051;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CXYGNSPKGFAY 13  
 Db 96 CALYNSPKGFAY 108  
 RESULT 3  
 AAB20388  
 ID AAB20388 standard; Peptide; 10 AA.  
 XX  
 AC AAB20388;  
 XX  
 DT 21-JUN-2001 (first entry)  
 DE Anti-FIX/FIXa antibody 193/AD3 CDR3.  
 XX  
 KM Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;  
 KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;  
 KM complementarity determining region; CDR.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO20011992-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 13-SEP-2000; 2000WO-EP08936.  
 XX  
 PR 14-SEP-1999; 99AT-0001576.  
 XX  
 XX (BAXT ) BAXTER AG.  
 XX Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 XX MPI

XX WPI; 2001-290358/30.

XX New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of Factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Claim 7; Page 74; 138pp; English.

CC The present sequence is that of complementarity determining region  
 CC 3 (CDR3) of the heavy chain of an antibody expressed by mouse  
 CC hybridoma 193/AD3. This antibody has anti-Factor IX (FIX) or  
 CC anti-activated Factor IX (FIXa) activity. It is an example of  
 CC anti-FIX/FIXa antibodies of the invention. Such antibodies and  
 CC their derivatives (including those that comprise the present CDR3  
 CC peptide) have Factor VIIa (FVIIa) cofactor activity or FIXa  
 CC activating activity. Administration of the antibodies or their  
 CC derivatives leads to an increase in the procoagulant activity of  
 CC FIXa, even in the presence of FVIIa inhibitors. This allows for  
 CC rapid blood coagulation even in the absence of FVII or FVIIa, and  
 CC in the case of FVII inhibitor patients. The antibodies or their  
 CC derivatives are used in a claimed pharmaceutical composition for  
 CC treating patients with blood coagulation disorders, especially  
 CC haemophilia A and haemorrhagic diathesis.

XX Sequence 10 AA;

Query Match 72.5%; Score 58; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13  
 |||||  
 Db 1 YGNSPKGFAY 10

#### RESULT 4

AAWS9884  
 ID AAW59884 standard; Protein; 365 AA.

XX AAW59884;  
 XX 20-NOV-1998 (first entry)

DE Amino acid sequence of the cDNA clone Bcl-like (HAICH29).

KW Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;  
 KW immunological disorder; autoimmune disease; anti-infectious agent.

XX Homo sapiens.

XX MO9831800-A2.

XX 23-JUL-1998.

XX 21-JAN-1998; 98WC-US00960.

XX 21-JAN-1997; 97US-0034205.

XX 21-JAN-1997; 97US-0034204.

XX (AUCK-) AUCKLAND UNISERVICES LTD.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Su dy;

XX WPI; 1998-414089/35.

XX N-FSDB; AAW1925.

PT New isolated polynucleotides and encoded polypeptides - used to  
 PT develop products for treating e.g. inflammatory diseases,  
 PT infections, immunological disorders, autoimmune diseases, allergies  
 PT or tumours

XX Claim 1; Fig 12A-12D; 120pp; English.

CC This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),  
 CC used in the method of the invention. The products of the clone can be  
 CC used for treating conditions associated with abnormal expression of  
 CC the polypeptides. They can be used for e.g. treating chronic  
 CC inflammatory diseases, immunological disorders, autoimmune diseases,  
 CC inflammatory diseases, various allergies, and as anti-infectious agents.  
 CC The products can also be used for detection and diagnosis.

XX Sequence 365 AA;

Query Match 55.0%; Score 44; DB 19; Length 365;  
 Best Local Similarity 53.8%; Pred. No. 35;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYNSPKGFAY 13  
 : |||||  
 Db 264 CDRFGHPKGFAY 276

#### RESULT 5

ABG95556  
 ID ABG95556 standard; Protein; 365 AA.

XX ABG95556;

DT 15-JAN-2003 (first entry)

DE Human novel secreted protein gene 120 polypeptide #1.

KW Human; secreted protein; autoimmune disease; chemotaxis;  
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
 KW cerebrovascular disorder; cerebral ischemia; angiogenesis; sunburn;  
 KW nervous system disorders; Alzheimer's disease; infection;  
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
 KW epithelial cell proliferation; organ transplantation; food additive;  
 KW preservative; nutritional.

XX Homo sapiens.

XX US6420526-B1.

XX 16-JUL-2002.

XX 08-SEP-1998; 98US-0149476.

XX 07-MAR-1997; 97US-038621P.

XX 07-MAR-1997; 97US-040161P.

XX 07-MAR-1997; 97US-040162P.

XX 07-MAR-1997; 97US-040163P.

XX 07-MAR-1997; 97US-040333P.

XX 07-MAR-1997; 97US-040334P.

XX 07-MAR-1997; 97US-040626P.

XX 11-APR-1997; 97US-043312P.

XX 11-APR-1997; 97US-043313P.

XX 11-APR-1997; 97US-043314P.

XX 11-APR-1997; 97US-043315P.

XX 11-APR-1997; 97US-043568P.

XX 11-APR-1997; 97US-043569P.

XX 11-APR-1997; 97US-043570P.

XX 11-APR-1997; 97US-043670P.

XX 11-APR-1997; 97US-043671P.

XX 11-APR-1997; 97US-043672P.

XX 23-MAY-1997; 97US-047492P.





XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB160511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pat\_sequences.  
 CC  
 XX Sequence 2515 AA;

Query Match 51.2%; Score 41; DB 22; Length 2515;  
 Best Local Similarity 87.5%; Pred. No. 8.4e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 4 CXXYGNSPKGF 11  
 DB 2171 YGNSPKSF 2178

RESULT 9  
 ABG76564  
 ID ABG76564 standard; Protein; 107 AA.  
 AC ABG76564;  
 XX  
 DT 05-NOV-2002 (first entry)

DE HCV E1 antigen monoclonal antibody #52.  
 XX  
 KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;  
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.  
 XX  
 OS Homo sapiens.

PN WO200260954-A1.

PO 08-AUG-2002.

PF 14-JAN-2002; 2002WO-SE00044.

PR 12-JAN-2001; 2001US-260889P.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Drakenberg K, Persson MA;

DR MPI, 2002-608502/65.

PT Vaccine comprising a human monoclonal antibody against hepatitis C  
 PT virus (HCV) E1 or E2 antigen, useful for treating or preventing HCV  
 PT infection -  
 XX  
 XX

PS Disclosure; Page 56; 64pp; English.

XX The invention relates to a human monoclonal antibody or its antigen  
 CC binding fragments, which exhibit immunological binding affinity for a  
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence  
 CC homologous to the binding portion of a human antibody Fab molecule from a  
 CC combinatorial antibody library. The vaccine composition comprising the  
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or  
 CC its hypervariable region is useful in treating or preventing HCV  
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human  
 CC monoclonal antibodies against HCV E1 antigen.  
 CC  
 XX Sequence 107 AA;

Query Match 50.0%; Score 40; DB 23; Length 107;  
 Best Local Similarity 63.6%; Pred. No. 45;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 CXXYGNSPKGF 11  
 DB 88 CQRYGTSPTF 98

RESULT 10  
 ABP62206  
 ID ABP62206 standard; Protein; 136 AA.  
 AC ABP62206;  
 XX  
 DT 10-OCT-2002 (first entry)

DE Human immunopeptide to HCV E2 glycoprotein Fab variable region #53.  
 XX  
 KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
 KW NS3 protein; viral infection.  
 XX  
 OS Homo sapiens.

PN WO200259340-A1.

PD 01-AUG-2002.

PF 25-JAN-2002; 2002WO-US02303.

PR 26-JAN-2001; 2001US-264451P.

PA (SCRI) SCRIPPS RES INST.

PI Maruyama T, Jones IM, Burton DR, Fox RI;

DR MPI, 2002-599801/64.

DR N-PSDB; ABQ92705.

PT New human immunopolypeptide with binding specificity for certain  
 PT envelope glycoproteins and nonstructural proteins of hepatitis C virus  
 PT (HCV), for diagnosing or treating patients having or suspected of  
 PT having HCV infection -  
 XX  
 XX

PS Claim 10; Fig 12; 308pp; English.

XX The present invention relates to human immunopolypeptides, produced by a  
 CC phage transduced cell library. The present sequence is one such  
 CC immunopolypeptide. The immunopolypeptides have binding specificity for  
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
 CC cell binding and contains neutralising epitopes, while NS3 is thought to  
 CC be involved in the replication of HCV. The immunopolypeptides are useful  
 CC for diagnosing and treating a patient having or suspected to be having  
 CC HCV infection.  
 CC  
 XX Sequence 136 AA;

Query Match 50.0%; Score 40; DB 23; Length 136;  
 Best Local Similarity 46.2%; Pred. No. 58;  
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXXYGNSPKGFAY 13  
 DB 89 CQRYGTSPTF 101

RESULT 11

ID ABP43671 standard; Protein; 261 AA.

AC ABP43671;

DT 26-FEB-2003 (first entry)

XX Methionine adenosyltransferase II alpha clone MGC:2907.  
 DE  
 XX  
 KM Neuroprotective; immunomodulator; cancer; chromosome 2p11.2;  
 KM cytoskeletal; anti-inflammatory; gene therapy; nutritional supplement;  
 KM wound; burn; ulcer; Alzheimer's disease; Huntington's disease;  
 KM amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 KM vulnerability.  
 XX  
 OS Homo sapiens.  
 XX  
 FN W0200231111-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 11-OCT-2001; 2001MO-US27760.  
 XX  
 PR 12-OCT-2000; 2000US-0687527.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Wehrman T, Dermanac RT;  
 XX  
 DR WPI; 2002-426278/45.  
 DR N-PSDB; AB060915.  
 XX  
 PS New polypeptides and their encoded proteins, useful as nutritional  
 PT sources or supplements, or in gene therapy, particularly for treating  
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
 PT inflammation -  
 XX  
 PS Claim 20; SEQ ID # 574; 357pp + sequence listing; English.  
 XX  
 CC The invention relates to 446 newly isolated polynucleotide sequences.  
 CC The activity of polynucleotides of the invention may be described as,  
 CC vulnerability, neuroprotective, immunomodulator, cytoskeletal and  
 CC anti-inflammatory. Compositions comprising nucleic acids of the invention  
 CC are useful for treating a mammalian subject, or as nutritional sources or  
 CC supplements. These are useful in gene therapy, particularly for treating  
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
 CC inflammation. The nucleic acids and polypeptides are also useful in  
 CC diagnostic and research methods. The sequences given in records  
 CC ABP43544-ABP43989 represent polypeptides encoded by polynucleotides of  
 CC the invention.  
 CC NOT3: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 261 AA;  
 XX  
 Query Match 50.0%; Score 40; DB 23; Length 261;  
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 QY 4 YGNSPKGFAYXXC 16  
 | : | | | | |  
 Db 92 YDSSKGFYKTC 104  
 XX  
 RESULT 12  
 ABB63366  
 ID ABB63366 standard; Protein; 291 AA.  
 XX  
 AC ABB63366;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 16890.  
 XX  
 KM Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.

XX Drosophila melanogaster.  
 OS  
 XX  
 FN W0200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001MO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li FMD, Myers EM;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; AB07469.  
 XX  
 PS New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 16890; 21bp + Sequence listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB01840-AB01875), expressed DNA  
 CC sequences (AB01840-AB01875) and the encoded proteins  
 CC (AB057737-AB072072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 291 AA;  
 XX  
 Query Match 50.0%; Score 40; DB 22; Length 291;  
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 5 GNSPKGFAY 13  
 | | | | |  
 Db 119 GKRPKGFAY 127  
 XX  
 RESULT 13  
 AAY95075  
 ID AAY95075 standard; Protein; 385 AA.  
 XX  
 AC AAY95075;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Candida albicans polypeptide sequence # 43.  
 XX  
 KM Candida albicans infection; growth; survival; medication; AIDS;  
 KM vulvovaginitis; immunocompromised patient; treat.  
 XX  
 OS Candida albicans.  
 XX  
 FN EP982401-A2.  
 XX  
 PD 01-MAR-2000.  
 XX  
 PF 23-DEC-1998; 98EP-0310694.  
 XX  
 PR 14-AUG-1998; 98GB-0017796.  
 XX  
 PA (JANC ) JANSSEN PHARM NV.



PT hyperproliferative disorders and autoimmune disorders -  
 XX Disclosure; SEQ ID 17654; 1037bp; English.

CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 116 AA;

Query March 48.8%; Score 39; DB 23; Length 116;  
 Best Local Similarity 77.8%; Fred. No. 71;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNSPKGFA 12  
 | | | | |  
 Db 65 YSNSPDGFA 73

Search completed: November 7, 2003, 07:27:04  
 Job time : 7.89987 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 14.0347 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992b-105  
Perfect score: 80  
Sequence: 1 CXXYGNSPKGFAYXXC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10C\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	55.0	249	15	US-10-153-668-118
2	44	55.0	306	15	US-10-153-668-120
3	44	55.0	365	11	US-09-809-391-696
4	44	55.0	365	12	US-09-882-171-696
5	38	47.5	105	10	US-09-828-708-3
6	38	47.5	107	8	US-08-844-215-10
7	38	47.5	108	15	US-10-269-805-32
8	38	47.5	108	15	US-10-269-805-36
9	38	47.5	211	9	US-09-764-903-39
10	38	47.5	351	10	US-09-978-295A-226
11	38	47.5	351	10	US-09-978-697-226
12	38	47.5	351	10	US-09-978-192A-226
13	38	47.5	351	10	US-09-999-832A-226
14	38	47.5	351	11	US-09-978-189-226
15	38	47.5	351	11	US-09-978-189-226

16	38	47.5	351	11	US-09-978-608A-226	Sequence 226, App
17	38	47.5	351	11	US-09-978-585A-226	Sequence 226, App
18	38	47.5	351	11	US-09-978-191A-226	Sequence 226, App
19	38	47.5	351	11	US-09-978-403A-226	Sequence 226, App
20	38	47.5	351	11	US-09-978-564A-226	Sequence 226, App
21	38	47.5	351	11	US-09-999-833A-226	Sequence 226, App
22	38	47.5	351	11	US-09-981-915A-226	Sequence 226, App
23	38	47.5	351	11	US-09-978-824-226	Sequence 226, App
24	38	47.5	351	11	US-09-918-585A-226	Sequence 226, App
25	38	47.5	351	11	US-09-978-423A-226	Sequence 226, App
26	38	47.5	351	11	US-09-978-193A-226	Sequence 226, App
27	38	47.5	351	11	US-09-999-830A-226	Sequence 226, App
28	38	47.5	351	11	US-09-978-757A-226	Sequence 226, App
29	38	47.5	351	11	US-09-978-187B-226	Sequence 226, App
30	38	47.5	351	11	US-09-978-643A-226	Sequence 226, App
31	38	47.5	351	12	US-09-978-375A-226	Sequence 226, App
32	38	47.5	351	12	US-09-978-375A-226	Sequence 226, App
33	38	47.5	351	12	US-09-978-188A-226	Sequence 226, App
34	38	47.5	351	12	US-10-143-031A-226	Sequence 226, App
35	38	47.5	351	12	US-10-143-031A-226	Sequence 226, App
36	38	47.5	351	12	US-10-002-967A-226	Sequence 226, App
37	38	47.5	351	12	US-10-017-083A-226	Sequence 226, App
38	38	47.5	351	12	US-10-143-030A-226	Sequence 226, App
39	38	47.5	351	12	US-10-199-672-80	Sequence 226, App
40	38	47.5	351	12	US-10-187-749-80	Sequence 80, App1
41	38	47.5	351	12	US-10-194-457-80	Sequence 80, App1
42	38	47.5	351	12	US-10-145-128A-226	Sequence 226, App
43	38	47.5	351	12	US-10-184-642-80	Sequence 80, App1
44	38	47.5	351	12	US-10-196-747-80	Sequence 80, App1
45	38	47.5	351	12	US-10-173-689-80	Sequence 80, App1
					US-10-173-690-80	Sequence 80, App1

## ALIGNMENTS

RESULT 1  
US-10-153-668-118  
Sequence 118, Application US/10153668  
Publication No. US2003092616A1  
GENERAL INFORMATION:  
APPLICANT: HONDA, Goichi  
APPLICANT: MATSUDA, Akio  
APPLICANT: MURAMATSU, Shuji  
APPLICANT: ISHIZAWA, Kenya  
TITLE OF INVENTION: STAT6 Activating Gene  
FILE REFERENCE: 1254-0207P  
CURRENT APPLICATION NUMBER: US/10/153,668  
PRIOR FILING DATE: 2002-05-24  
PRIOR APPLICATION NUMBER: US 60/293,172  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/316,031  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/328,403  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: JP 2001-157043  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: JP 2001-260681  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: JP 2001-313175  
PRIOR FILING DATE: 2001-10-10  
NUMBER OF SEQ ID NOS: 488  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 118  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-153-668-118

Query Match 55.0%; Score 44; DB 15; Length 249;  
Best Local Similarity 53.8%; Pred. No. 9.4;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CXXYGNSPKGFAY 13

Db 148 CDKFGHPKGFAY 160

RESULT 2  
US-10-153-668-120  
; Sequence 120, Application US/10153668  
; Publication No. US20030092618A1  
; GENERAL INFORMATION:  
; APPLICANT: HONDA, Goichi  
; APPLICANT: MATSUDA, Akio  
; APPLICANT: MURAMATSU, Shuji  
; APPLICANT: ISHIZAWA, Kenya  
; TITLE OF INVENTION: STAT6 Activating Gene  
; FILE REFERENCE: 1254-D207P  
; CURRENT APPLICATION NUMBER: US/10/153,668  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: US 60/293,172  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/316,031  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/328,403  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: JP 2001-157043  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: JP 2001-260681  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: JP 2001-313175  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 488  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-668-120

Query Match 55.0%; Score 44; DB 15; Length 306;  
Best Local Similarity 53.8%; Pred. No. 12;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXXYGNPKGFAY 13  
Db 205 CDKFGHPKGFAY 217  
RESULT 3  
US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PAM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 55.0%; Score 44; DB 11; Length 365;  
Best Local Similarity 53.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXXYGNPKGFAY 13  
Db 264 CDKFGHPKGFAY 276

RESULT 4  
US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
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; PRIOR APPLICATION NUMBER: 60/040,336  
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; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,584  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,492  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,601  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/043,580  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,568  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,314  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,569  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,311  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,671  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,674  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,669  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,312  
PRIOR FILING DATE: 1997-04-11  
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PRIOR FILING DATE: 1997-04-11  
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PRIOR APPLICATION NUMBER: 60/043,315  
PRIOR FILING DATE: 1997-04-11  
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PRIOR FILING DATE: 1997-08-22  
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PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,637  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,903  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/056,888  
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PRIOR APPLICATION NUMBER: 60/056,892

PRIOR FILING DATE: 1997-08-22  
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PRIOR APPLICATION NUMBER: 60/047,614  
PRIOR FILING DATE: 1997-05-23  
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PRIOR APPLICATION NUMBER: 60/043,576  
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PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/048,964  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/057,650  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/056,884  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: 60/057,669  
PRIOR FILING DATE: 1997-09-05

Query Match 55.0%; Score 44; DB 12; Length 365;  
Best Local Similarity 53.8%; Pred No. 14;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
Db 264 CDRFSGHPKGFAY 276

RESULT 5  
US-09-828-708-3  
Sequence 3, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.

APPLICANT: Burton, D.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 3  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-3

Query Match 47.5%; Score 38; DB 10; Length 105;  
Best Local Similarity 54.5%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11  
DB 82 CQYGGSSPRTF 92

RESULT 6  
US-09-828-708-7  
Sequence 7, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 7  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-7

Query Match 47.5%; Score 38; DB 10; Length 105;  
Best Local Similarity 54.5%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11  
DB 82 CQYGGSSPRTF 92

RESULT 7  
US-08-844-215-10  
Sequence 10, Application US/08844215  
Publication No. US20020016445A1  
GENERAL INFORMATION:  
APPLICANT: PERSSON, MATS AXEL  
APPLICANT: ALANDER, TOBIAS ERIC  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,215  
FILING DATE: 17-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/635,109  
FILING DATE: 19-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 80146.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-844-215-10

Query Match 47.5%; Score 38; DB 8; Length 107;  
Best Local Similarity 54.5%; Pred. No. 42;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11  
DB 88 CQYGGSSPRTF 98

RESULT 8  
US-10-269-805-32  
Sequence 32, Application US/10269805  
Publication No. US20030124129A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN D.  
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
FILE REFERENCE: A-722  
CURRENT APPLICATION NUMBER: US/10/269,805  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/328,604  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: Patentln version 3.1  
SEQ ID NO: 32  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-269-805-32

Query Match 47.5%; Score 38; DB 15; Length 108;  
Best Local Similarity 54.5%; Pred. No. 42;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11  
DB 89 CQYGGSSPRTF 99

RESULT 9  
US-10-269-805-36  
Sequence 36, Application US/10269805  
Publication No. US20030124129A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN D.  
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
FILE REFERENCE: A-722  
CURRENT APPLICATION NUMBER: US/10/269,805

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; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-36

Query Match
Best Local Similarity 47.5%; Score 38; DB 15; Length 108;
Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXGNSPKGF 11
Db 89 CQHTSSPRTF 99

RESULT 10
US-09-764-903-39
; Sequence 39, Application US/09764903
; Patent No. US2002009674A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT228
; CURRENT APPLICATION NUMBER: US/09/764,903
; CURRENT FILING DATE: 2001-02-17
; Prior application data removed - consult PAMM or file wrapper
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-903-39

Query Match
Best Local Similarity 47.5%; Score 38; DB 9; Length 211;
Pred. No. 84;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
Db 3 HGVSFGQFQWGC 15

RESULT 11
US-09-978-295A-226
; Sequence 226, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
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; APPLICANT: Paoul, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumae, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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;; PRIOR FILING DATE: 1998-04-01  
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;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.5%; Score 38; DB 10; Length 351;  
Best Local Similarity 46.2%; Pred. No. 1,4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 4 YGNSPKGAYXC 16  
Db 143 HGVSPQFQWGC 155

RESULT 12  
US-09-978-697-226  
;; Sequence 226, Application US/09978697  
;; Patent No. US20020169284A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerlitsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kilian, Kenneth J.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT FILING DATE: 2001-10-16  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
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PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
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PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.5%; Score 38; DB 10; Length 351;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

CY 4 YGNSPKGPAVXXC 16  
DB 143 HGVSPQGFQWGC 155

RESULT 13  
US-09-978-192A-226  
Sequence 226, Application US/09978192A  
Patent No. US2002017753A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kiljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Nadier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P26301C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR APPLICATION NUMBER: 60/085323  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.5%; Score 38; DB 10; Length 351;  
Best Local Similarity 46.2%; Pred. No. 1,4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXC 16  
DB 143 HGVSFGQFWSGC 155

RESULT 14  
US-09-999-832A-226  
Sequence 226, Application US/09999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kiljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918595  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364

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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.5%; Score 38; DB 10; Length 351;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGAYXXC 16  
Db 143 HGVSPQSFQMSGC 155

RESULT 15  
US-09-978-189-226  
Sequence 226, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Nadjler, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR FILING DATE: 1998-03-10  
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; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.5% Score 38; DB 11; Length 351;  
 Best Local Similarity 46.2%; Fred. NO. 1.4e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16  
 DB 143 HGVSPQGFQWGC 155

Search completed: November 7, 2003, 08:16:55  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 2.3498 Seconds  
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288.098 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80  
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Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, A1\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	55.0	365	4	US-09-149-476-696
2	33	48.8	109	4	US-09-025-769B-16
3	38	47.5	107	4	US-08-635-109-7
4	38	47.5	119	1	US-08-207-996-18
5	38	47.5	119	1	US-08-207-996-19
6	38	47.5	119	1	US-08-207-996-20
7	38	47.5	119	1	US-08-207-996-21
8	38	47.5	119	1	US-08-207-996-22
9	38	47.5	119	1	US-08-207-996-27
10	38	47.5	119	2	US-08-760-840A-18
11	38	47.5	119	2	US-08-760-840A-19
12	38	47.5	119	2	US-08-760-840A-20
13	38	47.5	119	2	US-08-760-840A-21
14	38	47.5	119	2	US-08-760-840A-22
15	38	47.5	119	2	US-08-760-840A-28
16	38	47.5	119	3	US-09-266-119-18
17	38	47.5	119	3	US-09-266-119-19
18	38	47.5	119	3	US-09-266-119-20
19	38	47.5	119	3	US-09-266-119-21
20	38	47.5	119	3	US-09-266-119-22
21	38	47.5	119	3	US-09-266-119-28
22	38	47.5	119	4	US-09-602-709-18
23	38	47.5	119	4	US-09-602-709-19
24	38	47.5	119	4	US-09-602-709-20
25	38	47.5	119	4	US-09-602-709-21
26	38	47.5	119	4	US-09-602-709-22
27	38	47.5	119	4	US-09-602-709-28

28	38	47.5	351	3	US-09-067-782A-2	Sequence 2, Appl
29	37	46.2	143	4	US-09-795-926-31	Sequence 21, Appl
30	37	46.2	240	3	US-09-795-926-33	Sequence 33, Appl
31	37	46.2	263	5	PCT-US94-00844-11	Sequence 11, Appl
32	37	46.2	426	4	US-09-252-991A-32215	Sequence 3215, A
33	37	46.2	572	2	US-09-032-315-7	Sequence 7, Appl
34	37	46.2	572	3	US-08-993-318A-7	Sequence 7, Appl
35	37	46.2	572	3	US-09-359-886-7	Sequence 7, Appl
36	37	46.2	572	3	US-09-396-260-7	Sequence 7, Appl
37	37	46.2	572	3	US-09-576-281-7	Sequence 7, Appl
38	36	45.0	149	4	US-08-252-991A-19973	Sequence 15973, A
39	36	45.0	396	4	US-09-325-932A-153	Sequence 153, App
40	36	45.0	484	4	US-09-134-001C-5402	Sequence 5402, Ap
41	36	45.0	3165	2	US-08-459-146-3	Sequence 3, Appl
42	36	45.0	3165	2	US-08-459-065-3	Sequence 3, Appl
43	35.5	44.4	2703	1	US-08-185-432-19	Sequence 19, Appl
44	35.5	44.4	2703	4	US-08-899-232-4	Sequence 4, Appl
45	35	43.8	49	2	US-08-766-858A-33	Sequence 33, Appl

## ALIGNMENTS

RESULT 1  
US-09-149-476-696  
Sequence 696, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23



EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 55.0%; Score 44; DB 4; Length 365;  
Best Local Similarity 53.8%; Pred. No. 9 6;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAY 13  
DB 264 CDKFSCHPKGFAY 276

RESULT 2  
US-09-025-769B-16

Sequence 16, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: 1189, Vic

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-09-025-769B-16

Query Match 48.8%; Score 39; DB 4; Length 109;  
Best Local Similarity 63.6%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNPKGF 11  
DB 89 CQYGNPKGF 99

RESULT 3

US-08-635-109-7  
Sequence 7, Application US/08635109

Patent No. 6538114

GENERAL INFORMATION:

APPLICANT: Peirson, Mats A. A.

APPLICANT: Allander, Tobias E.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 Hamilton Avenue, Suite 200

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/635,109

FILING DATE: 19-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McCracken, Thomas P

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 2300-6146

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-635-109-7

Query Match 47.5%; Score 38; DB 4; Length 107;  
Best Local Similarity 54.5%; Pred. No. 27;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNPKGF 11  
DB 88 CQYGNPKGF 98

RESULT 4  
US-08-207-996-18

Sequence 18, Application US/08207996

Patent No. 5646253

GENERAL INFORMATION:

APPLICANT: Scotgen Biopharmaceuticals, Inc.

APPLICANT: 1014 Hamilton Court

APPLICANT: Menlo Park, California 94025

APPLICANT: United States of America

APPLICANT: 1345 Avenue of the Americas

APPLICANT: New York, New York 10105

TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: IUD-5363  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-207-996-18

Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

CY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPMFAY 108

RESULT 5  
US-08-207-996-19  
Sequence 19, Application US/08207996  
Patent No. 5646253  
GENERAL INFORMATION:  
APPLICANT: Scotgen Biopharmaceuticals, Inc.  
APPLICANT: 1014 Hamilton Court  
APPLICANT: Menlo Park, California 94025  
APPLICANT: United States of America  
APPLICANT: 1345 Avenue of the Americas  
APPLICANT: New York, New York 10105  
APPLICANT: United States of America  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: IUD-5363  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-207-996-19

Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

CY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPMFAY 108

RESULT 6  
US-08-207-996-20  
Sequence 20, Application US/08207996  
Patent No. 5646253  
GENERAL INFORMATION:  
APPLICANT: Scotgen Biopharmaceuticals, Inc.  
APPLICANT: 1014 Hamilton Court  
APPLICANT: Menlo Park, California 94025  
APPLICANT: United States of America  
APPLICANT: 1345 Avenue of the Americas  
APPLICANT: New York, New York 10105  
APPLICANT: United States of America  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: IUD-5363  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-207-996-20

Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

CY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPMFAY 108

RESULT 7

US-08-207-996-21  
; Sequence 21, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotogen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Wordperfect 6.0/ASCII standard  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/207,996  
; FILING DATE: 08-MAR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pasqualini, Patricia A.  
; REGISTRATION NUMBER: 34,894  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-688-3884  
; TELEFAX: 212-838-3884  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-207-996-21  
  
Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPMFAY 108  
  
RESULT 8  
US-08-207-996-22  
; Sequence 22, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotogen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-3884  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-207-996-22  
  
Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPMFAY 108  
  
RESULT 9  
US-08-207-996-27  
; Sequence 27, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotogen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Wordperfect 6.0/ASCII standard  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/207,996  
; FILING DATE: 08-MAR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pasqualini, Patricia A.  
; REGISTRATION NUMBER: 34,894  
; REFERENCE/DOCKET NUMBER: LUD-5363

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-207-996-27

Query Match 47.5%; Score 38; DB 1; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXYGNSPKGFAY 13  
DB 96 CARHGDPAWFAY 108

RESULT 10  
US-08-760-840A-18  
Sequence 18, Application US/08760840A  
Patent No. 5952484  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTING;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Peife & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-760-840A-18

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CXYGNSPKGFAY 13

DB 96 CARHGDPAWFAY 108

RESULT 11  
US-08-760-840A-19  
Sequence 19, Application US/08760840A  
Patent No. 5952484  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTING;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Peife & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-760-840A-19

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXYGNSPKGFAY 13  
DB 96 CARHGDPAWFAY 108

RESULT 12  
US-08-760-840A-20  
Sequence 20, Application US/08760840A  
Patent No. 5952484  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTING;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: wordperfect

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946

## REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELEPHONE: 212-688-9200  
TELEFAX: 212-688-3884

## INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown

MOLECULE TYPE: protein  
US-08-760-840A-20

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best local Similarity 46.2%; Pred. No. 30;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 96 CASHGDDPAMFAY 108

## RESULT 13

US-08-760-840A-21  
Sequence 21, Application US/08760840A  
Patent No. 5952484

## GENERAL INFORMATION:

APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTING;  
APPLICANT: Pilar GARIN-CHESA;

APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES

NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: wordperfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946

## REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELEPHONE: 212-688-9200  
TELEFAX: 212-688-3884

## INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown

MOLECULE TYPE: protein  
US-08-760-840A-21

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best local Similarity 46.2%; Pred. No. 30;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 96 CASHGDDPAMFAY 108

## RESULT 14

US-08-760-840A-22  
Sequence 22, Application US/08760840A  
Patent No. 5952484

## GENERAL INFORMATION:

APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTING;  
APPLICANT: Pilar GARIN-CHESA;

APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES

NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: wordperfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946

## REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELEPHONE: 212-688-9200  
TELEFAX: 212-688-3884

## INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-760-840A-22

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPAWFAF 108

## RESULT 15

US-08-760-840A-28  
Sequence 28, Application US/08760840A  
Patent No. 5952484  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTIG;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,840A  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US 95/03094  
FILING DATE: 08-MAR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5952484man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-760-840A-28

Query Match 47.5%; Score 38; DB 2; Length 119;  
Best Local Similarity 46.2%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13  
DB 96 CARHGDPAWFAF 108

Search completed: November 7, 2003, 07:30:11  
Job time: 2.3498 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 2.0721 seconds  
(without alignments)  
742.581 Million cell updates/sec

Title: US-09-661-992b-106  
Perfect score: 82  
Sequence: 1 FRNRGWTALKVSSCD 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	2351	1 E2HU	coagulation factor
2	76	97.7	2319	2 A47004	coagulation factor
3	70	86.4	869	2 A25945	coagulation factor
4	70	85.4	2133	2 T42763	coagulation factor
5	44	53.7	275	2 B83412	streptomycin 3'-P
6	42	51.2	220	2 S44966	lmbr protein - Str
7	41	50.0	873	2 B86471	hypothetical prote
8	41	50.0	1120	2 T14275	myosin-like prote
9	40	48.8	76	2 A27957	hypothetical prote
10	40	48.8	536	2 B81319	N-acetylseruminate
11	40	48.8	573	2 B66639	protein T1P9.16 (1
12	39	47.6	157	2 A67117	probable phosphop
13	39	47.6	160	2 T44703	lipopolysaccharide
14	39	47.6	505	2 A97642	sugar transporter
15	39	47.6	512	2 A82865	hypothetical prote
16	39	47.6	558	2 T19269	hypothetical prote
17	39	47.6	1058	2 D82654	hypothetical prote
18	39	47.6	1099	2 A59311	ankyrin-like prote
19	39	47.6	1208	2 T44659	myosin VII, ZMW3
20	38.5	47.0	455	2 AD2620	mlab protein (impo
21	38.5	47.0	467	2 D97402	hypothetical 53.7K
22	38	46.3	300	2 T31149	hypothetical prote
23	38	46.3	485	2 T03426	sucrose phosphoryl
24	38	46.3	485	2 A83244	sucrose phosphoryl
25	37.5	45.7	172	2 E25358	hypothetical prote
26	37.5	45.7	376	2 T12673	hypothetical prote
27	37	45.1	58	2 A82880	hypothetical prote
28	37	45.1	129	2 F82515	conserved hypothet
29	37	45.1	151	2 E71547	hypothetical prote

30	37	45.1	304	2 A45989	peroxisome assembl
31	37	45.1	323	2 T25948	hypothetical prote
32	37	45.1	456	2 T46291	hypothetical prote
33	37	45.1	552	2 T33760	sphingosine-1-phos
34	37	45.1	717	2 H72208	conserved hypothet
35	37	45.1	772	2 A62955	GDEF family prote
36	37	45.1	772	2 G98327	hypothetical 91.8K
37	37	45.1	776	2 T29064	hyaluronate lyase
38	37	45.1	1243	2 S60138	sex factor aggrega
39	36.5	44.5	650	2 A34498	glycoprotein antri
40	36	43.9	89	1 S42609	sniga-like toxin I
41	36	43.9	89	2 S01033	sniga-like toxin I
42	36	43.9	89	2 I69156	sniga-like toxin I
43	36	43.9	89	2 A60279	sniga-like toxin I
44	36	43.9	89	2 S58344	sniga-like toxin I
45	36	43.9	89	2 P90779	sniga toxin 2 subu

## ALIGNMENTS

## RESULT 1

E2HU  
coagulation factor VIII precursor [validated] - human  
M/Alterate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant com  
C/Species: Homo sapiens (man)  
C/Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Dec-2000  
C/Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; F  
R/Gitcheiter, J.; Wood, W.I.  
Hum. Mol. Genet. 1, 199-200, 1992  
A/Title: Sequence of the exon-containing regions of the human factor VIII gene.  
A/Reference number: I54318; MUID:93265012; PMID:1303178  
A/Accession: I54318  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1921, 'S', 1923-2351 <RES>  
A/Cross-references: GB:M8648; NID:g182381; PID:AAA52420.1; PID:g182383  
R/Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Batton, D.L.; Gitcheiter, J.; Keyl, B.; Seeb  
Nature 312, 330-337, 1984  
A/Title: Expression of active human factor VIII from recombinant DNA clones.  
A/Reference number: A00525; MUID:85061548; PMID:6438526  
A/Accession: A00525  
A/Molecule type: mRNA  
A/Residues: 1-2351 <MCO>  
A/Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179  
R/Foote, J.T.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.  
s, D.N.; Hewick, R.M.  
Nature 312, 342-347, 1984  
A/Title: Molecular cloning of a cDNA encoding human antihemophilic factor.  
A/Reference number: I58059; MUID:85061550; PMID:6438528  
A/Accession: I58059  
A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-74, 'V', '76-1259, 'E', 1261-2351 <RE2>  
A/Cross-references: GB:X01740; NID:g182802; PID:AAA52484.1; PID:g182803  
R/Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Ka  
B.; Randolph, A.; Urdrea, M.S.; Valenzuela, P.; Dahl, H.H.; Favaloro, J.; Hansen, J.;  
DNA 4, 333-349, 1985  
A/Title: Characterization of the polypeptide composition of human factor VIII:C and t  
A/Reference number: A23584; MUID:86081164; PMID:3935400  
A/Accession: A23584  
A/Molecule type: mRNA  
A/Residues: 1-2351 <TRU>  
A/Cross-references: GB:M4113; NID:g182817; PID:AAA52485.1; PID:g182818  
R/Batton, D.; Rodriguez, H.; Venar, G.A.  
Biochemistry 25, 505-512, 1986  
A/Title: Proteolytic processing of human factor VIII. Correlation of specific cleavage  
ly.  
A/Reference number: A26174; MUID:86159740; PMID:3082357  
A/Accession: A26174  
A/Molecule type: protein  
A/Residues: 20-36; 392-399, 'X', 401-402; 1668-1676; 1709-1722, 'D', 1723-1725; 1741-1755 <SAJ  
R/Pittman, D.D.; Wang, J.H.; Kaufman, R.J.

Biochemistry 31, 3315-3325, 1992  
 A>Title: Identification and functional importance of tyrosine sulfate residues within re  
 A/Reference number: A42348; MUID:92207952; PMID:1554716  
 A/Accession: A42348  
 A/Molecule type: Protein  
 A/Residues: 20-36/356-371/392-408/582-594/1668-1669, 'X', 1671/1672-1692/1693-1708/1709-17  
 A/Experimental source: recombinant material from Chinese hamster ovary cells  
 A/Note: sequence extracted from NCBI backbone and corrected to correspond with the publi  
 J. Biol. Chem. 264, 14005-14010, 1989  
 A>Title: Inter-subunit fluorescence energy transfer in human factor VIII.  
 A/Reference number: A43986; MUID:89340500; PMID:2503509  
 A/Accession: A43986  
 A/Molecule type: Protein  
 A/Residues: 'X', 517-523/1853-1860, 'X', 1862-1864, 'X', 1866 <RAY>  
 R. Levte, A.; van Schijndel, H.B.; Niehs, C.; Hutterer, W.B.; Verbeet, M.P.; Mertens, K.;  
 J. Biol. Chem. 266, 740-745, 1991  
 A>Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for  
 A/Reference number: A56109; MUID:91093286; PMID:1898735  
 A/Contents: annotation; sulfation  
 R. Gitschler, J.; Wood, W.I.; Goralka, T.M.; Mion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,  
 Nature 312, 326-330, 1984  
 A>Title: Characterization of the human factor VIII gene.  
 A/Reference number: A56196; MUID:85061547; PMID:6438525  
 A/Contents: annotation; introns  
 R. Mullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.  
 Protein Sci. 4, 740-746, 1995  
 A>Title: Locations of disulfide bonds and free cysteines in the heavy and light chains c  
 A/Reference number: A56216; MUID:95338127; PMID:7614371  
 A/Contents: annotation; disulfide bonds  
 A/Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls  
 R. Kjaale, M.; Hedner, U.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.  
 Eur. J. Biochem. 234, 773-779, 1995  
 A>Title: Amino acid residues 721-729 are required for full factor VIII activity.  
 A/Reference number: S63527; MUID:96163459; PMID:8575434  
 A/Accession: S63527  
 A/Molecule type: Protein  
 A/Residues: 733-752/753-759 <KJA>  
 R. Lind, P.; Larsson, K.; Spitz, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg  
 Eur. J. Biochem. 232, 19-27, 1995  
 A>Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction  
 A/Reference number: S66445; MUID:96048024; PMID:7556150  
 A/Accession: S66445  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1668-1685 <LIN>  
 C/Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr  
 C/Genetics:  
 A/Genes: GDB:F8C  
 A/Cross-references: GDB:119124; OMIM:306700  
 A/Map position: Xq28-Xq28  
 A/Intons: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63  
 C/Function:  
 A/Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro  
 C/Superfamily: coagulation factor VIII, discoidin I amino-terminal homology; ferroxidase  
 C/Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla  
 F/1-19/DNA: signal sequence #status predicted <SIG>  
 F/20-2351/Product: coagulation factor VIII #status experimental <MAT>  
 F/20-740/Product: coagulation factor VIIa heavy chain #status experimental <ACH>  
 F/20-356/DNA: A1 <DA1>  
 F/23-348/DNA: ferroxidase repeat homology <FO1>  
 F/352-759/DNA: A2 <DA2>  
 F/402-730/DNA: ferroxidase repeat homology <FO2>  
 F/760-1667/DNA: B <DB0>  
 F/1668-2351/Product: coagulation factor VIIa light chain #status experimental <ACL>  
 F/1709-2038/DNA: A3 <DA3>  
 F/1716-2038/DNA: ferroxidase repeat homology <FO3>  
 F/2039-2191/DNA: C1 <DC1>  
 F/2039-2191/DNA: discoidin I amino-terminal homology <DN1>  
 F/2192-2351/DNA: C2 <DC2>  
 F/2192-2351/DNA: discoidin I amino-terminal homology <DN2>  
 F/60,258,601,776,803,847,919,962,982,1020,1024,1074,1085,1204,1274,1278,1301,1319,1403,1

F/172-198,267-348,547-573,649-730,1851-1877,1918-1922,2040-2188/Disulfide bonds: #sta  
 F/355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) #status predicted  
 F/355,337,738,742,1883,1659/Binding site: Sulfate (Tyr) (covalent) #status experiment  
 F/391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment  
 F/414,426/Binding site: Sulfate (Tyr) (covalent) #status predicted  
 F/759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment  
 F/1667-1668/Cleavage site: Arg-Glu (undifferentiated proteinase) #status experimental  
 F/1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experime  
 F/1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) #status experimental  
 F/2193-2345/Disulfide bonds: #status predicted

Query Match 100.0%; Score 82; DB 1; Length 2351;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 FRNGWTLTKVSSCD 731

## RESULT 2

A47004  
 Coagulation factor VIII precursor - mouse

C/Species: Mus musculus (house mouse)  
 C/Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text\_change 18-Jun-1999

C/Accession: A47004  
 R/Bider, B.; Larkich, D.; Gitschler, J.

Genomics 16, 374-379, 1993

A>Title: Sequence of the murine factor VIII cDNA.  
 A/Reference number: A47004; MUID:93300511; PMID:8314577

A/Accession: A47004  
 A/Status: preliminary

A/Molecule type: mRNA  
 A/Residues: 1-2319 <ELD>

A/Cross-references: GB:L05573; NID:9192456; PIDN:AA37385.1; PID:9192457  
 C/Superfamily: coagulation factor VIII, discoidin I amino-terminal homology; ferroxid

F/1-19/DNA: signal sequence #status predicted <SIG>  
 F/23-348/DNA: ferroxidase repeat homology <FO1>

F/402-730/DNA: ferroxidase repeat homology <FO2>  
 F/1886-2006/DNA: ferroxidase repeat homology <FO3>

F/2007-2156/DNA: discoidin I amino-terminal homology <DN1>  
 F/2160-2313/DNA: discoidin I amino-terminal homology <DN2>

Query Match 92.7%; Score 76; DB 2; Length 2319;  
 Best Local Similarity 93.8%; Pred. No. 1.7e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRNGWTLTKVSSCD 16  
 Db 716 FRNGWTLTKVSSCD 731

## RESULT 3

A25945  
 coagulation factor VIII - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 21-Jul-2000

C/Accession: A25945  
 R/Toole, J.T.; Pittman, D.D.; Orr, E.C.; Murtha, P.; Wasley, L.C.; Kaufman, R.J.

Proc. Natl. Acad. Sci. U.S.A. 83, 5939-5942, 1986  
 A>Title: A large region (approx 95 kDa) of human factor VIII is dispensable for in v

A/Reference number: A25945; MUID:86287369; PMID:3016730  
 A/Accession: A25945

A/Status: nucleic acid sequence not shown, not compared with conceptual translation  
 A/Molecule type: DNA

C/Superfamily: coagulation factor VIII, discoidin I amino-terminal homology; ferroxid

Query Match 85.4%; Score 70; DB 2; Length 869;  
 Best Local Similarity 93.3%; Pred. No. 8.7e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FRNGWTLTKVSSCD 16

DB 13 RNRGNTALLKXVSCD 27

## RESULT 4

T142763

coagulation factor VIII precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C&gt;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jun-2000

C:Accession: T142763

R:Lioliat, P.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z22269

A:Accession: T142763

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2133 &lt;LOL&gt;

A:Cross-references: EMBL:U49517; NID:G1511633; PID:G1511634; PIDN:AA06705.1

C:Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxidase

C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; Pla

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-2133/Product: coagulation factor VIII #status predicted &lt;MAT&gt;

F:23-349/Domain: ferroxidase repeat homology &lt;FOX1&gt;

F:402-730/Domain: ferroxidase repeat homology &lt;FOX2&gt;

F:1498-1820/Domain: ferroxidase repeat homology &lt;FOX3&gt;

Query Match 85.4%; Score 70; DB 2; Length 2133;

Best Local Similarity 93.3%; Pred. No. 0.00021;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RNRGNTALLKXVSCD 16  
DB 717 RNRGNTALLKXVSCD 731

## RESULT 5

B83412

streptomycin 3'-phosphotransferase PA1858 [imported] - Pseudomonas aeruginosa (strain F

C:Species: Pseudomonas aeruginosa

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83412

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.D.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,

; Lory, S.; Olsson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:2043737; PMID:10984043

A:Accession: B83412

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 &lt;STO&gt;

A:Cross-references: GB:AE004612; GB:AE004091; NID:9947846; PIDN:AA05247.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: str; PA1858

C:Superfamily: streptomycin 6-kinase

Query Match 53.7%; Score 44; DB 2; Length 275;  
Best Local Similarity 53.3%; Pred. No. 2.2;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 RNRGNTALLKXVSCD 16  
DB 34 RHRGMAAMKISSAS 48

## RESULT 6

S4966

lmbr protein - Streptomyces lincolnensis

C:Species: Streptomyces lincolnensis

C&gt;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Oct-1999

C:Accession: S69825; S4966

R:Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.

Mol. Microbiol. 16, 1137-1156, 1995

A:Title: Molecular characterization of the lincomycin-production gene cluster of Stre

A:Reference number: S69805; MUID:96020646; PMID:8577249

A:Accession: S69825

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-220 &lt;PE2&gt;

A:Cross-references: EMBL:X79146; NID:9499194; PIDN:CAAS5765.1; PID:G581696

A&gt;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994

C:Genetics:

A:Gene: lmbr

A:Start codon: GTG

C:Superfamily: Bacillus subtilis 23k phosphoprotein orfU

Query Match 51.2%; Score 42; DB 2; Length 220;  
Best Local Similarity 64.3%; Pred. No. 4.1;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 RNRGNTALLKXVSC 15  
DB 158 RHRGTAQLLVGSC 171

## RESULT 7

B86471

hypothetical protein T3269.38 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001

C:Accession: B86471

R:Rheologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Aloni

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallor

ke, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A6141; MUID:21016719; PMID:11130712

A:Accession: B86471

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-873 &lt;STO&gt;

A:Cross-references: GB:AE005172; NID:G11386301; PIDN:AA035092.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7

Query Match 50.0%; Score 41; DB 2; Length 873;  
Best Local Similarity 63.6%; Pred. No. 25;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNRGNTALLKX 11  
DB 624 RNRGTLQVVK 634

## RESULT 8

T14275

myosin-like protein my1 - common sunflower

N:Alternate names: ATMI homolog protein my1; unconventional myosin

C:Species: Helianthus annuus (common sunflower)

C&gt;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 08-Sep-2000

C:Accession: T14275

R:Yugrek, O.

submitted to the EMBL Data Library, March 1997

A:Description: Functional analysis of an unconventional myosin from sunflower express

A:Reference number: Z17957

A:Accession: T14275

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1120 &lt;VUG&gt;

A:Cross-references: EMBL:U94781; NID:G2444173; PIDD:AA671526.1; PID:G2444174  
 C:Genetics:  
 A:Gene: myl; hamyl  
 C:Superfamily: myosin heavy chain 95F; myosin motor domain homology  
 F:120-782/Domain: myosin motor domain homology <IMO>

Query Match 50.0%; Score 41; DB 2; Length 1120;  
 Best Local Similarity 50.0%; Pred. No. 31;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Db 793 RNRGWTALKVSSC 15  
 793 RNRGWTALKVSSC 806

RESULT 9  
 A97957  
 Hypothetical protein spr0681 [imported] - Streptococcus pneumoniae (strain R6)  
 C:Species: Streptococcus pneumoniae  
 C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
 C:Accession: A97957  
 R:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Bantz, R.H.; Jaskunas, S.R.;  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
 Y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001  
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A:Reference number: A97872; MUID:21439245; PMID:11544234  
 A:Accession: A97957  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-76 <DNR>  
 A:Cross-references: GB:AE007317; PIDD:AAK9485.1; PID:G15458269; GSPDB:GN00174  
 C:Genetics:  
 A:Gene: spr0681

Query Match 48.8%; Score 40; DB 2; Length 76;  
 Best Local Similarity 40.0%; Pred. No. 3.4;  
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 2 RNRGWTALKVSSC 16  
 7 KKKGVTLFWKSCN 21

RESULT 10  
 B8139  
 N-acetylneuraminate cyclidyltransferase (EC 2.7.7.43) Cj1143 [imported] - Campylobacter  
 C:Species: Campylobacter jejuni  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: B8139  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Randleam, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h  
 A:Reference number: A81250; MUID:20150912; PMID:10688204  
 A:Accession: B8139  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-536 <PAR>  
 A:Cross-references: GB:AL139077; GB:AL111168; NID:G6968444; PIDD:CA673398.1; PID:G696857  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: neuA; Cj1143  
 C:Keywords: nucleotidyltransferase

Query Match 48.8%; Score 40; DB 2; Length 536;  
 Best Local Similarity 43.8%; Pred. No. 23;  
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 1 FRNRGWTALKVSSC 16  
 434 FRNRGWTALKVSSC 449

## RESULT 11

B96639  
 protein TIF9.16 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: B96639  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloni  
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, T  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurce, J.S.; Maiti, R.; Marz  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor  
 ker, M.; Wu, D.; Xu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: B96639  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-573 <STO>  
 A:Cross-references: GB:AE005173; NID:G3056595; PIDD:AACT3906.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: TIF9.16  
 A:Map position: 1

Query Match 48.8%; Score 40; DB 2; Length 573;  
 Best Local Similarity 63.6%; Pred. No. 25;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 5 GMTALKVSSC 15  
 272 GVSALKVICSC 282

RESULT 12  
 A87117  
 probable phosphopantetheine adenylyltransferase [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: A87117  
 R:Cole, S.T.; Eiglsmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;  
 R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroy  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;  
 A:Title: Massive gene decay in the leprosy bacillus.  
 A:Reference number: A86909; MUID:21128732; PMID:11234002  
 A:Accession: A87117  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-157 <STO>  
 A:Cross-references: GB:AL450380; NID:G13093433; PIDD:CA630616.1; GSPDB:GN00147  
 C:Genetics:  
 A:Gene: coad  
 C:Superfamily: lipopolysaccharide core biosynthesis protein kdtB

Query Match 47.6%; Score 39; DB 2; Length 157;  
 Best Local Similarity 70.0%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 2 RNRGWTALKVSSC 11  
 75 RSRGWTALKVSSC 84

RESULT 13  
 T44703  
 lipopolysaccharide core biosynthesis protein [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000

C:/Accession: T44703  
 R.Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, May 1998  
 A/Reference number: 222830

A/Accession: T44703  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA

A/Residues: 1-160 <PAR>

A/Cross-references: EMBL:AL023635; PIDN:CA19191.1

A/Experimental source: cosmid B1243

C/Genetics:

A/Note: KdtB  
 C/Superfamily: lipopolysaccharide core biosynthesis protein kdtB

Query Match

47.6%; Score 39; DB 2; Length 160;

Best Local Similarity 70.0%; Pred. No. 11;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FRNGMTALLK 11

Db 78 RSRGWTATVK 87

#### RESULT 14

A/97642

sugar transporter AGR\_C\_4264 (U91632) [imported] - Agrobacterium tumefaciens (strain C58)

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

C/Accession: A97642

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A/Reference number: A97642; MUID:21608551; PMID:11743194

A/Accession: A97642

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-505 <KUR>

A/Cross-references: GB:AB07869; PIDN:AXK8090.1; PID:G15157518; GSPDB:GN00169

C/Genetics:

A/Map position: circular chromosome

Query Match

47.6%; Score 39; DB 2; Length 505;

Best Local Similarity 60.0%; Pred. No. 34;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNGMTALL 10

Db 182 FRNGMTSII 191

#### RESULT 15

AB2865

hypothetical protein gyaA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

C/Accession: AB2865

R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AB2865

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-512 <KUR>

A/Cross-references: GB:AB008688; PIDN:AAL43336.1; PID:G17740829; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Accession: T44703  
 R.Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, May 1998  
 A/Reference number: 222830

A/Accession: T44703  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA

A/Residues: 1-160 <PAR>

A/Cross-references: EMBL:AL023635; PIDN:CA19191.1

A/Experimental source: cosmid B1243

C/Genetics:

A/Note: KdtB  
 C/Superfamily: lipopolysaccharide core biosynthesis protein kdtB

Query Match

47.6%; Score 39; DB 2; Length 512;

Best Local Similarity 60.0%; Pred. No. 35;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNGMTALL 10

Db 189 FRNGMTSII 198

#### RESULT 16

A/97642

sugar transporter AGR\_C\_4264 (U91632) [imported] - Agrobacterium tumefaciens (strain C58)

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

C/Accession: A97642

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A/Reference number: A97642; MUID:21608551; PMID:11743194

A/Accession: A97642

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-505 <KUR>

A/Cross-references: GB:AB07869; PIDN:AXK8090.1; PID:G15157518; GSPDB:GN00169

C/Genetics:

A/Map position: circular chromosome

Query Match

47.6%; Score 39; DB 2; Length 512;

Best Local Similarity 60.0%; Pred. No. 34;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNGMTALL 10

Db 182 FRNGMTSII 191

#### RESULT 17

AB2865

hypothetical protein gyaA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

C/Accession: AB2865

R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AB2865

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-512 <KUR>

A/Cross-references: GB:AB008688; PIDN:AAL43336.1; PID:G17740829; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

Search completed: November 7, 2003, 07:36:23  
 Job time : 4.1721 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 1.15354 Seconds  
(without alignments)  
652.278 Million cell updates/sec

Title: US-09-661-992B-106

Sequence: 1 FRNRGNTALNKVSSCD 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	82	100.0	2351	FA8_HUMAN	P00451 homo sapien
2	76	92.7	2319	FA8_MOUSE	Q06194 mus musculu
3	70	85.4	2133	FA8_PIG	P12263 sus scrofa
4	41	50.0	324	CAHF_MOUSE	Q09233 mus musculu
5	39	47.6	160	COAD_MYCLE	Q69466 mycobacteri
6	38	46.3	514	ATPA_THRPE	P11677 chibacilli
7	37	45.1	304	PRX2_CRIGR	Q06438 cricetus
8	37	45.1	419	IRKG_RAT	P82191 rattus norv
9	36.5	44.5	650	BR86_BOOMI	P20736 boophilus m
10	36	43.9	89	SLTB_YEAST	P09336 bacteriophag
11	36	43.9	142	YB9E_YEAST	P38337 bacteriophag
12	36	43.9	160	RI5F_ARATH	Q9fma6 arabidopsis
13	36	43.9	167	APB2_AERPE	Q73943 aeropyrum p
14	36	43.9	207	YVYZ_YEAST	P47087 saccharomyc
15	36	43.9	375	DUS4_CHICK	Q9pwt1 gallus gall
16	36	43.9	394	DUS4_HUMAN	Q33115 homo sapien
17	36	43.9	395	DUS4_RAT	Q42877 rattus norv
18	36	43.9	405	LEPB_HABIN	P64833 haemophilus
19	36	43.9	419	IRKG_MOUSE	Q92307 mus musculu
20	36	43.9	442	HRB6_XANCV	P80153 xanthomonas
21	36	43.9	1150	NRDC_HUMAN	Q43847 homo sapien
22	36	43.9	1161	NRDC_MOUSE	Q8B841 mus musculu
23	36	43.9	1161	NRDC_RAT	P47245 rattus norv
24	35.5	43.3	261	PSB7_YEAST	P25043 saccharomyc
25	35	42.7	117	RS26_CAEEL	Q45499 caenorhabdi
26	35	42.7	164	UCRP_HUMAN	P05161 homo sapien
27	35	42.7	226	RNS7_PYPYR	P12779 rhizobium f
28	35	42.7	295	H1A_RHIFR	P12779 rhizobium f
29	35	42.7	306	BUB2_YEAST	P26448 saccharomyc
30	35	42.7	307	GPDA_AANSP	Q2Yw62 anabaena sp
31	35	42.7	336	USG_AZOVI	P66129 acetobacter
32	35	42.7	400	VG78_HSV1	Q00157 icetaurid h
33	35	42.7	418	IRKG_HUMAN	Q9npi9 homo sapien

34	35	42.7	444	1	OAR_CAEEL	Q02213 caenorhabdi
35	35	42.7	456	1	TRME_BUCAP	Q44633 buchnera ap
36	35	42.7	467	1	SIL5_MOUSE	Q31957 mus musculu
37	35	42.7	539	1	OSF_SHEEP	Q28542 ovis aries
38	35	42.7	587	1	RGPI_HUMAN	P40650 homo sapien
39	35	42.7	702	1	ERF_THICU	Q50565 chibacilli
40	35	42.7	1033	1	TIRI_ECOLI	P10486 escherichia
41	35	42.7	1849	1	BIG1_HUMAN	Q96656 homo sapien
42	34.5	42.1	415	1	Y207_METJA	Q60269 methanococc
43	34.5	42.1	497	1	KPYC_ARATH	Q65555 arabidopsis
44	34	41.5	108	1	R33A_SCHPO	Q3584 schizosacch
45	34	41.5	146	1	SP22_BACST	Q32727 bacillus st

## ALIGNMENTS

RESULT 1	FA8_HUMAN	STANDARD;	PRT; 2351 AA.
ID	FA8_HUMAN		
AC	P00451;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Coagulation factor VIII precursor (Procoagulant component)		
DE	(Antihemophilic factor) (AHF).		
GN	F8 OR F8C.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86081164; PubMed=3935400;		
RA	Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D., Harlog K., Kuo C.H., Maslarz F.R., Merryweather J.P., Najarian R., Pachl C., Porter S.J., Puma J., Quiroga M., Rall L.B., Randolph A., Urdia M.S., Valenzuela P., Dahl H.-H.M., Favaloro J., Hansen J., Nordfang O., Ezban M.,		
RT	"Characterization of the polypeptide composition of human factor VIII: C and the nucleotide sequence and expression of the human kidney cDNA."		
RT	DNA 4:333-349(1985).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=86061548; PubMed=6438526;		
RX	Wood W.T., Capon D.V., Simonsen C.C., Baton D.L., Gitschier J., Key B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L., Delwart B., Tuddenham E.G.D., Vohar G.A., Lawn R.M.,		
RT	"Expression of active human factor VIII from recombinant DNA clones."		
RT	Nature 312:330-337(1984).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=85061550; PubMed=6438528;		
RA	Toole J.J., Knopf J.L., Wozney J.M., Soltzman L.A., Buecker J.L., Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C., Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fass D.N., Hewick R.M.,		
RT	"Molecular cloning of a cDNA encoding human antihemophilic factor."		
RT	Nature 312:342-347(1984).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93265012; PubMed=1303178;		
RA	Gitschier J., Wood W.L.,		
RT	"Sequence of the exon-containing regions of the human factor VIII gene."		
RT	Hum. Mol. Genet. 1:199-200(1992).		
RN	[5]		
RP	SEQUENCE OF 2064-2070 FROM N.A.		
RA	de Water N.S., Williams R., Browett P.J.,		
RT	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	SULFATION OF TYR-1699.		

RX MEDLINE=91093266; PubMed=1898735;  
 RA Leyte A., van Schijndel H.B., Nierns C., Hutterer W.B., Verbeet M.P.,  
 RA Mertens K., van Mourik J.A.;  
 RT "Sulfation of Tyr1680 of human blood coagulation factor VIII is  
 RT essential for the interaction of factor VIII with von Willebrand  
 RT factor.";  
 RL J. Biol. Chem. 266:740-746(1991).  
 RN [7]  
 RP SUPFATION.  
 RX MEDLINE=92207952; PubMed=1554716;  
 RA Pittman D.D., Wang J.H., Kaufman R.J.;  
 RT "Identification and functional importance of tyrosine sulfate  
 RT residues within recombinant factor VIII.";  
 RL Biochemistry 31:3315-3325(1992).  
 RN [8]  
 RP STRUCTURE BY NMR OF 2322-2343.  
 RX MEDLINE=95200924; PubMed=7893714;  
 RA Gilbert G.E., Baleja J.D.;  
 RT "Membrane-binding peptide from the C2 domain of factor VIII forms an  
 RT amphipathic structure as determined by NMR spectroscopy.";  
 RL Biochemistry 34:3022-3031(1995).  
 RN [9]  
 RP REVIEW ON MOLECULAR BASIS OF HEMA.  
 RX MEDLINE=91221499; PubMed=1902642;  
 RA Gitschler J.;  
 RT "The molecular basis of hemophilia A.";  
 RL Ann. N.Y. Acad. Sci. 614:89-96(1991).  
 RN [10]  
 RP REVIEW ON MOLECULAR BASIS OF HEMA.  
 RX MEDLINE=89088506; PubMed=2491949;  
 RA White G.C. Jr., Shoemaker C.B.;  
 RT "Factor VIII gene and hemophilia A.";  
 RL Blood 73:11-12(1989).  
 RN [11]  
 RP REVIEW ON MOLECULAR BASIS OF HEMA.  
 RX MEDLINE=95245332; PubMed=7728145;  
 RA Antonarakis S.E., Kazazian H.H., Tuddenham E.G.D.;  
 RT "Molecular etiology of factor VIII deficiency in hemophilia A.";  
 RL Hum. Mutat. 5:1-22(1995).  
 RN [12]  
 RP VARIANT HEMA GLN-2326.  
 RX MEDLINE=86235434; PubMed=3012775;  
 RA Gitschler J., Wood W.I., Shuman M.A., Lawn R.M.;  
 RT "Identification of a missense mutation in the factor VIII gene of a  
 RT mild hemophiliac.";  
 RL Science 232:1415-1416(1986).  
 RN [13]  
 RP VARIANT HEMA PRO-2135.  
 RX MEDLINE=88096539; PubMed=3122181;  
 RA Levinson B., Jancso R.L., Phillips J.A. III, Gitschler J.;  
 RT "A novel missense mutation in the factor VIII gene identified by  
 RT analysis of amplified hemophilia DNA sequences.";  
 RL Nucleic Acids Res. 15:9797-9805(1987).  
 RN [14]  
 RP VARIANT HEMA GLN-2228.  
 RX MEDLINE=88191889; PubMed=2833855;  
 RA Yousoufian H., Antonarakis S.E., Bell W., Griffin A.M.,  
 RA Kazazian H.H.;  
 RT "Nonsense and missense mutations in hemophilia A: estimate of the  
 RT relative mutation rate at CG dinucleotides.";  
 RL Am. J. Hum. Genet. 42:718-725(1988).  
 RN [15]  
 RP VARIANT HEMA GLY-291.  
 RX MEDLINE=88220354; PubMed=2835904;  
 RA Yousoufian H., Wong C., Aronis S., Platakoukis H., Kazazian H.H. Jr.,  
 RA Antonarakis S.E.;  
 RT "Moderately severe hemophilia A resulting from Glu-->Gly substitution  
 RT in exon 7 of the factor VIII gene.";  
 RL Am. J. Hum. Genet. 42:867-871(1988).  
 RN [16]  
 RP VARIANT HEMA CYS-1708.  
 RX MEDLINE=89274393; PubMed=2499363;  
 RA O'Brien D.P., Tuddenham E.G.;  
 RT "Purification and characterization of factor VIII 1,689-Cys: a  
 RT nonfunctional cofactor occurring in a patient with severe hemophilia  
 RT A.";  
 RL Blood 73:2117-2122(1989).  
 RN [17]  
 RP VARIANT HEMA CYS-391.  
 RX MEDLINE=90001543; PubMed=2506948;  
 RA Shima M., Ware J., Yoshioaka A., Fukui H., Fulcher C.A.;  
 RT "An arginine to cysteine amino acid substitution at a critical  
 RT thrombin cleavage site in a dysfunctional factor VIII molecule.";  
 RL Blood 74:1612-1617(1989).  
 RN [18]  
 RP VARIANT HEMA LEU-189.  
 RX MEDLINE=90057680; PubMed=2510835;  
 RA Chan V., Chan T.K., Tong T.M., Todd D.;  
 RT "A novel missense mutation in exon 4 of the factor VIII:C gene  
 RT resulting in moderately severe hemophilia A.";  
 RL Blood 74:2688-2691(1989).  
 RN [19]  
 RP VARIANT HEMA LEU-2326.  
 RX MEDLINE=89197216; PubMed=2495245;  
 RA Inaba H., Fujimaki M., Kazazian H.H. Jr., Antonarakis S.E.;  
 RT "Wild hemophilia A resulting from Arg-to-Leu substitution in exon 26  
 RT of the factor VIII gene.";  
 RL Hum. Genet. 81:335-338(1989).  
 RN [20]  
 RP VARIANT HEMA HIS-391.  
 RX MEDLINE=89264602; PubMed=2498882;  
 RA Arai M., Inaba H., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,  
 RA Fujimaki M., Hoyer L.W.;  
 RT "Direct characterization of factor VIII in plasma: detection of a  
 RT mutation altering a thrombin cleavage site  
 RT (arginine-372-->histidine).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).  
 RN [21]  
 RP VARIANT HEMA CYS-1708.  
 RX MEDLINE=90105723; PubMed=2104766;  
 RA Arai M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,  
 RA Phillips J.A. III, Jancso R.L., Hoyer L.W.;  
 RT "Characterization of a thrombin cleavage site mutation (Arg 1689 to  
 RT Cys) in the factor VIII gene of two unrelated patients with  
 RT cross-reacting material-positive hemophilia A.";  
 RL Blood 75:384-389(1990).  
 RN [22]  
 RP VARIANTS HEMA GLN-2228 AND LEU-2326.  
 RX MEDLINE=90123183; PubMed=2105106;  
 RA Casula I., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,  
 RA Mancuso G., Morfini M., de Biasi R., Bauda F., Carbonara A.;  
 RT "Recurrent mutations and three novel rearrangements in the factor  
 RT VIII gene of hemophilia A patients of Italian descent.";  
 RL Blood 75:662-670(1990).  
 RN [23]  
 RP VARIANT HEMA CYS-391.  
 RX MEDLINE=90329422; PubMed=1973901;  
 RA Patterson J.K., McVey J.H., Boon M., Ajani A., Tuddenham E.G.;  
 RT "CRH+ hemophilia A due to a missense mutation (372-->Cys) at the  
 RT internal heavy chain thrombin cleavage site.";  
 RL Br. J. Haematol. 75:73-77(1990).  
 RN [24]  
 RP VARIANTS HEMA PHE-1699 AND CYS-1708.  
 RX MEDLINE=90152691; PubMed=2105906;  
 RA Higuchi M., Wong C., Kochan L., Olek K., Aronis S., Kasper C.K.,  
 RA Kazazian H.H., Antonarakis S.E.;  
 RT "Characterization of mutations in the factor VIII gene by direct  
 RT sequencing of amplified genomic DNA.";  
 RL Genomics 6:65-71(1990).  
 RN [25]  
 RP VARIANTS HEMA CYS-1728 AND ASP-1941.  
 RX MEDLINE=90169988; PubMed=2106480;  
 RA Traystman M.D., Higuchi M., Kasper C.K., Antonarakis S.E.,  
 RA Kazazian H.H.;  
 RT "Use of denaturing gradient gel electrophoresis to detect point  
 RT mutations in the factor VIII gene."



```

RL  submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN
RP  [2]
RX  SEQUENCE OF 705-1573 FROM N.A.
RA  MEDLINE=86287369; PubMed=3016730;
RA  Toole J.J., Pittman D.D., Orr E.C., Martha P., Wasley L.C.,
RA  Kaufman R.J.
RT  "A large region (approximately equal to 95 kDa) of human factor VIII
RT  is dispensable for in vitro procoagulant activity.";
RT  Proc. Natl. Acad. Sci. U.S.A. 83:5939-5942(1986).
RN
RP  [3]
RX  SEQUENCE OF 392-759 FROM N.A.
RA  MEDLINE=94179260; PubMed=7510693;
RA  Lublin I.M., Healey J.F., Scandella D., Runge M.S., Lollar P.;
RA  "Elimination of a major inhibitor epitope in factor VIII.";
RA  J. Biol. Chem. 269:8639-8641(1994).
CC  -I- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS
CC  AS A COFACTOR FOR FACTOR IXA WHEN IT CONVERTS FACTOR X TO THE
CC  ACTIVATED FORM, FACTOR XA.
CC  -I- SUBCELLULAR LOCATION: Extracellular.
CC  -I- SIMILARITY: Contains 3 F5/8 type A domains.
CC  -I- SIMILARITY: Contains 2 F5/8 type C domains.
CC  -I- SIMILARITY: STRONG. TO COAGULATION FACTOR V.
CC
CC  -----
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CC
CC  -----
DR  EMBL, U49517; AAB06705.1; -.
DR  PIR, A25945; A25945.
DR  PIR, T42763; T42763.
DR  HSSP, P00451; ICRG.
DR  InterPro: IPR001117; Cu-oxidase.
DR  InterPro: IPR000421; FA58_C.
DR  Pfam: PF00394; Cu-oxidase; 3.
DR  Pfam: PF00754; F5_F8_type_C; 2.
DR  SMART, SM00231; FA58C; 2.
DR  PROSITE, PS01285; FA58C_1; 2.
DR  PROSITE, PS01286; FA58C_2; 2.
DR  PROSITE, PS00022; FA58C_3; 2.
DR  PROSITE, PS00079; MULTICOPPER_OXIDASE1; 3.
KM  blood coagulation; Repeat; Plasma; Acute phase; Calcium;
KM  signal; Glycoprotein; Sulfation.
FT  SIGNAL 1
FT  CHAIN 19
FT  DOMAIN 20 2133
FT  DOMAIN 20 357
FT  DOMAIN 20 199
FT  DOMAIN 207 357
FT  DOMAIN 399 730
FT  DOMAIN 583 730
FT  DOMAIN 760 1599
FT  DOMAIN 1495 1822
FT  DOMAIN 1495 1659
FT  DOMAIN 1669 1822
FT  DOMAIN 1822 1970
FT  DOMAIN 1975 2127
FT  SITE 391 392
FT  SITE 759 760
FT  SITE 1449 1450
FT  MOD_RES 737 737
FT  MOD_RES 738 738
FT  MOD_RES 742 742
FT  DISULFID 173 199
FT  DISULFID 547 573
FT  DISULFID 1633 1659
FT  DISULFID 1822 1970
FT  DISULFID 1975 2127
FT  CARBOHYD 233 233

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Query Match Best Local Similarity 85.4%; Score 70; DB 1; Length 2133;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RNRGMTALLKYSQCD 16  
Db 717 RNRGMTALLKYSQCD 731

RESULT 4  
CAHF\_MOUSE STANDARD; PRT; 324 AA.

ID CAHF\_MOUSE STANDARD; PRT; 324 AA.  
AC Q99N23;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DS Carbonic anhydrase XIV precursor (EC 4.2.1.1) (Carbonate dehydratase  
XV) (CA-XV).  
GN CA15 OR CAR15.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
OX NCBI\_TaxID=10090;  
EN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Kidney;  
RA Hewlett-Emmett D., Shlimm L.C.;  
RT "Characterization and evolution of two new members of the alpha-  
carbonic anhydrase gene family in mouse: Car15 and Car15.1";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA DiCicco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Tothyluki S., Carninci P., Prange C.J.,  
RA Rana S.A., Lomuello N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
RA Villalón D.R., Motley D.M., Sodegryn E.J., Lu X., Gibbs R.A.,  
RA Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC -1- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC -1- COFACTOR: Zinc (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC family.
-----
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CC EMBL: AF231123; AAK16671.1; -.
CC EMBL: BC019975; AAH19975.1; -.
CC HSSP: G64444; 2ZNC.
CC MGD: MGI:1931324; Car15.
CC InterPro: IPR001148; Euk_Coandh.
CC Pfam: PF00194; carb_anhydriase; 1.
CC Prodom: PD000865; Euk_Coandh; 1.
CC PROSITE: PS00162; Euk_CO2_ANHYDRASE; FALSE_NEG.
CC Lysase; Zinc; Glycoprotein; Signal.
CC SIGNAL 1 18
CC CHAIN 19 324 CARBONIC ANHYDRASE XV.
CC METL 122 122 ZINC (CATALYTIC) (BY SIMILARITY).
CC METL 124 124 ZINC (CATALYTIC) (BY SIMILARITY).
CC METL 147 147 ZINC (CATALYTIC) (BY SIMILARITY).
CC CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 324 AA; 35482 MW; D285DD086476372F CRC64;
SQ
Query Match 50.0%; Score 41; DB 1; Length 324;
Best Local Similarity 61.5%; Pred. No. 3.1;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 NRGMTALLKVSQC 15
Db 87 NDGHTVLRLVNSC 99

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RA Holroyd S., Hornsby T., Jégals K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RT "Massive gene decay in the leprosy bacillus";
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: Reversibly transfers an adenylyl group from ATP to 4'-
CC phosphopantetheine, yielding dephospho-CoA (dPPCoA) and
CC pyrophosphate (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC 3'-dephospho-CoA.
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC -1- SUBUNIT: Homohexamer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the bacterial coad family.
-----
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CC EMBL: AL023635; CAA19191.1; -.
CC EMBL: AL583923; CAC30616.1; ALT_INTR.
CC PIR: T44703; T44703.
CC HSSP: P23875; 1B6T.
CC Leproma; ML1663; -.
CC HAMAP: MF_00151; -.
CC InterPro: IPR004821; Cyt tran rel.
CC InterPro: IPR004820; Cytidylyltransf.
CC InterPro: IPR001980; LPS biosynth.
CC Pfam: PF01467; CTP transf 2; 1.
CC PRINTS: PRO1020; LPSBIOSYNTHS.
CC TIGRPFAMS: TIGR01510; coad_prev_kdtb; 1.
CC TIGRPFAMS: TIGR00125; Cyt_tran_rel; 1.
CC Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis;
CC Complete proteome.
CC SEQUENCE 160 AA; 17496 MW; 1F762492F3C0676C CRC64;
SQ
Query Match 47.6%; Score 39; DB 1; Length 160;
Best Local Similarity 70.0%; Pred. No. 3.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 2 NRGMTALLK 11
Db 78 RSRGMTALIVK 87

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RESULT 5
COAD_MYCLE STANDARD; PRT; 160 AA.
ID COAD_MYCLE
AC 069466;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DS Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DS phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DS pyrophosphorylase).
DS COAD OR KDTB OR ML1663 OR MLCB1243.10.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OK NCBI_TaxID=1769;
RN NCB1_TaxID=1769;
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eismaster K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown S., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

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RESULT 6
ATPA_THIFE STANDARD; PRT; 514 AA.
ID ATPA_THIFE
AC P41167;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS ATP synthase alpha chain (EC 3.6.3.14).
DS ATPA.
OS Thibacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OK NCBI_TaxID=920;
RN NCB1_TaxID=920;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33020;
RX MEDLINE=95047244; PubMed=7958772;
RA Brown L.D., Demehy M.E., Rawlings D.B.;
RT "The fl genes of the Rf0 ATP synthase from the acidophilic bacterium
RT Thibacillus ferrooxidans complement Escherichia coli F1 unc
RT mutants";
RL FEMS Microbiol. Lett. 122:19-26(1994).

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CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
CC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC H(+) (out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
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-----
CC EMBL: M61087; AAA53125.1; -.
CC InterPro: IPR000793; ATPase_a/AC.
CC InterPro: IPR000194; ATPase_a/DNcentr.
CC InterPro: IPR004100; ATPase_a/DN.
CC InterPro: IPR000790; ATPase_AC.
CC InterPro: IPR005294; ATPsynthf1_alpha.
CC Pfam: PF00006; ATP-synt_ab; 1.
CC Pfam: PF00306; ATP-synt_ab_C; 1.
CC Pfam: PF02874; ATP-synt_ab_N; 1.
CC ProDom: PD001099; ATPase_ac; 1.
CC TrRfam: TR000962; atpA; 1.
CC PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
CC ATP synthesis; CF(1); ATP-binding; Hydrolyase;
CC Hydrogen ion transport.
CC K1M BIND 170 177 ATP (BY SIMILARITY).
CC ACT SITE 374 374 BY SIMILARITY.
CC SEQUENCE 514 AA; 55600 MW; 8349B6C651BC6B CRC64;

Query Match 46.3%; Score 38; DB 1; Length 514;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRNRGNTALL 10
DB 250 FRDRGNMALL 259

RESULT 7
PEX2_CRIGR STANDARD; PRT; 304 AA.
AC Q06438;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxisome assembly factor-1 (PAF-1) (Peroxin-2) (Peroxisomal membrane
DE protein 3).
GN PMP3 OR PEX2 OR PAF1 OR PMP35.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_Taxid=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=93286102; PubMed=7685346;
RT Thieringer R., Raetz C.R.H.;
RT "peroxisome-deficient Chinese hamster ovary cells with point
RT mutations in peroxisome assembly factor-1.";
RU J. Biol. Chem. 268:12631-12636(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=94309666; PubMed=8035823;
RA Tsukamoto T., Shimozawa N., Fujiki Y.;

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RT "Peroxisome assembly factor 1: nonsense mutation in a peroxisome-
RT deficient Chinese hamster ovary cell mutant and deletion analysis.";
RU Mol. Cell. Biol. 14:5458-5465(1994).
CC -1- FUNCTION: SOMEWHAT IMPLICATED IN THE BIOGENESIS OF PEROXISOMES.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
-----
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-----
CC EMBL: Z17220; CA478929.1; -.
CC EMBL: D30618; BA06308.1; -.
CC PIR: A45989; A45989.
CC InterPro: IPR006845; Pex2_Pex12.
CC InterPro: IPR001841; Znf_fing.
CC Pfam: PF04757; Pex2_Pex12; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; 1.
CC PROSITE: PS00891; ZF_RING_2; 1.
CC Transmembrane; Peroxisome; Zinc-finger.
FT TRANSMEM 139 212 BY SIMILARITY.
FT TRANSMEM 194 212 BY SIMILARITY.
FT ZN FING 243 283 RING-TYPE.
FT MUTGEN 246 246 C-Y: LOSS OF FUNCTION.
SQ SEQUENCE 304 AA; 34794 MW; 84ECFPA613C148BF CRC64;

Query Match 45.1%; Score 37; DB 1; Length 304;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRNRGNTALLKVSNC 15
DB 123 FRNRHLASFGKVKOC 137

RESULT 8
IRKG_RAT STANDARD; PRT; 419 AA.
AC P52191; G9J187;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inward rectifier potassium channel 16 (Potassium channel, inwardly
DE rectifying, subfamily J, member 16) (Inward rectifier K+ channel
DE Kir5.1) (Kir5).
GN KCNJ16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Brain;
RA MEDLINE=95179470; PubMed=7874445;
RA Bond C.T., Pessia M., Xia X.-M., Lagrutta A., Kavanaugh M.P.,
RA Adelman J.P.;
RA "Cloning and expression of a family of inward rectifier potassium
RA channels.";
RT Recept. Channels 2:183-191(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20287495; PubMed=10764726;
RA Tucker S.J., Imbrici P., Salvatore L., D'Adamo M.C., Pessia M.;
RT "pH dependence of the inwardly rectifying potassium channel, Kir5.1,
RT and localization in renal tubular epithelia.";
RU J. Biol. Chem. 275:16404-16407(2000).
CC -1- FUNCTION: INWARD RECTIFIER K+ CHANNELS ARE CHARACTERIZED BY A

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GREATER TENDANCY TO ALLOW POTASSIUM TO FLOW INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLTAGE DEPENDANCE IS REGULATED BY THE CONCENTRATION OF EXTRACELLULAR POTASSIUM; AS EXTERNAL K+ IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL MAGNESIUM. KCNU16 MAY BE INVOLVED IN THE REGULATION OF FLUID AND PH BALANCE (BY SIMILARITY).

-1- SUBUNIT: SEEMS TO FORM HETERODIMER WITH KIR4.1/KCNJ10 OR KIR2.1/KCNJ2.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: IN THE BRAIN, TESTIS, LIVER, SPLEEN, KIDNEY, SUPRAXILIARY GLAND, AND ADRENALS.

-1- SIMILARITY: BELONGS TO THE INWARD RECTIFIER-TYPE K+ CHANNEL FAMILY.

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EMBL: X85851; CAAS8564.1; -.

EMBL: AF249676; AAF74265.1; -.

InterPro: IPR001838; K+channel\_IR.

InterPro: IPR001622; K+channel\_pore.

Pfam: PF01007; IRK; 1.

PRINTS: PR01320; KIRCHANNEL.

ProDom: PD001103; K+channel\_IR; 2.

Ionic channel; Ion transport; Voltage-gated channel; Transmembrane; Potassium transport.

DOMAIN 1 75 CYTOPLASMIC (POTENTIAL).

TRANSMEM 76 98 M1 (POTENTIAL).

DOMAIN 121 137 H5 (PORE-FORMING) (POTENTIAL).

TRANSMEM 146 170 M2 (POTENTIAL).

DOMAIN 171 419 CYTOPLASMIC (POTENTIAL).

SITE 161 161 ROLE IN THE CONTROL OF POLYAMINE-MEDIATED CHANNEL GATING AND IN THE BLOCKING BY INTRACELLULAR MAGNESIUM (BY SIMILARITY).

CONFLICT 361 419 RGSCSTDTNRRSFSAVAVVSCNPEPSTSPDCEKCV  
PYKALLTNRIKISMSOM -> PRILHGHQHEBILQSC  
HGEOL (IN REF. 1).

SEQUENCE 419 AA; 47936 MW; AC654A72D51A1IC CRC64;

Query Match 45.14; Score 37; DB 1; Length 419;  
Best Local Similarity 46.74; Pred. No. 24;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 RNRGNTALKVSQCD 16

DB 371 RRRSFSAVAVVSCSE 385

RESULT 9

BM86\_BOOMI STANDARD; PRT; 650 AA.

AC P20736; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Glycoprotein antigen BM86 precursor (Protective antigen).

OS Boophilus microplus (Cattle tick).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Acari;

OC Parasitiformes; Ixodidae; Ixodidae; Boophilus.

ON NCB1\_Taxid=6941;

RX TISSUE=Gut;

RX MEDLINE=9009323; Pubmed=2690068;

RA Rand K.N., Moore T., Srikantha A., Spring K., Teljam R.L., Willadsen P., Cobon G.S.;

"Cloning and expression of a protective antigen from the cattle tick Boophilus microplus.";  
Proc. Natl. Acad. Sci. U.S.A. 86:9657-9661(1989).

RP PARTIAL SEQUENCE.

RX MEDLINE=89309823; Pubmed=2745982;

RA Willadsen P., Riding G.A., McKenna R.V., Kemp D.H., Teljam R.L., Nielsen J.N., Lahnstein J., Cobon G.S., Gough J.M.;

RA "Immunologic control of a parasitic arthropod. Identification of a protective antigen from Boophilus microplus.";  
J. Immunol. 143:1346-1351(1989).

-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Probable).

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-1- SIMILARITY: Contains 7 EGF-like domains.

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EMBL: M29321; AAA30098.1; -.

PIR: A34498; A34498.

InterPro: IPR006209; EGF\_Like.

InterPro: IPR006210; IEGF.

Pfam: PF00008; EGF; 2.

SMART: SM00181; EGF; 2.

PROSITE: PS00022; EGF\_1; FALSE NEG.

PROSITE: PS01186; EGF\_2; FALSE NEG.

KW Glycoprotein; Antigen; Signal; EGF-like domain; Repeat; GPI-anchor.

CHAIN 1 19

PROPEP 628 650

DOMAIN 20 627 GLYCOPROTEIN ANTIGEN BM86.

DOMAIN 67 104 HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).

DOMAIN 205 247 EGF-LIKE 1.

DOMAIN 251 292 EGF-LIKE 2.

DOMAIN 291 335 EGF-LIKE 3.

DOMAIN 482 530 EGF-LIKE 4.

DOMAIN 531 568 EGF-LIKE 5.

DOMAIN 601 627 EGF-LIKE 6.

DISULFID 32 49 SER/THR-RICH.

DISULFID 51 65 BY SIMILARITY.

DISULFID 71 81 BY SIMILARITY.

DISULFID 76 91 BY SIMILARITY.

DISULFID 93 103 BY SIMILARITY.

DISULFID 209 222 BY SIMILARITY.

DISULFID 218 231 BY SIMILARITY.

DISULFID 233 246 BY SIMILARITY.

DISULFID 255 269 BY SIMILARITY.

DISULFID 263 278 BY SIMILARITY.

DISULFID 280 291 BY SIMILARITY.

DISULFID 295 307 BY SIMILARITY.

DISULFID 300 316 BY SIMILARITY.

DISULFID 318 334 BY SIMILARITY.

DISULFID 486 500 BY SIMILARITY.

DISULFID 492 516 BY SIMILARITY.

DISULFID 518 529 BY SIMILARITY.

DISULFID 535 550 BY SIMILARITY.

DISULFID 543 559 BY SIMILARITY.

DISULFID 561 567 BY SIMILARITY.

LIPID 627 627 GPI-ANCHOR (BY SIMILARITY).

CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).

VARIANT 235 237 SCS -> RAF.

FT VARIANT 507 507 F -> C.

SEQUENCE 650 AA; 71721 MW; 5DBD71B354D8312A CRC64;

Query Match 44.5%; Score 36.5; DB 1; Length 650;  
 Best Local Similarity 45.0%; Pred. No. 49;  
 Matches 9; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 RNRGNTALKV-----SSCD 16  
 DB 114 RNRGNTALKV-----SSCD 133

RESULT 10  
 SLTB\_BP933 STANDARD; PRT; 89 AA.  
 AC P03385; Q96198;  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE SHIGA-like toxin II subunit B precursor (Verotoxin 2 subunit B)  
 DE (SLT-IIb).  
 GN STX2B.  
 OS Bacteriophage 933W.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC Lambda-like viruses.  
 CX NCBI\_TaxID=10730;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA Jackson M.P., Neill R.J., O'Brien A.D., Holmes R.K., Newland J.W.;  
 RT "Nucleotide sequence analysis and comparison of the structural genes  
 RT for Shiga-like toxin I and Shiga-like toxin II encoded by  
 RT bacteriophages from *Escherichia coli* 933.";  
 RL FEMS Microbiol. Lett. 44:109-114(1987).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RA MEDLINE=97257502; PubMed=9103976;  
 RX Schmidt H., Scheef J., Janetzki-Mittmann C., Datz M., Karch H.;  
 RT "An *lex* RNA gene is located close to the Shiga toxin II operon in  
 RT enterohemorrhagic *Escherichia coli* O157 and non-O157 strains.";  
 RL FEMS Microbiol. Lett. 143:39-44(1997).  
 CC -1- FUNCTION: THE B SUBUNIT IS RESPONSIBLE FOR BINDING THE TOXIN TO  
 CC SPECIFIC RECEPTORS ON THE TARGET CELL SURFACE.  
 CC -1- SUBUNIT: THE SHIGA-LIKE TOXINS CONTAIN A SINGLE A SUBUNIT AND  
 CC MULTIPLE COPIES OF A B SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE SLT BETA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X07865; CAA30715.1; -;  
 DR EMBL; Y10775; CAA71748.1; -;  
 DR PIR; S01033; S01033.  
 DR HSSP; P08027; IBOV.  
 DR InterPro; IPR003189; SLT\_beta.  
 DR Pfam; PF02258; SLT\_beta; 1.  
 DR ProDom; PD006042; SLT\_beta; 1.  
 KM Toxin; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 89 SHIGA-LIKE TOXIN II SUBUNIT B.  
 FT DISULFD 22 75 BY SIMILARITY  
 SO SEQUENCE 89 AA; 9874 MW; 0EFDDBB7CC581D9 CRC64;

Query Match 43.9%; Score 36; DB 1; Length 89;  
 Best Local Similarity 50.0%; Pred. No. 6.8;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMTALKVSSCD 16  
 DB 65 GMTALKVSSCD 76

RESULT 11  
 YB9E\_YEAST STANDARD; PRT; 142 AA.  
 AC P38337;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical 16.4 kDa protein in POP4-SH1 intergenic region.  
 GN YBR258C OR YBR1726.  
 OS *Saccharomyces cerevisiae* (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CX NCBI\_TaxID=4932;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN=8288C;  
 RC MEDLINE=93220397; PubMed=8465606;  
 RX Daignon F., Bileau N., Crouzet M., Nigle M.;  
 RA "The complete sequence of a 19,482 bp segment located on the right  
 RT arm of chromosome II from *Saccharomyces cerevisiae*.";  
 RL Yeast 9:189-199(1993).  
 CC -----

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 CC -----  
 DR EMBL; X70529; CAA49922.1; -;  
 DR EMBL; Z36127; CAA85221.1; -;  
 DR PIR; S32960; S32960.  
 DR SGD; S0000462; SHG1.  
 DR GO; GO:0018024; F-histone-lysine N-methyltransferase activity; IDA.  
 DR GO; GO:0018571; F-histone methylation; IDA.  
 DR Pfam; PF05205; Cpaf15; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 142 AA; 16429 MW; 12E73F0C3DD225D7 CRC64;

Query Match 43.9%; Score 36; DB 1; Length 142;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNRGNTALK 10  
 DB 67 RNRGNTALK 76

RESULT 12  
 R1SF\_ARATH STANDARD; PRT; 160 AA.  
 ID R1SF\_ARATH  
 AC O9FML6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 40S ribosomal protein S15-6.  
 GN RPS15 OR A15G63070 OR MD12.3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 CX NCBI\_TaxID=702;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN=cv. Columbia;  
 RX MEDLINE=98162728; PubMed=9501997;  
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asanizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.  
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen  
 RT physically assigned P1 clones.";

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RL DNA Res. 4:401-414(1997).
RN (2)
RP GENE FAMILY ORGANIZATION, AND NOMENCLATURE.
RC STRAIN=CV, Columbia;
RX MEDLINE=21482694; PubMed=11598216;
RA Barakat A., Szick-Miranda K., Chang I.-F., Guyot R., Blanc G.,
RT Cooke R., Delensy M., Bailey-Serres J.;
RT "The organization of cytoplasmic ribosomal protein genes in the
RT Arabidopsis genome.";
RL Plant Physiol. 127:398-415(2001).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC EMBL; AB008265; BAB10549.1; -.
CC HSSP; P80381; 1QKF.
CC InterPro; IPR002222; Ribosomal_S19.
CC InterPro; IPR005713; S15_euk_arch.
CC Pfam; PF00203; Ribosomal_S19; 1.
CC PRINTS; PR00975; RIBOSOMAL_S19.
CC PRODOM; PD001012; Ribosomal_S19; 1.
CC TIGRFAMs; TIGR01025; rps_arch; 1.
CC PROSITE; PS00323; RIBOSOMAL_S19; 1.
CC Ribosomal protein; Multigene family.
SQ SEQUENCE 160 AA; 18576 MW; A85F03A3ADA37649 CRC64;

Query Match 43.9%; Score 36; DB 1; Length 160;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FNRGRTALTKYSSCD 16
DB 26 FRGPNVDALTKMSND 41

RESULT 13
APE2_AERPE STANDARD; PRT; 167 AA.
ID APE2_AERPE STANDARD; PRT; 167 AA.
AC 073943; G9YAM2; (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Homing endonuclease I-ApeII (EC 3.1.1.-) (rRNA intron-encoded homing
DE endonuclease 2).
GN APEII OR APEI1921.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98324973; PubMed=9658008;
RA Nomura N., Sako Y., Uchida A.;
RT "Molecular characterization and postsplicing fate of three introns
RT within the single rRNA operon of the hyperthermophilic archaeon
RT Aeropyrum pernix K1.";
RT Aeropyrum pernix K1.";
RL J. Bacteriol. 180:3635-3643(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Aoki A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

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RA Yamazaki J., Kuehida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -1- FUNCTION: ENDONUCLEASE INVOLVED IN RNA INTRON I-GAMMA HOMING.
CC -----
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CC -----
CC EMBL; AB008745; BAA31988.1; ALT_INIT.
CC EMBL; AP000062; BAA80926.1; -.
CC PIR; A72580; A72580.
CC InterPro; IPR001982; Endonuc_LAG/HNH.
CC Pfam; PF00961; LAGLIDADG_1; 1.
CC Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome.
FT CONFLICT 131 167
FT KSYSLSSLNKKSKRRSRSEITIKTIIPCDKAVEPPGER ->
FT NRTPYLA (IN REF. 1).
SQ SEQUENCE 167 AA; 19140 MW; 52D500B57FBC75CB CRC64;

Query Match 43.9%; Score 36; DB 1; Length 167;
Best Local Similarity 40.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 FNRGRTALTKYSSCD 16
DB 144 KRSLERITKIRPCD 158

RESULT 14
YVY2_YEAST STANDARD; PRT; 207 AA.
ID YVY2_YEAST STANDARD; PRT; 207 AA.
AC P47087.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 23.2 kDa protein in SPCL-1IV3 intergenic region.
GN YUR012C OR J1440 OR YUR83.25.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RC de Haan M., Smits P.H.M., Grivell L.A.;
RL Submitted (May-1995) to the EMBL/Genbank/DBJ databases.
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CC -----
CC EMBL; X87611; CA60934.1; -.
CC EMBL; Z49512; CAA89536.1; -.
CC PIR; S55200; S55200.
CC SGD; S0005773; YUR012C.
CC Hypothetical protein; Transmembrane.
KW HYPOHETICAL YUR012C.
FT TRANSMEM 17
FT POTENTIAL.
SQ SEQUENCE 207 AA; 23190 MW; FDC11EBED5AFA90A CRC64;

Query Match 43.9%; Score 36; DB 1; Length 207;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 5 GMTALKVSSC 15  
 |||:|:|:|  
 Db 154 GMTSLTRLSEC 164

Db 202 GITALKVSS 211  
 :|:|:|:|:|

Search completed: November 7, 2003, 07:28:11  
 Job time : 3.15354 secs

RESULT 15  
 DUSA4 CHICK STANDARD; PRT; 375 AA.  
 ID DUSA4 CHICK STANDARD; PRT; 375 AA.  
 AC 09FW71;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)  
 DE (Mitogen-activated protein kinase phosphatase-2) (MAP kinase  
 DE phosphatase-2) (MKP-2).  
 GN DUSP4 OR MKP2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn;  
 RX MEDLINE=20379359; PubMed=10918612;  
 RA Fu S.-L., Waha A., Vogt P.K.;  
 RT "Identification and characterization of genes upregulated in cells  
 RT transformed by v-Jun.";  
 RL Oncogene 19:3537-3545(2000).  
 CC -1- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY  
 CC DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES  
 CC ERK1 AND ERK2 (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
 CC phosphate.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-  
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.  
 CC -1- SIMILARITY: Contains 1 rhodanese domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF167286; AAD46656.1; -.  
 DR HSSP: Q16828; IMKP.  
 DR InterPro: IPR000340; DS\_phosphatase.  
 DR InterPro: IPR001763; Rhodanese-like.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR Pfam: PF00782; DSpC; 1.  
 DR Pfam: PF00581; Rhodanese; 1.  
 DR SMART: SM00195; DSpC; 1.  
 DR SMART: SM00450; RHOD; 1.  
 DR PROSITE: PS50206; RHODANESE\_3; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50054; TYR\_PHOSPHATASE\_DUAL; 1.  
 KM Hydrolase; Nuclear protein.  
 FT DOMAIN 25 143 RHODANESE.  
 FT ACT SITE 178 375 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT SITE 261 261 BY SIMILARITY.  
 SQ SEQUENCE 375 AA; 41052 MW; 179290DC2BEEF1 CRC64;

QY 5 GMTALKVSS 14  
 Query Match 43.9%; Score 36; DB 1; Length 375;  
 Best Local Similarity 80.0%; Pred. No. 33;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 5.27637 seconds

(without alignments)  
782.516 Million cell updates/sec

Title: US-09-661-992b-106

Perfect score: 82  
Sequence: 1 FRNRGMTALKVSSCD 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_podent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	93.9	2343	6	062730
2	77	93.9	2343	6	018806
3	44	53.7	275	16	0912N7
4	43	52.4	265	10	08S3T6
5	43	52.4	311	4	08NGLO
6	43	52.4	312	11	08VGA8
7	42	51.2	220	2	054372
8	42	51.2	221	2	093MP7
9	42	51.2	221	2	0933W2
10	42	51.2	221	2	09K387
11	42	51.2	221	2	09F0M6
12	42	51.2	221	2	0938X3
13	41	50.0	324	11	099N23
14	41	50.0	381	16	09KX14
15	41	50.0	537	16	08FTK2
16	41	50.0	843	10	09FXK5

17	41	50.0	872	10	09S916	09S916 arabidopsis
18	41	50.0	872	10	09CED8	09CED8 arabidopsis
19	41	50.0	875	10	09LVZ1	09LVZ1 arabidopsis
20	41	50.0	884	10	09FWZ8	09FWZ8 arabidopsis
21	41	50.0	1120	10	024515	024515 helianthus
22	40.5	49.4	782	4	075659	075659 homo sapien
23	40.5	49.4	1104	4	075180	075180 homo sapien
24	40.5	49.4	1158	4	09B087	09B087 homo sapien
25	40.5	49.4	1158	4	09C058	09C058 homo sapien
26	40.5	49.4	1158	4	09C058	09C058 homo sapien
27	40	48.8	76	16	08CJZ4	08CJZ4 streptococc
28	40	48.8	220	10	09HLA8	09HLA8 thermoplas
29	40	48.8	355	10	09SGH8	09SGH8 arabidopsis
30	40	48.8	355	10	094413	094413 arabidopsis
31	40	48.8	355	10	094413	094413 arabidopsis
32	40	48.8	407	5	09N3Y7	09N3Y7 caenorhabd
33	40	48.8	425	5	08WTW2	08WTW2 caenorhabd
34	40	48.8	536	16	09PWF1	09PWF1 campylobact
35	40	48.8	573	10	093ZEA	093ZEA arabidopsis
36	40	48.8	573	10	064785	064785 arabidopsis
37	39	47.6	897	3	09HDS6	09HDS6 arabidopsis
38	39	47.6	194	16	08CUP6	08CUP6 arabidopsis
39	39	47.6	195	2	030797	030797 mycobacteri
40	39	47.6	320	11	08VGB1	08VGB1 mus musculu
41	39	47.6	356	10	08GMD6	08GMD6 arabidopsis
42	39	47.6	357	10	08LGC7	08LGC7 arabidopsis
43	39	47.6	442	16	08PB87	08PB87 xanthomonas
44	39	47.6	461	4	08NAV7	08NAV7 homo sapien
45	39	47.6	499	10	09LAV9	09LAV9 arabidopsis
			512	16	005176	005176 agrobacteri

## ALIGNMENTS

RESULT 1  
ID 062730 PRELIMINARY; PRT; 2343 AA.

AC 062730:  
DT 01-AUG-1998 (TEMBUREL. 07, Created)  
DT 01-AUG-1998 (TEMBUREL. 07, last sequence update)  
DT 01-MAR-2003 (TEMBUREL. 23, last annotation update)  
DE Factor VIII.  
OS Canis familiaris (Dog).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney, and Spleen;  
RA Gordy P.W., Bowen R.A.;  
RT "Characterization of the canine factor VIII cDNA."  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 2 P5/8 TYPE C DOMAINS.  
DR EMBL; AF049489; AAC05384.1; -.  
DR HSSP; P00451; ICFG.  
DR InterPro; IPR001117; Cu-oxidase.  
DR InterPro; IPR000421; FAS8\_C.  
DR Pfam; PF00394; Cu-Oxidase; 3.  
DR Pfam; PF00754; F5\_F8\_Type\_C; 2.  
DR SMART; SM00231; FAS8C; 2.  
DR PROSITE; PS01285; FAS8C\_1; 2.  
DR PROSITE; PS01286; FAS8C\_2; 2.  
DR PROSITE; PS00079; MUTITCOPER\_OXIDASEL; 3.  
SQ SEQUENCE 2343 AA; 265613 MW; F612D744ADADD99 CRC64;

Query Match 93.9%; Score 77; DB 6; Length 2343;

Best Local Similarity 93.8%; Pred. No. 38-05; Mismatches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGMTALKVSSCD 16  
DB 710 FRNRGMTALKVSSCD 725



DR PRINTS: PR00237; GPCRHDOPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM Receptor; Transmembrane.  
 SQ SEQUENCE 311 AA; 34682 MW; C680187C542C27DA CRC64;

Query Match 52.4%; Score 43; DB 4; Length 311;  
 Best Local Similarity 75.0%; Pred. No. 10;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 NRGMTALLKVVSS 14  
 DB 42 NLGWTALLIVSS 53

## RESULT 6

Q8VGAB PRELIMINARY; PRT; 312 AA.  
 AC Q8VGAB;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE Olfactory receptor MOR174-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang X., Firestein S.J.;  
 RT "The olfactory receptor gene superfamily of the mouse.";  
 RL Nat. Neurosci. 0:0-0(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A070244; AAL60907.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopn.  
 DR Pfam: PF00001; Tm1.1; 1.  
 DR PRINTS: PR00237; GPCRHDOPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM Receptor.  
 SQ SEQUENCE 312 AA; 34685 MW; 9AA8CDBE70E0A274 CRC64;

Query Match 52.4%; Score 43; DB 11; Length 312;  
 Best Local Similarity 75.0%; Pred. No. 10;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 NRGMTALLKVVSS 14  
 DB 42 NLGWTALLIVSS 53

## RESULT 7

Q54372 PRELIMINARY; PRT; 220 AA.  
 AC Q54372;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE lmbR protein.  
 GN LMBR.  
 OS Streptomyces lincolnensis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 NCBI\_TaxID=1915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=78-11;  
 RA MEDLINE=96020646; PubMed=8577249;  
 RA Peschke U., Schmidt H., Zhang H.Z., Piepersberg W.;  
 RT "Molecular characterization of the lincomycin-production gene cluster

RT of Streptomyces lincolnensis 78-11.";  
 RL Mol. Microbiol. 16:1137-1156(1995).  
 DR EMBL: X79146; CAAS5765.1; -  
 DR InterPro: IPR001585; Transaldolase.  
 DR Pfam: PF00923; Transaldolase; 1.  
 DR PROSITE: PS01054; TRANSALDOLASE\_1; 1.  
 SQ SEQUENCE 220 AA; 23491 MW; 59158145A16AAEF7 CRC64;

Query Match 51.2%; Score 42; DB 2; Length 220;  
 Best Local Similarity 64.3%; Pred. No. 11;  
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NRGMTALLKVVSSC 15  
 DB 158 RRRGMTAQLVSSC 171

## RESULT 8

Q93MP7 PRELIMINARY; PRT; 221 AA.  
 AC Q93MP7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE CMP-Neu5Ac synthetase.  
 GN NEU5A1.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Campylobacteraceae; Campylobacter.  
 NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43438;  
 RA Gilbert M., Michlewicz J., Karwaki M.-F., Cunningham A.,  
 RA Wakarchuk W.W.;  
 RT "The genetic basis for the variation in the lipo-oligosaccharide of  
 the mucosal pathogen, Campylobacter jejuni: Biosynthesis of sialylated  
 ganglioside mimics in the core oligosaccharide.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF400048; AAK91728.1; -  
 DR InterPro: IPR003329; Cytidylyl-trans.  
 DR Pfam: PF02348; CMP\_transf\_3; 1.  
 SQ SEQUENCE 221 AA; 24915 MW; CC7F77F601A28684 CRC64;

Query Match 51.2%; Score 42; DB 2; Length 221;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 PRNRGMTALLKVVSSCD 16  
 DB 118 YXNSNANALISVSBCD 133

## RESULT 9

Q933W2 PRELIMINARY; PRT; 221 AA.  
 AC Q933W2;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE CMP-Neu5Ac synthetase (CMP-Neu5Ac synthetase).  
 GN NEU5A1.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Campylobacteraceae; Campylobacter.  
 NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=81-176;  
 RA Guerry P., Szymanski C.M., Prendergast M.M., Hickey T.B., Ewing C.P.,  
 RA Patariani D.L., Moran A.P.;  
 RT "Phase Variation of Campylobacter jejuni 81-176 Lipooligosaccharide  
 affects Virulence.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43456, and ATCC 43449;  
 RA Gilbert M., Michniewicz J., Karwaski M.-F., Cunningham A.,  
 RA Makarchuk W.W.;  
 RT "The genetic basis for the variation in the lipo-oligosaccharide of  
 RT the mucosal pathogen, *Campylobacter jejuni*: biosynthesis of sialylated  
 RT ganglioside mimics in the core oligosaccharide."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF305571; AAL09372.1; -  
 DR EMBL; AF401529; AAL05994.1; -  
 DR EMBL; AF401529; AAL06008.1; -  
 DR InterPro: IPR003329; Cytidylyl\_trans.  
 DR Pfam; PF02348; CTP\_transf\_3; 1.  
 SQ SEQUENCE 221 AA; 25002 MW; 3358AB8A64493AE CRC64;  
 QY  
 Query Match 51.2%; Score 42; DB 2; Length 221;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Db 1 FRNRGMTALLKVSSED 16  
 118 YKSNANALISVSECD 133  
 RESULT 10  
 Q9K387 PRELIMINARY; PRT; 221 AA.  
 ID Q9K387;  
 AC Q9K387;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE CMP-sialic acid synthetase.  
 OS *Campylobacter jejuni*.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; *Campylobacterales*;  
 OC *Campylobacteraceae*; *Campylobacter*.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43446, and OH4384;  
 RX MEDLINE=20127862; PubMed=10660542;  
 RA Gilbert M., Britson J.-R., Karwaski M.-F., Michniewicz J.,  
 RA Cunningham A.-M., Wu Y., Young N.M., Makarchuk W.W.;  
 RT "Biosynthesis of ganglioside mimics in *Campylobacter jejuni* OH4384:  
 RT identification of the glycosyltransferase genes, enzymatic synthesis  
 RT of model compounds, and characterization of nanomole amounts by 600-  
 RT MHz 1H and 13C NMR analysis."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF167344; AAF31774.1; -  
 DR EMBL; AF167344; AAF31774.1; -  
 DR InterPro: IPR003329; Cytidylyl\_trans.  
 DR Pfam; PF02348; CTP\_transf\_3; 1.  
 SQ SEQUENCE 221 AA; 24991 MW; 25B3BEF7AB5000FA CRC64;  
 QY  
 Query Match 51.2%; Score 42; DB 2; Length 221;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Db 1 FRNRGMTALLKVSSED 16  
 118 YKSNANALISVSECD 133  
 RESULT 11  
 Q9F0M6 PRELIMINARY; PRT; 221 AA.  
 ID Q9F0M6;  
 AC Q9F0M6;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE CMP-sialic acid synthetase.  
 OS *Campylobacter jejuni*.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; *Campylobacterales*;  
 OC *Campylobacteraceae*; *Campylobacter*.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43432;  
 RA Gilbert M., Michniewicz J., Makarchuk W.W.;  
 RT "The LOS biosynthesis locus of *Campylobacter jejuni* O:4."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF215659; AAC43982.1; -  
 DR InterPro: IPR003329; Cytidylyl\_trans.  
 DR Pfam; PF02348; CTP\_transf\_3; 1.  
 SQ SEQUENCE 221 AA; 25015 MW; CA321B85C6314377 CRC64;  
 QY  
 Query Match 51.2%; Score 42; DB 2; Length 221;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Db 1 FRNRGMTALLKVSSED 16  
 118 YKSNANALISVSECD 133  
 RESULT 12  
 Q938X3 PRELIMINARY; PRT; 221 AA.  
 ID Q938X3;  
 AC Q938X3;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE CMP-Neu5Ac synthetase.  
 OS *NeutA*.  
 OS *Campylobacter jejuni*.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; *Campylobacterales*;  
 OC *Campylobacteraceae*; *Campylobacter*.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43460;  
 RA Gilbert M., Michniewicz J., Karwaski M.-F., Cunningham A.,  
 RA Makarchuk W.W.;  
 RT "The genetic basis for the variation in the lipo-oligosaccharide of  
 RT the mucosal pathogen, *Campylobacter jejuni*: Biosynthesis of sialylated  
 RT ganglioside mimics in the core oligosaccharide."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY044868; AAK96004.1; -  
 DR InterPro: IPR003329; Cytidylyl\_trans.  
 DR Pfam; PF02348; CTP\_transf\_3; 1.  
 SQ SEQUENCE 221 AA; 25014 MW; FC3AB85C6396371 CRC64;  
 QY  
 Query Match 51.2%; Score 42; DB 2; Length 221;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Db 1 FRNRGMTALLKVSSED 16  
 118 YKSNANALISVSECD 133  
 RESULT 13  
 Q99N23 PRELIMINARY; PRT; 324 AA.  
 ID Q99N23;  
 AC Q99N23;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Carbonic anhydrase XV (EC 4.2.1.1) (Carbonic anhydrase 15).  
 GN CAR15.  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Kidney;
RA Hewitt-Barnett D., Shimlin L.C.;
RT "Characterization and evolution of two new members of the alpha-
RL carbonic anhydrase gene family in mouse: Carls and Carls."
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Straube R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF231122; AAK16671.1;
DR EMBL; BC019975; AAK19975.1;
DR HSSP; O64444; 22NC.
DR MGD; MGI:1931324; Carls.
DR InterPro; IPR001148; Euk_Coanhd.
DR Pfam; PF00194; carl_ahydase; 1.
DR ProDom; PD000865; Euk_Coanhd; 1.
KM Lyase.
SQ SEQUENCE 324 AA; 35482 MW; D285DD086476372F CRC64;

Query Match 50.0%; Score 41; DB 11; Length 324;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 NRGMATLKYSSC 15
DB 87 MDGHTVLRVNSC 99

RESULT 14
ID O9KY14 PRELIMINARY; PRT; 381 AA.
AC O9KY14;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE Ribocitavin-specific deaminase.
GN RIBD OR SCO2688 OR SCC61A.09.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
the 8 kb Streptomyces coelicolor A3(2) chromosome."
RN M01. Microbiol. 21:77-96(1996).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,

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RA Warren T., Nietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2)."
RN Nature 417:141-147(2002).
DR EMBL; AL939113; CAB92254.1;
DR HSSP; Q60034; 1CZ3.
DR InterPro; IPR002125; dCMP_cyt_deam.
DR InterPro; IPR004794; Eubact_ribd.
DR InterPro; IPR002734; RibD_C.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR Pfam; PF01872; RibD_C; 1.
DR TIGRPFAM; TIGR00326; eubact_ribd; 1.
DR TIGRPFAM; TIGR00227; ribD_Cterm; 1.
DR PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
KM Complete proteome.
SQ SEQUENCE 381 AA; 39437 MW; 6D94B85AE5595E7 CRC64;

Query Match 50.0%; Score 41; DB 16; Length 381;
Best Local Similarity 46.7%; Pred. No. 30;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 NRGMATLKYSSC 16
DB 57 NRGHTAVVTEPCD 71

RESULT 15
ID O8FTK2 PRELIMINARY; PRT; 537 AA.
AC O8FTK2;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE Putative ABC transporter permease protein.
GN CE1564.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriinae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN SEQUENCE FROM N.A.
RC STRAIN=XS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens XS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005219; BAC18374.1;
KM Complete proteome.
SQ SEQUENCE 537 AA; 57162 MW; 1B1067CE463ADB2F CRC64;

Query Match 50.0%; Score 41; DB 16; Length 537;
Best Local Similarity 61.1%; Pred. No. 43;
Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 FRNRGMTA--LKYSSC 16
DB 136 FRGGRTAGGLSVASSD 153

Search completed: November 7, 2003, 07:34:40
Job time : 8.37637 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 ; Search time 14.0347 Seconds  
(without alignments)  
195.799 Million cell updates/sec

Title: US-09-661-992B-106

Perfect score: 82

Sequence: 1 FRNKGMTALKVSSCD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	82	100.0	1438	14	US-10-006-091-1
2	82	100.0	1438	14	US-10-047-257-1
3	82	100.0	1438	15	US-10-225-900-1
4	82	100.0	1471	14	US-10-095-718-2
5	82	100.0	2332	10	US-09-957-641-2
6	82	100.0	2332	12	US-10-131-510A-2
7	82	100.0	2332	15	US-10-187-319-2
8	82	100.0	2351	12	US-10-133-907-4
9	82	100.0	2351	15	US-10-132-829-4
10	82	100.0	2351	15	US-10-172-712-27
11	82	100.0	2351	15	US-10-095-718-4
12	82	100.0	2351	15	US-10-131-510A-6
13	82	100.0	2351	15	US-10-187-319-6
14	82	100.0	2351	15	US-10-131-510A-4
15	82	100.0	2351	15	US-10-187-319-4

16	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, Appl
17	70	85.4	1443	15	US-10-187-319-39	Sequence 39, Appl
18	70	85.4	2133	15	US-10-131-510A-37	Sequence 37, Appl
19	70	85.4	2133	15	US-10-187-319-37	Sequence 37, Appl
20	43	52.4	311	12	US-10-017-161-284	Sequence 284, Appl
21	43	52.4	311	15	US-10-023-597-52	Sequence 52, Appl
22	42	51.2	221	9	US-09-816-028A-37	Sequence 37, Appl
23	42	51.2	221	12	US-10-303-161-37	Sequence 37, Appl
24	42	51.2	221	12	US-10-303-118-37	Sequence 37, Appl
25	42	51.2	221	12	US-10-303-128-37	Sequence 37, Appl
26	42	51.2	221	12	US-10-303-134-37	Sequence 37, Appl
27	42	51.2	221	12	US-10-303-162-37	Sequence 37, Appl
28	40.5	49.4	1160	12	US-10-137-870-234	Sequence 234, App
29	40.5	49.4	1160	12	US-10-140-018-234	Sequence 234, App
30	40.5	49.4	1160	12	US-10-140-021-234	Sequence 234, App
31	40.5	49.4	1160	12	US-10-140-274-234	Sequence 234, App
32	40.5	49.4	1160	12	US-10-140-471-234	Sequence 234, App
33	40.5	49.4	1160	12	US-10-140-807-234	Sequence 234, App
34	40.5	49.4	1160	12	US-10-140-922-234	Sequence 234, App
35	40.5	49.4	1160	12	US-10-140-924-234	Sequence 234, App
36	40.5	49.4	1160	12	US-10-140-926-234	Sequence 234, App
37	40.5	49.4	1160	12	US-10-141-698-234	Sequence 234, App
38	40.5	49.4	1160	12	US-10-141-702-234	Sequence 234, App
39	40.5	49.4	1160	12	US-10-141-704-234	Sequence 234, App
40	40.5	49.4	1160	12	US-10-142-421-234	Sequence 234, App
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44	40.5	49.4	1160	12	US-10-144-994-234	Sequence 234, App
45	40.5	49.4	1160	12	US-10-145-628-234	Sequence 234, App

#### ALIGNMENTS

RESULT 1  
US-10-006-091-1  
Sequence 1, Application US/10006091  
Publication No. US20020102730A1  
GENERAL INFORMATION:  
APPLICANT: Cho, Myung-Sam  
APPLICANT: Chan, Sham-Yuen  
APPLICANT: Kelsey, William  
APPLICANT: Yee, Helena  
TITLE OF INVENTION: Expression System for Factor VIII  
FILE REFERENCE: MSB-7255.1  
CURRENT APPLICATION NUMBER: US/10/006,091  
CURRENT FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1438  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Derived from  
US-10-006-091-1

Query Match 100.0%; Score 82; DB 14; Length 1438;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNKGMTALKVSSCD 16  
DB 637 FRNKGMTALKVSSCD 712

RESULT 2  
US-10-047-257-1  
Sequence 1, Application US/10047257  
Publication No. US20020115152A1  
GENERAL INFORMATION:

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/ APPLICANT: Cho, Myung-Sam
/ APPLICANT: Chan, Shan-Yuen
/ APPLICANT: Kelsey, William
/ APPLICANT: Yee, Helena
/ TITLE OF INVENTION: Expression System for Factor VIII
/ FILE REFERENCE: MSB-7255.2
/ CURRENT APPLICATION NUMBER: US/10/047,257
/ PRIORITY FILING DATE: 2002-01-15
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1438
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-047-257-1
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Query Match 100.0%; Score 82; DB 14; Length 1438;

Best Local Similarity 100.0%; Pred. No. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALLKVSSCD 16

DB 697 FRNRGNTALLKVSSCD 712

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RESULT 3
US-10-225-900-1
/ Sequence 1, Application US/10225900
/ Publication No. US2003007752A1
/ GENERAL INFORMATION:
/ APPLICANT: Cho, Myung-Sam
/ APPLICANT: Chan, Shan-Yuen
/ APPLICANT: Kelsey, William
/ APPLICANT: Yee, Helena
/ TITLE OF INVENTION: Expression System for Factor VIII
/ FILE REFERENCE: MSB-7255
/ CURRENT APPLICATION NUMBER: US/10/225,900
/ PRIORITY FILING DATE: 2002-08-22
/ PRIOR APPLICATION NUMBER: US/09/209,916
/ PRIOR FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1438
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-225-900-1
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Query Match 100.0%; Score 82; DB 15; Length 1438;

Best Local Similarity 100.0%; Pred. No. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALLKVSSCD 16

DB 697 FRNRGNTALLKVSSCD 712

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RESULT 4
US-10-095-718-2
/ Sequence 2, Application US/10095718
/ Publication No. US2002013156A1
/ GENERAL INFORMATION:
/ APPLICANT: Walsh, Christopher
/ APPLICANT: Chao, Hengjun
/ APPLICANT: Burshtein, Haim
/ APPLICANT: Lynch, Carmel
/ APPLICANT: Stepan, Tony
```

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/ APPLICANT: Munson, Keith
/ TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
/ TITLE OF INVENTION: Methods of Using the Same
/ FILE REFERENCE: 35052/204375
/ CURRENT APPLICATION NUMBER: US/10/095,718
/ PRIORITY FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 09/589,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/158,780
/ PRIOR FILING DATE: 1999-10-12
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1471
/ TYPE: PRT
/ ORGANISM: Homo sapiens B-domain deleted factor VIII
/ FEATURE:
/ OTHER INFORMATION: Homo sapiens BDD FVIII
US-10-095-718-2
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Query Match 100.0%; Score 82; DB 14; Length 1471;

Best Local Similarity 100.0%; Pred. No. 4.9e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALLKVSSCD 16

DB 716 FRNRGNTALLKVSSCD 731

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RESULT 5
US-09-957-641-2
/ Sequence 2, Application US/09957641
/ Publication No. US20020182670A1
/ GENERAL INFORMATION:
/ APPLICANT: Emory University
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: 75-00
/ CURRENT APPLICATION NUMBER: US/09/957,641
/ PRIORITY FILING DATE: 2001-09-16
/ PRIOR APPLICATION NUMBER: US 60/234047
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: US 60/236460
/ PRIOR FILING DATE: 2000-09-29
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 2332
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-957-641-2
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Query Match 100.0%; Score 82; DB 10; Length 2332;

Best Local Similarity 100.0%; Pred. No. 8.2e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALLKVSSCD 16

DB 697 FRNRGNTALLKVSSCD 712

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RESULT 6
US-10-131-510A-2
/ Sequence 2, Application US/10131510A
/ Publication No. US2003016536A1
/ GENERAL INFORMATION:
/ APPLICANT: Lollar, John S
/ TITLE OF INVENTION: Modified Factor VIII
/ FILE REFERENCE: 75-953
/ CURRENT APPLICATION NUMBER: US/10/131,510A
/ PRIORITY FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: U.S. 09/315,179
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: U.S. 09/037,601
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PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: U.S. 08/670,707  
PRIOR FILING DATE: 1996-06-26  
PRIOR APPLICATION NUMBER: PCT/US97/11155  
PRIOR FILING DATE: 1997-06-26  
PRIOR APPLICATION NUMBER: PCT/US94/13200  
PRIOR FILING DATE: 1994-11-15  
PRIOR APPLICATION NUMBER: U.S. 08/212,133  
PRIOR FILING DATE: 1994-03-11  
PRIOR APPLICATION NUMBER: U.S. 07/864,004  
PRIOR FILING DATE: 1992-04-07  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 2332  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-510A-2

Query Match 100.0%; Score 82; DB 12; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALXVSSCD 16  
DB 697 FRNRGNTALXVSSCD 712

RESULT 7  
US-10-187-319-2  
Sequence 2, Application US/10187319  
Publication No. US20030068785A1  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S.  
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winnet and Sullivan, P.C.  
STREET: 5370 Manhattan Circle Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/187,319  
FILING DATE: 27-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/523,656  
FILING DATE: 2000-03-10  
APPLICATION NUMBER: US 09/037,601  
FILING DATE: 1998-03-10  
APPLICATION NUMBER: WO PCT/US97/11155  
FILING DATE: 1997-06-26  
APPLICATION NUMBER: US 08/670,707  
FILING DATE: 1996-06-26  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenlee, Lorraine L.  
REGISTRATION NUMBER: 27,894  
REFERENCE/DOCKET NUMBER: 75-95K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: <Unknown>  
MOLECULE TYPE: protein  
HYDROTHERMAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Liver  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-187-319-2

Query Match 100.0%; Score 82; DB 15; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALXVSSCD 16  
DB 697 FRNRGNTALXVSSCD 712

RESULT 8  
US-10-133-907-4  
Sequence 4, Application US/10133907  
Publication No. US20030195223A1  
GENERAL INFORMATION:  
APPLICANT: Chien, Kenneth R.  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor V  
TITLE OF INVENTION: with vesicle vector  
FILE REFERENCE: 6627-P41170  
CURRENT APPLICATION NUMBER: US/10/133,907  
CURRENT FILING DATE: 2002-04-25  
PRIOR APPLICATION NUMBER: 60/286,314  
PRIOR FILING DATE: 2001-04-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 2351  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-133-907-4

Query Match 100.0%; Score 82; DB 12; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGNTALXVSSCD 16  
DB 716 FRNRGNTALXVSSCD 731

RESULT 9  
US-10-132-829-4  
Sequence 4, Application US/10132829  
Publication No. US20030044982A1  
GENERAL INFORMATION:  
APPLICANT: Chien, Kenneth R.  
TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor V  
TITLE OF INVENTION: with vesicle vector  
FILE REFERENCE: 6627-P41170  
CURRENT APPLICATION NUMBER: US/10/132,829  
CURRENT FILING DATE: 2002-04-25  
PRIOR APPLICATION NUMBER: 60/286,314  
PRIOR FILING DATE: 2001-04-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 2351  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-132-829-4

Query Match 100.0%; Score 82; DB 15; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGTMALTKVSSCD 16  
DB 716 FRNRGTMALTKVSSCD 731

RESULT 10  
US-10-172-712-27  
; Sequence 27, Application US/10172712  
; Publication No. US20030125232A1  
; GENERAL INFORMATION:  
; APPLICANT: GRIFFIN, JOHN H.  
; APPLICANT: GALE, ANDREW J.  
; APPLICANT: GETZOFF, ELIZABETH D.  
; APPLICANT: PELIBOUER, JEAN-LUC  
; TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS  
; FILE REFERENCE: 4198-4001US1  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/10/172,712  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; TYPE: PRT  
; LENGTH: 2351  
; ORGANISM: Homo sapiens  
US-10-172-712-27

Query Match 100.0%; Score 82; DB 15; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGTMALTKVSSCD 16  
DB 716 FRNRGTMALTKVSSCD 731

RESULT 11  
US-10-095-718-4  
; Sequence 4, Application US/10095718  
; Publication No. US20020131956A1  
; GENERAL INFORMATION:  
; APPLICANT: Walsh, Christopher  
; APPLICANT: Chao, Hengjun  
; APPLICANT: Birstein, Haim  
; APPLICANT: Lynch, Carmel  
; APPLICANT: Stepan, Tony  
; APPLICANT: Munson, Keith  
; TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 35052/204375  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: US/10/095,718  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/158,780  
; PRIOR FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; TYPE: PRT  
; LENGTH: 1431  
; ORGANISM: canine B-domain deleted factor VIII  
US-10-095-718-4

Query Match 93.9%; Score 77; DB 14; Length 1431;  
Best Local Similarity 93.8%; Pred. No. 3.9e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRNRGTMALTKVSSCD 16  
DB 710 FRNRGTMALTKVSSCD 725

RESULT 12  
US-10-131-510A-6  
; Sequence 6, Application US/10131510A  
; Publication No. US20030166536A1  
; GENERAL INFORMATION:  
; APPLICANT: Lollar, John S  
; TITLE OF INVENTION: Modified Factor VIII  
; FILE REFERENCE: 75-957  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US/10/131,510A  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: U.S. 09/037,601  
; PRIOR FILING DATE: 1994-11-15  
; PRIOR APPLICATION NUMBER: U.S. 08/670,707  
; PRIOR FILING DATE: 1996-06-26  
; PRIOR APPLICATION NUMBER: PCT/US97/11155  
; PRIOR FILING DATE: 1997-06-26  
; PRIOR APPLICATION NUMBER: PCT/US94/13200  
; PRIOR FILING DATE: 1994-11-15  
; PRIOR APPLICATION NUMBER: U.S. 08/212,133  
; PRIOR FILING DATE: 1994-03-11  
; PRIOR APPLICATION NUMBER: U.S. 07/864,004  
; PRIOR FILING DATE: 1992-04-07  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 2319  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-131-510A-6

Query Match 92.7%; Score 76; DB 12; Length 2319;  
Best Local Similarity 93.8%; Pred. No. 0.0001;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FRNRGTMALTKVSSCD 16  
DB 716 FRNRGTMALTKVSSCD 731

RESULT 13  
US-10-187-319-6  
; GENERAL INFORMATION:  
; APPLICANT: Lollar, John S.  
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT FILING DATE: 2002-03-10  
; APPLICATION NUMBER: US 09/523,656  
; FILING DATE: 2000-03-10  
; APPLICATION NUMBER: US 09/037,601  
; FILING DATE: 1998-03-10  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/523,656  
; FILING DATE: 2000-03-10  
; APPLICATION NUMBER: US 09/037,601  
; FILING DATE: 1998-03-10

APPLICATION NUMBER: WO PCT/US97/11155  
FILING DATE: 1997-06-26  
APPLICATION NUMBER: US 08/670,707  
FILING DATE: 1996-06-26  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenlee, Lorance L.  
REGISTRATION NUMBER: 27,894  
REFERENCE/DOCKET NUMBER: 75-95K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
TITLE: Sequence of the Murine Factor VIII CDNA  
JOURNAL: Genomics  
VOLUME: 16  
PAGES: 374-379  
DATE: 1993  
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 2319  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-187-319-6

Query Match 92.7%; Score 76; DB 15; Length 2319;  
Best Local Similarity 93.8%; Pred. No. 0.0001;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNRGWTALKVSSCD 16  
Db 716 FRRGWTALKVSSCD 731

RESULT 14  
US-10-131-510A-4  
Sequence 4, Application US/10131510A  
Publication No. US2003016536A1  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S  
TITLE OF INVENTION: Modified Factor VIII  
FILE REFERENCE: 75-95J  
CURRENT APPLICATION NUMBER: US/10/131,510A  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: U.S. 09/315,179  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: U.S. 09/037,601  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: U.S. 08/670,707  
PRIOR FILING DATE: 1996-06-26  
PRIOR APPLICATION NUMBER: PCT/US97/11155  
PRIOR FILING DATE: 1997-06-26  
PRIOR APPLICATION NUMBER: PCT/US94/13200  
PRIOR FILING DATE: 1994-11-15  
PRIOR APPLICATION NUMBER: U.S. 08/212,133  
PRIOR FILING DATE: 1994-03-11  
PRIOR APPLICATION NUMBER: U.S. 07/864,004  
PRIOR FILING DATE: 1992-04-07  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 368  
TYPE: PRT  
ORGANISM: Sus scrofa  
US-10-131-510A-4

Query Match 85.4%; Score 70; DB 12; Length 368;  
Best Local Similarity 93.3%; Pred. No. 0.00016;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RNRGWTALKVSSCD 16  
Db 326 RNRGWTALKVSSCD 340

RESULT 15  
US-10-187-319-4  
Sequence 4, Application US/10187319

Publication No. US20030068785A1  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S.  
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Lorance L.  
STREET: 5370 Manhattan Circle Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/187,319  
FILING DATE: 27-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/523,656  
FILING DATE: 2000-03-10  
APPLICATION NUMBER: US 09/037,601  
FILING DATE: 1998-03-10  
APPLICATION NUMBER: WO PCT/US97/11155  
FILING DATE: 1997-06-26  
APPLICATION NUMBER: US 08/670,707  
FILING DATE: 1996-06-26

ATTORNEY/AGENT INFORMATION:  
NAME: Greenlee, Lorance L.  
REGISTRATION NUMBER: 27,894  
REFERENCE/DOCKET NUMBER: 75-95K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 368 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
AMTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Porcine  
TISSUE TYPE: spleen  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..368  
OTHER INFORMATION: /note= "Predicted amino acid  
sequence of porcine factor VIII A2 domain, defined as residues  
homologous to human factor VIII, amino acids 373-740. Residues  
1-4 are from known porcine amino acid sequence."  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-187-319-4

Query Match 85.4%; Score 70; DB 15; Length 368;  
Best Local Similarity 93.3%; Pred. No. 0.00016;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RNRGWTALKVSSCD 16  
Db 326 RNRGWTALKVSSCD 340

Search completed: November 7, 2003, 08:16:56  
Job time: 15.0347 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 (Search time 2.3498 Seconds  
(without alignments)  
288.098 Million cell updates/sec

Title: US-09-661-992B-106  
Perfect score: 82  
Sequence: 1 FRNKGMTALKVSSCD 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5E\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfl1eal.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	1438	4 US-09-209-916-1	Sequence 1, Appl 1
2	82	100.0	1471	1 US-08-683-839B-3	Sequence 3, Appl 1
3	82	100.0	2332	1 US-07-864-004B-4	Sequence 4, Appl 1
4	82	100.0	2332	1 US-08-251-937A-2	Sequence 2, Appl 1
5	82	100.0	2332	1 US-08-212-133A-2	Sequence 2, Appl 1
6	82	100.0	2332	1 US-08-276-594A-2	Sequence 2, Appl 1
7	82	100.0	2332	1 US-08-474-503-2	Sequence 2, Appl 1
8	82	100.0	2332	2 US-08-670-707A-2	Sequence 2, Appl 1
9	82	100.0	2332	2 US-09-037-601-2	Sequence 2, Appl 1
10	82	100.0	2332	4 US-09-315-179-2	Sequence 2, Appl 1
11	82	100.0	2332	4 US-09-523-656-2	Sequence 2, Appl 1
12	82	100.0	2332	5 PCT-US93-03275-4	Sequence 4, Appl 1
13	82	100.0	2332	5 PCT-US94-13200-2	Sequence 2, Appl 1
14	82	100.0	2351	1 US-08-121-202-2	Sequence 2, Appl 1
15	82	100.0	2351	1 US-08-366-851A-2	Sequence 2, Appl 1
16	82	100.0	2351	6 5171844-2	Sequence 2, Appl 1
17	82	100.0	2351	6 5171844-2	Sequence 2, Appl 1
18	77	93.9	2343	3 US-09-324-867-2	Sequence 2, Appl 1
19	76	92.7	1661	2 US-08-882-083-2	Sequence 2, Appl 1
20	76	92.7	1661	2 US-08-558-107-2	Sequence 2, Appl 1
21	76	92.7	21	2 US-09-243-539-2	Sequence 2, Appl 1
22	76	92.7	2304	3 US-08-324-867-4	Sequence 2, Appl 1
23	76	92.7	2319	1 US-08-212-133A-8	Sequence 8, Appl 1
24	76	92.7	2319	1 US-08-474-503-6	Sequence 6, Appl 1
25	76	92.7	2319	2 US-08-670-707A-6	Sequence 6, Appl 1
26	76	92.7	2319	3 US-09-037-601-6	Sequence 6, Appl 1
27	76	92.7	2319	4 US-09-315-179-6	Sequence 6, Appl 1

28	76	92.7	2319	4 US-09-523-656-28	Sequence 28, Appl 1
29	76	92.7	2319	5 PCT-US94-13200-6	Sequence 6, Appl 1
30	70	85.4	367	1 US-07-864-004B-2	Sequence 2, Appl 1
31	70	85.4	367	1 US-08-251-937A-2	Sequence 2, Appl 1
32	70	85.4	367	5 PCT-US93-03275-2	Sequence 2, Appl 1
33	70	85.4	368	1 US-08-212-133A-6	Sequence 4, Appl 1
34	70	85.4	368	1 US-08-474-503-4	Sequence 4, Appl 1
35	70	85.4	368	2 US-08-670-707A-4	Sequence 4, Appl 1
36	70	85.4	368	3 US-09-037-601-4	Sequence 4, Appl 1
37	70	85.4	368	4 US-09-315-179-4	Sequence 4, Appl 1
38	70	85.4	368	4 US-09-523-656-4	Sequence 4, Appl 1
39	70	85.4	368	5 PCT-US94-13200-4	Sequence 4, Appl 1
40	70	85.4	541	1 US-08-121-202-4	Sequence 4, Appl 1
41	70	85.4	868	1 US-07-864-004B-6	Sequence 6, Appl 1
42	70	85.4	868	1 US-08-251-937A-6	Sequence 6, Appl 1
43	70	85.4	868	1 US-08-212-133A-3	Sequence 3, Appl 1
44	70	85.4	1090	5 PCT-US93-03275-6	Sequence 6, Appl 1
45	70	85.4	1443	2 US-08-670-707A-39	Sequence 39, Appl 1

## ALIGNMENTS

RESULT 1  
US-09-209-916-1  
Sequence 1, Application US/09209916  
Patent No. 6358703  
GENERAL INFORMATION:  
APPLICANT: Cho, Myung-Sam  
APPLICANT: Chan, Shun-Yuen  
APPLICANT: Kelsey, William  
APPLICANT: Yee, Helena  
TITLE OF INVENTION: Expression System for Factor VIII  
FILE REFERENCE: MSB-7255  
CURRENT APPLICATION NUMBER: US/09/209,916  
CURRENT FILING DATE: 1998-12-10  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1438  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Derived from  
US-09-209-916-1

Query Match 100.0%; Score 82; DB 4; Length 1438;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNKGMTALKVSSCD 16  
DB 697 FRNKGMTALKVSSCD 712

RESULT 2  
US-08-683-839B-3  
Sequence 3, Application US/086838398  
Patent No. 5744326  
GENERAL INFORMATION:  
APPLICANT: Ili, Charles . R. et al.  
TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional  
TITLE OF INVENTION: Regulatory Sequences To Increase Expression of  
TITLE OF INVENTION: Intronsless Genes Containing Near-Consensus Splice Sites  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/683,839B  
FILING DATE: 11-MARCH-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Remillard, Jane E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: TTI-138  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1471 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-683-839B-3

Query Match 100.0%; Score 82; DB 1; Length 1471;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALLKVS SCD 16  
Db 716 FRNRGWTALLKVS SCD 731

RESULT 3  
US-07-864-004B-4  
Sequence 4, Application US/07864004B  
Patent No. 5364771  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S.  
APPLICANT: Runge, Marschall S.  
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/864,004B  
FILING DATE: 07 APRIL 1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: EMU106  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Liver cDNA sequence  
US-07-864-004B-4

Query Match 100.0%; Score 82; DB 1; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALLKVS SCD 16  
Db 697 FRNRGWTALLKVS SCD 712

RESULT 4  
US-08-251-937A-4  
Sequence 4, Application US/08251937A  
Patent No. 5583209  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S.  
APPLICANT: Runge, Marschall S.  
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/251,937A  
FILING DATE: 31-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/864,004  
FILING DATE: 07-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pratt, John S.  
REGISTRATION NUMBER: 29,476  
REFERENCE/DOCKET NUMBER: EMU106DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6367  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Liver cDNA sequence  
US-08-251-937A-4

Query Match 100.0%; Score 82; DB 1; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRMGTALLKVVSSCD 16  
|||||  
Db 697 FRNRMGTALLKVVSSCD 712

## RESULT 5

US-08-212-133A-2  
/ Sequence 2, Application US/08212133A  
/ Patent No. 5663060  
/ GENERAL INFORMATION:  
/ APPLICANT: Lollar, John S.  
/ APPLICANT: Runge, Werschall S.  
/ TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
/ NUMBER OF SEQUENCES: 12  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Kilpatrick & Cody  
/ STREET: 100 Peachtree Street  
/ CITY: Atlanta  
/ STATE: Georgia  
/ COUNTRY: US  
/ ZIP: 30303  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/212,133A  
/ FILING DATE: March 11, 1994  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/864,004  
/ FILING DATE: 07-APR-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Pabst, Patricia L.  
/ REGISTRATION NUMBER: 31,284  
/ REFERENCE/DOCKET NUMBER: EMU/76677  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 404-572-6508  
/ TELEFAX: 404-572-6555  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 2332 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ HYPOTHEICAL: YES  
/ ANTI-SENSE: NO  
/ FRAGMENT TYPE: N-terminal  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapien  
/ TISSUE TYPE: Liver cDNA sequence  
US-08-212-133A-2

Query Match 100.0%; Score 82; DB 1; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRNRMGTALLKVVSSCD 16  
|||||  
Db 697 FRNRMGTALLKVVSSCD 712

## RESULT 6

US-08-276-594A-2  
/ Sequence 2, Application US/08276594A  
/ Patent No. 5693499  
/ GENERAL INFORMATION:  
/ APPLICANT: YONEMURA, Hiroshi  
/ APPLICANT: TAJIMA, Yoshitaka  
/ APPLICANT: SUGAWARA, Keishin  
/ APPLICANT: MASUDA, Kenichi

TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION  
/ TITLE OF INVENTION: FACTOR VIII PROTEIN COMPLEX  
/ NUMBER OF SEQUENCES: 11  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Foley & Lardner  
/ STREET: 3000 K Street, N.W., Suite 500  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20007-5109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/276,594A  
/ FILING DATE: 18-JUL-1994  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/950,191  
/ FILING DATE: 24-SEP-1992  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: JP 243262/1991  
/ FILING DATE: 24-SEP-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: WEGNER, Harold C.  
/ REGISTRATION NUMBER: 25,258  
/ REFERENCE/DOCKET NUMBER: 74129/195/AOPA  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202) 672-5300  
/ TELEFAX: (202) 672-5399  
/ TELEX: 904136  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 2332 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-276-594A-2

Query Match 100.0%; Score 82; DB 1; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRNRMGTALLKVVSSCD 16  
|||||  
Db 697 FRNRMGTALLKVVSSCD 712

## RESULT 7

US-08-474-503-2  
/ Sequence 2, Application US/08474503  
/ Patent No. 5744446  
/ GENERAL INFORMATION:  
/ APPLICANT: Emory University  
/ TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
/ NUMBER OF SEQUENCES: 12  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Kilpatrick & Cody  
/ STREET: 1100 Peachtree Street, Suite 2800  
/ CITY: Atlanta  
/ STATE: Georgia  
/ COUNTRY: US  
/ ZIP: 30309  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/474,503  
/ FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pratt, John S.  
REGISTRATION NUMBER: 29,476  
REFERENCE/DOCKET NUMBER: EMU106CIP(3)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6500  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Liver cDNA sequence  
US-08-474-503-2

Query Match 100.0%; Score 82; DB 1; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNRGMTALKVSSCD 16  
DB 697 FNNRGMTALKVSSCD 712

RESULT 8  
US-08-670-707A-2  
Sequence 2, Application US/08670707A  
Patent No. 5859204  
GENERAL INFORMATION:  
APPLICANT: Iollar, John S.  
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/670,707A  
FILING DATE: 26-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US94/13200  
FILING DATE: 15-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,133  
FILING DATE: 11-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/864,004  
FILING DATE: 07-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenlee, Lorance L.  
REGISTRATION NUMBER: 27,894  
REFERENCE/DOCKET NUMBER: 75-95F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Liver  
US-08-670-707A-2

Query Match 100.0%; Score 82; DB 2; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNRGMTALKVSSCD 16  
DB 697 FNNRGMTALKVSSCD 712

RESULT 9  
US-09-037-601-2  
Sequence 2, Application US/09037601  
Patent No. 6180371  
GENERAL INFORMATION:  
APPLICANT: Iollar, John S.  
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,601  
FILING DATE: 26-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US94/13200  
FILING DATE: 15-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,133  
FILING DATE: 11-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/864,004  
FILING DATE: 07-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Feider, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 75-95F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Liver  
US-09-037-601-2

Query Match 100.0%; Score 82; DB 3; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALIKVSSCD 16  
DB 697 FRNRGWTALIKVSSCD 712

RESULT 10  
US-09-315-179-2  
Sequence 2, Application US/09315179  
Patent No. 6376463  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S  
TITLE OF INVENTION: Modified Factor VIII  
FILE REFERENCE: 75-954  
CURRENT APPLICATION NUMBER: US/09/315,179  
CURRENT FILING DATE: 1999-05-20  
EARLIER APPLICATION NUMBER: U.S. 09/037,601  
EARLIER FILING DATE: 1998-03-10  
EARLIER APPLICATION NUMBER: U.S. 08/670,707  
EARLIER FILING DATE: 1996-06-26  
EARLIER APPLICATION NUMBER: PCT/US97/11155  
EARLIER FILING DATE: 1997-06-26  
EARLIER APPLICATION NUMBER: PCT/US94/13200  
EARLIER FILING DATE: 1994-11-15  
EARLIER APPLICATION NUMBER: U.S. 08/212,133  
EARLIER FILING DATE: 1994-03-11  
EARLIER APPLICATION NUMBER: U.S. 07/864,004  
EARLIER FILING DATE: 1992-04-07  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 2332  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-315-179-2

Query Match 100.0%; Score 82; DB 4; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALIKVSSCD 16  
DB 697 FRNRGWTALIKVSSCD 712

RESULT 11  
US-09-523-656-2  
Sequence 2, Application US/09523656  
Patent No. 6458563  
GENERAL INFORMATION:  
APPLICANT: Lollar S., John  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: 75-951  
CURRENT APPLICATION NUMBER: US/09/523,656  
CURRENT FILING DATE: 2000-03-10  
EARLIER APPLICATION NUMBER: 09/037,601  
EARLIER FILING DATE: 1998-03-10  
EARLIER APPLICATION NUMBER: 08/670,707  
EARLIER FILING DATE: 1996-06-26  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 2332  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-523-656-2

Query Match 100.0%; Score 82; DB 4; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALIKVSSCD 16  
DB 697 FRNRGWTALIKVSSCD 712

RESULT 12  
PCT-US93-03275-4  
Sequence 4, Application PC/TUS9303275  
GENERAL INFORMATION:  
APPLICANT: Lollar, John S.  
APPLICANT: Runge, Marshall S.  
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03275  
FILING DATE: 19930407  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/864004  
FILING DATE: 07-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: EMU 106PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Liver CDNA sequence  
PCT-US93-03275-4

Query Match 100.0%; Score 82; DB 5; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGWTALIKVSSCD 16  
DB 697 FRNRGWTALIKVSSCD 712

RESULT 13  
PCT-US94-13200-2  
Sequence 2, Application PC/TUS9413200  
GENERAL INFORMATION:

APPLICANT: Emory University  
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Suite 2800  
City: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13200  
FILING DATE: 15-NOV-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: EMU106CIP(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Liver cdna sequence  
PCT-US94-13200-2

Query Match 100.0%; Score 82; DB 5; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGTALKVSSCD 16  
|||||  
Db 697 FRNRGTALKVSSCD 712

RESULT 14  
US-08-121-202-2  
Sequence 2, Application US/08121202  
Patent No. 5563045  
GENERAL INFORMATION:  
APPLICANT: Pittman, Debora  
APPLICANT: Rehenculla, Alimawaz  
APPLICANT: Mozney, John M.  
APPLICANT: Kaufman, Randal J.  
TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
City: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,202  
FILING DATE: 14-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinert, M. C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5195A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1210 X6574  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-202-2

Query Match 100.0%; Score 82; DB 1; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRNRGTALKVSSCD 16  
|||||  
Db 716 FRNRGTALKVSSCD 731

RESULT 15  
US-08-366-851A-2  
Sequence 2, Application US/08366851A  
Patent No. 5681746  
GENERAL INFORMATION:  
APPLICANT: Bodner, Mordechai  
APPLICANT: De Polo, Nicolas J.  
APPLICANT: Hsu, David Chi-Tang  
APPLICANT: Chang, Steven  
TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Viagene, Inc.  
STREET: 11055 Roselle Street  
City: San Diego  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,851A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 930049.438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 452-1288  
TELEFAX: (619) 452-2616  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-366-851A-2

Query Match 100.0%; Score 82; DB 1; Length 2351;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNRGWTALLKVSSCD 16  
|||  
Db 716 FNRGWTALLKVSSCD 731

Search completed: November 7, 2003, 07:30:12  
Job time : 3.3498 secs